

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

Annual Report 2022

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Contents

1	WOAH	I/FAO FMD Reference Laboratory Network	3			
	1.1	Principle Goals	3			
	1.2	Reporting Period	4			
	1.3	Collated input from	4			
2	Globa	l distribution and impact of foot-and-mouth disease	6			
	2.1	Introduction	6			
	2.2	Overview of the activities of the OIE/FAO FMD Laboratory Network during 2022	. 11			
	2.3	Regional distribution of different FMD viral lineages	. 13			
	2.4	Vaccine matching and recommendations	. 17			
3	Overv	iew of Network surveillance activities in each of the regional endemic pools	18			
	3.1	Pool 1 Regional synopsis	. 18			
	3.2	Pool 2 Regional synopsis	. 19			
	3.3	Pool 3 Regional synopsis	. 21			
	3.4	Pool 4 Regional synopsis	. 23			
	3.5	Pool 5 Regional synopsis	. 25			
	3.6	Pool 6 Regional synopsis	. 26			
	3.7	Pool 7 Regional synopsis	. 28			
4	Impro	ving the quality of laboratory tests from FMD reference laboratories	29			
	4.1	Proficiency testing schemes (PTS) organised by the Network Partners	. 29			
	4.2	Supply of reagents	. 31			
	4.3	Training courses organised by Network partners	. 36			
	4.4	Collaborative projects	. 39			
	4.5	In vivo potency studies undertaken during 2021	. 45			
A re	ppendix 1 gions tes	Details of clinical samples from field cases from countries in FMDV endemic ted during 2021	48			
A	ppendix 2	Vaccine matching studies undertaken by Network partners during 2021	50			
Appendix 3 Nucleotide sequence analysis57						
A	Appendix 4 Selected phylogenetic trees for 202259					
A	ppendix 5	The 17th Annual Meeting of the WOAH/FAO FMD Reference Laboratory Network	71			



1 WOAH/FAO FMD Reference Laboratory Network

1.1 Principle Goals

The Network of WOAH/FAO FMD Reference Laboratories has been established with two principal goals:

1) To understand global virus distribution patterns and use these data to inform vaccine recommendations

and

2) To harmonise and improve the quality of laboratory testing carried out by international and national reference laboratories.

These activities require sharing and joint evaluation of surveillance information from laboratory diagnosis, serotyping, genetic characterisation and vaccine matching tests and harmonisation of standards for diagnostic procedures.

This report is divided into two parts providing an update on progress towards each of these goals.



1.2 Reporting Period

1st January 2022 - 31st December 2022

1.3 Collated input from



Figure 1-1: Participating laboratories









2 Global distribution and impact of foot-and-mouth disease

Foot-and-mouth disease (FMD) is a highly contagious viral disease that infects a wide variety of domestic and wild cloven-hooved hosts. Its presence impacts upon rural livelihoods and restricts trade opportunities for countries where the disease is endemic and poses a constant threat to those countries that are free of the disease. In endemic countries, the economic costs associated with FMD are estimated to be US\$6.5–21 billion annually, with outbreaks in FMD-free countries and zones potentially causing economic losses of >\$1.5 billion. FMD virus lineages are not randomly dispersed throughout the world but are associated with particular ecological niches. The distribution of these FMD virus lineages is affected by cyclical upsurges in the prevalence of particular strains that may be associated with the evolution of FMD virus sto escape protective immunity in susceptible livestock populations and/or opportunities presented by movements of animals and their products. These features can give rise to pandemic events where FMDV lineages spread widely to affect new regions.

Global surveillance for FMD is necessary to identify the current hazards and to predict heightened risk so that appropriate diagnostic tools and vaccines are available for detection and control. This requires sustained effort directed towards the monitoring of FMD outbreaks and ideally also of FMDV circulation and persistence, along with collection and characterisation of FMD viruses and integration of findings with associated epidemiological intelligence. Such an extensive effort requires a coordinated approach encompassing national and international disease laboratories of the **WOAH/FAO FMD Laboratory Network** (www.foot-and-mouth.org) along with partnering laboratories, commercial vaccine and diagnostic providers. The worldwide distribution of the different serotypes and variants of FMD virus (as compiled in 2022) and the associated activities of the Network laboratories are presented in this report.

2.1 Introduction

Global surveillance undertaken by the WOAH/FAO FMD Laboratory Network aims to monitor the distribution of FMD viruses to predict risk for endemic and FMD-free countries. FMDV is unevenly distributed throughout the world reflecting factors such as livestock density and species mix, patterns of husbandry, animal movement and trade, wildlife reservoirs and incentives and capacities for disease control. The virus exists as seven serotypes and multiple subtypes where cross-immunity is absent or incomplete. The situation is dynamic and complex and affected by viral evolution, waxing and waning of host immunity and changing ecosystems and trading patterns. Despite the opportunities for spread of FMDV into new regions, viruses tend to recur in the same parts of the world, presumably reflecting some degree of either ecological isolation or adaptation. On this basis, the global pool of FMD viruses can be subdivided into seven 'regional pools' in which genetically and antigenically distinctive virus strains tend to occur within a defined region.



The seven 'Regional Pools' referred to throughout this report are shown below (Figure 2-1) and represent:

- Pool 1 Southeast Asia with spill over into Eastern Asia
- Pool 2 Southern Asia
- Pool 3 Western Asia with spill over into North Africa
- Pool 4 Eastern Africa with spill over into North Africa
- Pool 5 Western Africa
- Pool 6 Southern Africa
- Pool 7 South America



Figure 2-1: Distribution of the seven endemic pools of FMD showing conjectured status of FMD in countries during 2022. Periodically, viruses spread between pools and to free regions, and countries at the interfaces between pools (such as in North Africa and Central Asia) often experience FMD outbreaks from different regional sources. Note on Pools 4-6: In Africa there are currently three FMD virus pools loosely defined as covering East Africa (pool 4), West Africa (pool 5) and Southern Africa (pool 6). A map describing the official WOAH status for these countries can be found at: https://www.woah.org/en/what-we-do/animal-health-and-welfare/official-disease-status/

The clustering of FMD viruses into 7 virus pools, with 3 pools covering West Eurasia, South Asia and Southeast Asia, 3 pools covering East, West and Southern Africa and 1 pool covering South America, enables a targeted approach to be applied to the 'Progressive Global Control of FMD' initiative overseen by the WOAH and FAO and for which the Network laboratories will play a pivotal role.

Overview of the Global situation in 2022

Headline events (Figure2-2) in 2022 include:

 A new clade within the O/ME-SA/PanAsia-2^{ANT-10} sub-lineage has caused outbreaks in Eastern Mediterranean countries (Jordan, Palestine and Israel). These FMD viruses are most closely related to those found in Pakistan and UAE and this lineage appears



to have become more dominant than sub-lineage O/ME-SA/PanAsia-2^{QOM-15} that was previously found in this region.

- There continues to be increased dominance of O/ME-SA/Ind-2001e over other serotype O lineages. For example, in mainland southeast Asia there were previously four lineages of serotype O; however, since 2020/2021 only O/ME-SA/2001e has been detected. Indonesia, which has previously been free from FMD (since 1990) has reported the first FMD cases due to O/ME-SA/Ind-2001e. FMD cases due to O/ME-SA/Ind-2001e have also been detected in Kazakhstan (2022) and Russia (2021).
- For Pools 2 and 3, an emerging lineage called O/ME-SA/SA-2018 has been detected in India, Sri Lanka and UAE. There is an increased number of reports for this lineage; however, vaccine matching data from reference laboratories suggests that many existing serotype O vaccines are well matched to field viruses from this lineage.



Figure 2-2: Headline FMD events for 2022

- FMD outbreaks in the Maghreb in North Africa have been due to the O/EA-3 topotype and sequence data shared within the Network shows that these cases are due to a new introduction of the virus that is distinct to cases that occurred in 2018.
- For Southern Africa (Pool 6), the O/EA-2 topotype continues to cause more outbreaks and has now been reported in Zambezi, Namibia, Malawi and Mozambique. Together with cases in Zambia (2018-2021) this is the first detection of serotype O in southern Africa for ~20yrs. These findings are important because serotype O vaccines are not widely used in the southern Africa region.



• Published reports of FMD cases in Egypt have been associated with FMD viruses from the EURO-SA and A/EURO-SA lineages that are normally only found in South America. These unexpected outbreaks need to be monitored closely since there is potential for onward spread in North Africa and the Eastern Mediterranean.

Specific information regarding contemporary FMD outbreaks can be found on the World Animal Health Information System (WAHIS) located on the WOAH website (<u>https://wahis.woah.org/#/home</u>), as well as the EMPRES-i+ Global Animal Disease Information System (<u>https://empres-i.apps.fao.org/</u>) provided by FAO. Further supplementary data and updates are provided in the WRLFMD/EuFMD Quarterly Report for FMD (<u>https://www.wrlfmd.org/ref-lab-reports</u>).

During 2022, FMD outbreaks have continued to affect countries in the established endemic regions of the world. Particular attention has been focussed upon new FMD outbreaks and events that have occurred at the margins of these endemic regions (reported on the WOAH WAHIS Interface: <u>https://wahis.woah.org/#/home</u>, summarised in Figure 2-3, Table 2-1 and described elsewhere in this report). Further details of many of the characterisation of viruses retrieved from these outbreaks are provided later in this report.



Figure 2-3: Map indicating the location of significant epidemiological events and disease outbreaks reported to OIE in immediate notifications or follow-up reports in 2022 (data, available from: https://wahis.woah.org/#/home, downloaded on 7 April 2023)



Table 2-1: New FMD outbreaks reported to WOAH during 2022 (data retrieved from WAHIS on www.oie.int on 9th February 2023).

	စ္ Number of Animals						
Country	New outbrea	Susceptible	Cases	Killed and disposed of	Slaughtered	Deaths	Vaccinated
Afghanistan	0	18098	158	0	47	3	6494
Algeria	23	1525	112	0	6	3	0
Benin	22	193260	10696	25	0	75	0
Bhutan	3	32	6	0	0	0	0
Botswana	1	7940	240	0	0	0	8459
China (People's Rep. of)	1	454	21	454	0	0	0
Comoros	30	78	63	0	0	15	0
Ethiopia	67	589005	6100	0	0	169	4677
Indonesia	19	70013	67150	0	0	1	0
Iraq	53	4238	1374	0	0	56	0
Israel	95	81824	4795	19	0	1006	44951
Jordan	1	36000	31	0	0	0	0
Kazakhstan	1	65	2	25	0	0	0
Kenya	4	170	14	0	0	0	370
Malawi	4	45467	711	0	0	0	42581
Malaysia	5	712	27	0	0	0	1619
Mongolia	3	1368	55	0	0	0	101000
Mozambique	4	21306	1063	0	0	0	0
Namibia	2	278	15	0	0	0	0
Palestine	5	2145	112	0	0	69	352
Saudi Arabia	79	24572	662	0	0	117	5019406
South Africa	184	346011	7863	73	2099	0	0
Sudan	9	12035	408	0	0	17	0
Thailand	29	2188	504	0	0	16	2770
Tunisia	61	5022	418	0	0	0	805
Türkiye	29	21795	589	0	0	25	567502
United Arab Emirates	10	12880	671	658	0	13	0
Zambia	2	767	22	0	0	0	0
Zimbabwe	12	36642	918	0	0	0	35896



2.2 Overview of the activities of the OIE/FAO FMD Laboratory Network during 2022

The WOAH/FAO FMD Reference Laboratory Network provides important support to the global control of FMD and provides opportunities and expertise for developing and sustaining laboratory capacity and capability, exchange of materials and technologies, harmonising approaches to diagnosis and supporting complementary research. Laboratories within the Network regularly receive samples for FMD diagnosis from many parts of the world. The *in vitro* antigenic properties of selected isolates are assessed for vaccine matching and nucleotide sequencing allows precise characterisation of new isolates and tracing of their origin by comparison with viruses held in virus collections. This analysis assists the monitoring of the 'real time' emergence and spread of FMD virus globally.

3315 clinical samples from suspect cases of FMD were tested by laboratories in the Network (and associated laboratories) during 2022. These samples were collected from 34 countries from all seven FMD endemic pools (Figure 2-4). **However, sampling within these pools is not equivalent:** and efforts are currently underway with the Network to improve sample collection in regions where sampling is under-represented.



Figure 2-4: Distribution of samples collected from suspect cases of FMD and reported by the WOAH/FAO FMD Laboratory Network during 2022. Routine surveillance that is undertaken in countries that are FMD-free without vaccination is not shown.





Figure 2-5: Clinical samples (n=3315) tested for FMD investigation (virology) by the WOAH/FAO FMD Laboratory Network from FMD endemic countries during 2022 and their distribution across the seven FMD endemic pools (see Figure 2-1).



Figure 2-6: Summary of results for characterised isolates (n=1240) from FMD endemic countries were reported by the Network during 2022. FMDV GD denotes samples that were only positive using molecular (RT-PCR methods), while a further 2081 samples were tested but found to be negative for FMDV using all diagnostic methods.





Figure 2-7: Summary of 713 samples (viruses and field isolates) that were sequenced (VP1/capsid/complete genome) during 2021 (see Appendix 3).

The results for the individual samples are reported later in this report. Characterization results obtained on samples received by WRLFMD and PANAFTOSA can also be found respectively at: <u>http://www.wrlfmd.org/</u> and at: <u>http://new.paho.org/panaftosa</u>.

2.3 Regional distribution of different FMD viral lineages

In regions where FMD is endemic, continuous evolution of the virus generates geographically discrete lineages that are genetically distinct from FMD viruses found elsewhere. The conjectured global status for FMD (see Figure 2-1) masks the underlying complexity of FMDV virus distribution in the different pools (at serotype, topotype and lineage levels). This report showcases a new format to display how different FMD lineages circulate in different regions of the world. Using a new tool (called PRAGMATIST) that has been developed in partnership between WRLFMD and EuFMD, analyses accommodate the latest epidemiological data collected by the Network and presented in this report regarding FMDV lineages detected in samples to assess the relative importance of the viral strains circulating within each *source regions* (see Table 2-2 below).



Table 2-2: Conjectured distribution of important FMDV lineages in different endemic regions. For each of the regions, data represent the relative importance of the different lineages [prevalence score estimated as a proportion (%) of total FMD cases that occur in domesticated host animals]. NB: Arrows highlight changes from the figures published in this table in last year's report

	Vest Eurasia	East Asia	Vorth Africa	South Asia	East Africa	West & entral Africa	Southern Africa	South America
FMDV Lineage	>					ပ ပ		
O/ME-SA/PanAsia-2	35							
O/ME-SA/PanAsia		10						
O/SEA/Mya-98		₽ 21.5₃₃						
O/ME-SA/Ind2001	7	140 20	₽ 10	186 80				
O/EA/WA	3		55		1 55.5₅	465 70	1 16 °	
O/EURO-SA								190 80
O/CATHAY		10.5						
A/ASIA/Sea-97		18 26						
A/ASIA/Iran-05	132 27	0						
A/ASIA/G-VII	10 15			10 16				
A/AFRICA			133 25		22	17 15		
A/EURO-SA								10 20
Asia-1	12.5	0 0.5		4				
SAT 1			0		8	J 3 5	16 27	
SAT 2	0.5		10		14	115 10	1 52 57	
SAT 3					0.5 1		16	
С								

Based on these data, a *prevalence score* is defined by estimating the proportion of each of the local viral strains that would be represented if 100 animals infected with FMDV were randomly selected from each source area.

In order to help visualise the changing patterns in FMDV distribution and recognise risks for the emergence of new lineages, the Network has reviewed available intelligence for epidemiologically important FMDV lineages (Table 2-2), focussing on those that have already demonstrated a potential for long-distance trans-pool spread: O/ME-SA/Ind-2001, O/ME-SA/PanAsia, O/ME-SA/PanAsia-2, O/SEA/Mya-98, O/EA-3, A/ASIA/G-VII, A/ASIA/Iran-05, A/ASIA/Sea-97 and SAT 2/VII.

The current known and conjectured distribution of these different FMD viral lineages are represented in the maps below: The extent of current distribution for each of the viral



lineages is represented within the black lines, while the location of individual outbreaks (dots) and affected countries (shaded colours, according to dates) are shown. NB: Arrows are drawn to highlight the regions that are now threatened by these lineages and text boxes highlight some of the headline events and changes that have occurred during 2021-22.



FMDV O



FMDV A



FMDV Asia 1



Figure 2-10: Conjectured distribution of serotype Asia 1.

Main events in 2022:

 No further spread of this serotype in Southeast Asia (beyond cases reported in 2017)

FMDV SAT 2



Figure 2-11: Conjectured distribution of serotype the SAT 2 (topotype VII) FMDV lineage.

Main events in 2022:

• First detection of SAT2/XIV in Ethiopia since 1991 (data not shown)



2.4 Vaccine matching and recommendations

These take two forms: regional recommendations and details of locally produced vaccines for each of the FMD endemic pools are summarised later in this report, whilst the WRLFMD recommendations for FMD free countries are given in Figure 2-12 below. Details of vaccine matching work undertaken by the Network are summarised in Appendix 2.



Figure 2-12: Recommendations from WRLFMD on FMD virus strains to be included in FMDV vaccine antigen bank for Europe (January 2023)

Outputs from WRLFMD are generated with a tool (called PRAGMATIST¹) that has been developed in partnership between WRLFMD and EuFMD. These analyses accommodate the latest epidemiological data collected by the Network regarding FMDV lineages that are present in different source regions (see Table 2-2 above), as well as available *in vitro*, *in vivo* and field data to score the ability of vaccines to protect against these FMDV lineages. Further information about FMD vaccine producers is available on the Network website: <u>https://www.foot-and-mouth.org/fmd-vaccine-producers</u>

The figure highlights the importance of these source regions for Europe (using data collected at the EU-RL Workshop); please contact WRLFMD/EuFMD for assistance to tailor these outputs to other geographical regions. NB: Vaccine-coverage data presented is based on available data and may under-represent the true performance of individual vaccines.

¹ Ludi *et al.*, (2022) PRAGMATIST: A tool to prioritize foot-and-mouth disease virus antigens held in vaccine banks. *Front Vet Sci.* **9**:1029075. doi: <u>10.3389/fvets.2022.1029075</u>



3 Overview of Network surveillance activities in each of the regional endemic pools

3.1 Pool 1 Regional synopsis

3.1.1 Conjectured circulating FMD viral lineages in Pool 1 during 2022

- Serotype O:
 - o SEA/Mya-98
 - ME-SA/PanAsia
 - o ME-SA/Ind2001e
 - CATHAY
- Serotype A:
 - o ASIA/Sea-97
- Serotype Asia-1 (no outbreaks detected since 2017, Myanmar)

 Table 3-1: Overview of clinical samples collected and tested from Pool 1 in 2022 (countries highlighted in blue; graph represents clinical submissions to Network laboratories since 2005)





Laboratory	Countries of Origin	Number of Clinical Field Cases	f Samples Surveillance Activities
AQPA	Cambodia, Republic of Korea, Vietnam	23	1237711
FGBI ARRIAH	Mongolia	3	0
LVRI	China	14	4580
RRLSEA	Thailand	313	4305
WRLFMD	Indonesia, Mongolia, Thailand	39	0



Pool 1 headlines:

- New FMD outbreaks due to the O/ME-SA/Ind-2001e lineage have been detected in Indonesia (see Appendix 4.1).
- Antigenic variability observed for serotype A viruses in Thailand has led to a switch in the locally produced FMD vaccine used in the country (see Appendix 4.2)
- In China, three FMD serotype O lineages have been detected since 2020 (see Appendix 4.3): O/SEA/Mya-98, O/CATHAY and O/ME-SA/Ind-2001, while the last case of serotype A was seen in 2019. During 2022, there has been only one official FMD outbreak reported in China due to O/CATHAY, although surveillance has identified positive samples comprising O/SEA/Mya-98 (n=3), O/ME-SA/Ind-2001e (n=12) as well as O/CATHAY (n=24).
- No FMD outbreaks have been reported in the Republic of Korea since 2019.
- No new outbreaks due to serotype Asia1 were detected in 2021. This serotype has been absent since 1998, except for outbreaks in Vietnam (2006) and Myanmar (2017).

3.1.2 Vaccine recommendations for Pool 1

- Internationally produced vaccines:
 - o O: Campos, O₁ Manisa, Primosky, TUR/5/2009 & 3039
 - A: Arg2001, A24 Cruzeiro, Iran/05, A22/Iraq/64, Malaysia/97, TUR/20/06 & Zabaikalsky.
 - Asia 1: Shamir
- Locally produced vaccines (in Thailand):
 - o 0: 189/87 (Udornthani/87)
 - A: Lopburi/12, Sakolnakorn/97
- Locally produced vaccines (at FGBI ARRIAH):
 - o O: Ind-2001, Mya-98, PanAsia-2
 - o A; G-VII, Iran-05, Sea-97
 - o Asia1: Shamir, Sindh-08
- Locally used vaccine strains (by Chinese manufactures):
 - o O/Mya-98 (O/Mya98/BY/2010 and Re-O/Mya98), O/HK99
 - Re-Á/Sea-97 (Re-A/WH/09)
 - Asia1/GV (Asia1/JSL/06).

3.2 Pool 2 Regional synopsis

3.2.1 Conjectured circulating FMD viral lineages in Pool 2 during 2022

- Serotype O:
 - o ME-SA/Ind-2001e
 - o ME-SA/SA-2018
- Serotype A:
 - ASIA/IND (genotype VII also known as genotype 18)
- Serotype Asia-1



Table 3-2: Overview of clinical samples collected and tested from Pool 2 in 2022 (countries highlighted in blue; graph represents clinical submissions to Network laboratories since 2005)



Pool 2 headlines:

- The emerging O/ME-SA/SA-2018 lineage has now been detected in many Indian states and there is almost an equal number of O/ME-SA/Ind-2001e and O/ME-SA/SA-2018 outbreaks (see Appendix 4.4).
- O/ME-SA/PanAsia-2^{ANT10} could not be detected anywhere in India except for the two sporadic incidences in Jammu & Kashmir in 2021 (see Appendix 4.4).
- Vaccine protection studies highlight the antigenic differences between A/ASIA/G-VII and A/ASIA/Iran-05²

² Singanallur *et al.*, (2022) A Vaccine Based on the A/ASIA/G-VII Lineage of Foot-and-Mouth Disease Virus Offers Low Levels of Protection against Circulating Viruses from the A/ASIA/Iran-05 lineage. *Viruses* **14**(1):97. doi: <u>10.3390/v14010097</u>

3.2.2 Vaccine recommendations for Pool 2

- Internationally produced vaccines:
 - O/ME-SA/PanAsia-2 (or suitable alternative). *In vitro* vaccine matching data for O/ME-SA/Ind2001 provides evidence for an antigenic match with O/TUR/09 vaccine (MSD) and O-3039 (Boehringer Ingelheim).
- Locally produced vaccines (by Indian suppliers):
 - o O/IND/R2/1975
 - o A/IND/27/2011 *
 - o Asia1/IND/63/1972

* Serotype A FMD virus strains circulating in India since 2012–13 have been found to be antigenically divergent from the currently used vaccine strain (IND40/2000). Taking into account the studies carried out by ICAR-NIFMD regarding the selection of suitable (alternate) FMDV serotype A vaccine strains, A/IND27/2011 emerged as the candidate strain of choice out of a panel of 8 strains.



3.3 Pool 3 Regional synopsis

3.3.1 Conjectured circulating FMD viral lineages in Pool 3 during 2022

- Serotype O:
 - o ME-SA/SA-2018 in Oman
 - ME-SA/PanAsia-2 [comprising at least two viral sublineages (ANT-10 and QOM-15) present in different countries].
 - o ME-SA/Ind-2001 (via introductions from South Asia: Pool 2)
 - EA-3 (in Israel & Palestinian Autonomous Territories)
- Serotype A:
 - ASIA/Iran-05 [comprising 4 predominant viral sublineages (SIS-10, SIS-12, SIS-13 and FAR-11)]
 - o ASIA/G-VII
 - Serotype Asia-1:
 - Sindh-08

Table 3-3: Overview of clinical samples collected and tested from Pool 3 in 2022 (countries highlighted in blue; graph represents clinical submissions to Network laboratories since 2005)



			oumpies
Laboratory	Countries of Origin	Clinical Field	Surveillance
		Cases	Activities
ANSES	Oman	149	146
CVDRL	Afghanistan	160	160
FGBI ARRIAH	Russia, Kazakhstan, Pakistan	154*	50986*
ŞAP Institute	Türkiye	148	106850
WRLFMD	Israel, Palestine, Pakistan, UAE	87	0

* 152 diagnostic and 50686 surveillance samples from Russia. Some of these samples may be from Pool 1



Pool 3 headlines:

- FMD outbreaks due to O/ME-SA/Ind-2001e have been reported in Kazakhstan (Jan 2022) and Russia (Dec 2021). Sequences from these countries are closely related to each other and highlight an epidemiological connection to Pool 1 as a source (perhaps via Mongolia – see Appendix 4.5).
- O/ME-SA/SA-2018 has been detected in UAE and Oman (in samples collected in 2021), representing the first time that this lineage has been detected outside of Pool 2.
- A/AFRICA/G-I viruses have been detected in Oman highlighting the epidemiological connectivity to East Africa (via trade or movement of people).
- Only serotype O FMD outbreaks have been reported in Turkey during 2022 due to viruses from the O/ME-SA/PanAsia-2^{QOM-15} and O/ME-SA/PanAsia-2^{ANT-10} sub-lineages.
- A new viral clade within the O/ME-SA/PanAsia-2^{ANT-10} sub-lineage has caused extensive outbreaks in Eastern Mediterranean countries (Jordan, Palestine and Israel). These viruses are most closely relation to those detected in the Gulf States and Pakistan and appears to have supplanted the O/ME-SA/PanAsia-2^{QOM-15} lineage that was previously dominant in some of these countries (see Appendix 4.6).

3.3.2 Vaccine recommendations for Pool 3

Internationally produced vaccines

- MSD and Boehringer-Ingelheim (Merial)*:
 - O/ME-SA/PanAsia-2 (or suitable alternative)
 - o O/Manisa
 - A Iran-05 (or A TUR 06)
 - o A22/Iraq
 - Asia-1 Shamir
 - o A/G-VII
- Locally produced vaccines (at FGBI ARRIAH):
 - o O: Ind-2001, Mya-98, PanAsia-2
 - o A; G-VII, Iran-05, Sea-97
 - o Asia1: Shamir, Sindh-08
- Locally produced vaccines:
 - o O/TUR/07 (PanAsia 2)
 - A05 (A/IRN/17)
 - o A/ASIA/Iran 05^{FAR-11}
 - o A/Asia/G-VII
 - Asia 1/Sindh-08
- Locally produced vaccines (other suppliers in the region):
 - o Vetal
 - o MEVAC



3.4 Pool 4 Regional synopsis

3.4.1 Conjectured circulating FMD viral lineages in Pool 4 during 2022

- Serotype O:
 - EA-2 (Namibia, Zambia, Kenya, Tanzania, DR Congo, Uganda)
 - o EA-3 (Algeria, Tunisia, Egypt, Ethiopia, Eritrea, Sudan)
 - o EA-4 (Ethiopia, Kenya, Uganda)
 - ME-SA/Sharqia-72 (detected in samples collected in Egypt in 2009)
 - o ME-SA/Ind2001 (in Libya, Tunisia, Algeria and Morocco)
- Serotype A
 - o AFRICA/I (Kenya, Tanzania, D.R. Congo)
 - o AFRICA/IV (Algeria, Sudan, Eritrea, Egypt)
 - o AFRICA/VII (Ethiopia, Egypt)
 - ASIA/Iran-05^{BAR-08} (Egypt)
- Serotype SAT 1
 - o I (Kenya, Tanzania)
 - o IX (Ethiopia)
- Serotype SAT 2:
 - o IV (Kenya, Tanzania)
 - VII (Sudan, Egypt, Mauritania)
 - o XIII (Ethiopia, Sudan)
 - XIV (Ethiopia)
- Serotype SAT 3
 - Only detected in African buffalo in the south of the Queen Elizabeth National Park, Uganda in 1970, 1997 and 2013).

Table 3-4: Overview of clinical samples collected and tested from Pool 4 in 2022 (countries highlighted in blue; graph represents clinical submissions to Network laboratories since 2005). *Note: These figures include samples collected in countries in North Africa where FMD outbreaks have occurred since 2013.*





FMD Laboratory	Kenya	61	2187
AHI	Ethiopia	181	2570
WRLFMD	Algeria, Egypt, Ethiopia,	130	0
	Sudan. Tunisia		

Pool 4 headlines:

- There has been a new introduction of the O/EA-3 topotype into the Maghreb (Tunisia & Algeria) that is most closely related to FMD viruses detected in West Africa see Appendix 4.7
- The have been published reports of FMD outbreaks in Egypt due to exotic serotype O and A viruses with a South American origin ^{3,4}. These unexpected outbreaks need to be closely monitored since there is potential for onward spread in North Africa and the Eastern Mediterranean.
- SAT 2 topotype XIV has been detected in Ethiopia for the first time since 1991 (Appendix 4.8).

³ Soltan *et al.*, (2022) Emergence of foot-and-mouth disease virus, serotype O, Europe-South America topotype in Egypt, 2022. *Transbound Emerg. Dis.* **69**(5): 2409-2411. doi: <u>10.1111/tbed.14612</u>

⁴ Hagag *et al.*, (2022). Molecular detection and phylogenetic analysis of newly emerging FMDV type A, lineage EURO-SA in Egypt in 2022. Virus Res. **323**:198960. doi: <u>10.1016/j.virusres.2022.198960</u>

3.4.2 Vaccine recommendations for Pool 4

- Internationally produced vaccines:
 - o O: Manisa, 3039
 - O: PanAsia-2 (or equivalent)
 - o A: Eritrea
 - o SAT 1: Sat105, SAT109
 - o SAT 2: SAT251, Eritrea
 - o SAT 3: SAT306, SAT309
- Locally produced vaccines from KEVIVAPI (Kenya):
 - O: K 77/78 EA1
 - o A: K5/80 G1
 - SAT1: T155/71 NWZ
 - o SAT2: K52/84 IV
- Locally produced vaccines from Ethiopia:
 - Serotype O (EA-3)
 - Serotype A (Africa/G-III)
 - Serotype SAT 2 (XIII)
- Locally produced vaccines from BVI (Botswana including the following strains O/Manisa 1/78, O/3039, SAT105, SAT109,SAT2035, SAT251, SAT306 & SAT309



3.5 Pool 5 Regional synopsis

3.5.1 Conjectured circulating FMD viral lineages in Pool 5 during 2022

- Serotype O:
 - WA and EA-3 (Nigeria)
- Serotype A:
 - o AFRICA/G-IV & G-VI
- Serotype SAT 1
 - Topotype X (Nigeria and Cameroon)
- Serotype SAT 2:
 - Topotype VII (Mauritania)

Table 3-5: Overview of clinical samples collected and tested from Pool 5 in 2022 (countries highlighted in blue; graph represents clinical submissions sent to Network laboratories since 2005)



Pool	5 hos	adlin	06'

NCFAD

NVRI

- The O/EA-3 topotype appears to be widely spread across the region including in Niger where new cases have been detected (see Appendix 4.9).
- The A/AFRICA/G-IV genotype has also been detected during 2002 in Niger.

Ghana

Nigeria

20

31

0

2229

- New cases due to SAT2/VII have been detected in Mali (for samples collected in 2021).
- New transboundary risks have been identified associated with increased animal movements from the Central African Republic.



3.5.2 Vaccine recommendations for Pool 5

- Internationally produced vaccines:
 - o **O/Manisa**
 - o O/Maghreb
 - o O/PanAsia-2 (or equivalent)
 - o O: 3039
 - o A: Eritrea
 - SAT 2: Eritrea & Zimbabwe
 - Locally produced vaccines
 - o O: NIG 04/14
 - O: WA and EA-3 topotypes
 - A: NIG 07/13
 - A: West Africa (G-IV lineage)
 - SAT 1: Topotype X
 - SAT 2: NIG 03/12
 - SAT 2: Topotype VII
 - o O, A, SAT 1 & SAT 2 (Boru-Vacc, Nigeria)

3.6 Pool 6 Regional synopsis

3.6.1 Conjectured circulating FMD viral lineages in pool 6 during 2022

- Serotype O
 - o O/EA-2 topotype
- Serotype SAT 1:
 - o Topotypes I, II and III
- Serotype SAT 2:
 - o Topotypes I, II and III
- Serotype SAT 3:
 - o Topotypes I, II and III

 Table 3-6:
 Overview of clinical samples collected and tested from Pool 6 in 2022 (countries highlighted in blue; graph represents clinical submissions since 2005)





		Clinical Field Cases	Surveillance Activities
ARC-OVI	Eswatini, Lesotho, Malawi, Mozambique, South Africa, Zimbabwe	1175	199345
BVI	Botswana, Lesotho, Malawi, Mozambique, Namibia, Zimbabwe	75	1825
WRLFMD	Botswana, Malawi, Namibia, Zambia	10	0

Pool 6 headlines:

- FMD outbreaks continue in South Africa where SAT 2 cases have been detected for almost two years. During 2022, 119 outbreaks have been detected in KwaZulu-Natal caused by viruses that are closely related to those recovered from cases in 2021 (see: Appendix 4.10). SAT 3 outbreaks have occurred in Limpolo and the central provinces of North-West, Gauteng, Mpumalnga and Free State (See Appendix 4.11). The outbreaks are mostly in cattle, but cases have also been seen in small ruminants (particularly sheep). There are some reports of FMDV circulation in buffalo, but this is only for serotype SAT 2 in the North of the country.
- Serotype O viruses (O/EA-2 topotype) have spread from Pool 4 to cause outbreaks in central/southern Zambia, Namibia, Mozambique and Malawi (see Appendix 4.12). These cases pose new risks to countries in southern Africa where serotype O has not been detected since 2000.

3.6.2 Vaccine recommendations for Pool 6

- Internationally produced vaccines:
 - o O: Manisa, 3039
 - o SAT 1: SAT105, SAT 109
 - SAT 2: SAT251
 - SAT 3: SAT306, SAT 309
- Locally produced vaccines
 - o O: Manisa
 - SAT 1: SAT105, SAT109
 - o SAT 2: SAT251, SAT2035
 - o SAT 3: SAT306, SAT309



3.7 Pool 7 Regional synopsis

 Table 3-7:
 Overview of clinical samples collected and tested from Pool 7 in 2022 (countries highlighted in blue; graph represents clinical submissions since 2005)



Pool 7 headlines:

• Except for Venezuela which has no official FMD status with the WOAH, there have been no confirmed cases of FMD anywhere in South America during 2022.

3.7.1 Vaccine recommendations for Pool 7

- Internationally produced vaccines:
 - All vaccines used in the region are produced in South America (Argentina, Brazil, Colombia, Paraguay & Venezuela have vaccine manufacturers)
- Locally produced vaccines
 - \circ O: O₁ Campos
 - o A: A₂₄ Cruzeiro, A/Arg/2001
 - o C: C₃ Indaial



4 Improving the quality of laboratory tests from FMD reference laboratories

4.1 Proficiency testing schemes (PTS) organised by the Network Partners

ANSES, France

- FMD/SVD Proficiency testing scheme 2022
 - 46 laboratories from 40 countries participated
 - Registration in February 2022 with shipment of samples in May 2022
 - Sample analysis June 2022 (4 weeks)
 - Panel 1: Live virus (4 samples of 3 ml)
 - Panel 2: Inactivated virus (4 samples of 4 ml)
 - Panel 3: Sera (FMDV antibodies) (5 samples of 1.8 ml)
 - Panel 4: Sera (FMDV antibodies) (4 samples of 0.5 ml)

APQA, Republic of Korea

- FMD Proficiency testing scheme
 - o 46 Regional Diagnostic Laboratories
 - Virological test panel: 6 samples (inactivated virus)
 - Test: RT-PCR and real time RT-PCR
 - Serological test panel: 6 sera (Sero-positive and negative against type O)
 - Test: two commercial NSP ELISA kits and a single SP-O ELISA kit
 - Objective: to evaluate FMD diagnostic capability of the laboratories using virological and serological methods

FGBI ARRIAH, Russia

- In June 2022, panels for FMD proficiency tests were sent to 12 laboratories:
 - two Russian veterinary laboratories
 - eight border countries: Armenia, Azerbaijan, Belarus, Moldova, Kazakhstan (2 laboratories), Kyrgyzstan (2 laboratories), Uzbekistan, Mongolia.
 - \circ $\,$ To date, results have been submitted by nine laboratories.

ICAR-NIFMD, India

- ICAR-NIFMD conducted FMD Proficiency Testing Scheme (PTS) for 3AB3 indirect DIVA ELISA and SPCE for state FMD regional and collaborating laboratories.
- In SPC-ELISA Proficiency Testing.
 - A total of 11 operators from NIFMD laboratories and State FMD Regional and Collaborating Centres participated.
 - Except for a few of the samples with borderline titre values, the overall interpretation of all operators with respect to protective status showed concordance with the ICFMD result.



- In 3AB3 NSP ELISA (DIVA) Proficiency Testing
 - A total of 21 operators from NIFMD laboratories and state FMD Regional and Collaborating Centres participated.
 - It was observed that all operators judged the positive sample as positive except for a few operators who misinterpreted the weak positive sample as negative.

IZSLER, Italy

- National (Italy) Proficiency test
 - Objective: To practise the regional laboratories in the use of serological tests for maintaining preparedness in case of national emergency
 - Panel composition: 22 sera (naive and various SP-Ab profiles against FMD type O and A)
 - Test used: IZSLER manufactured kits (SP-ELISA type O)
 - Task: providing results for each sera

PANAFTOSA/VPH, PAHO/WHO

- 22 National and international reference laboratories from 14 countries
- 4 panels for the detection/typing of FMDV and Vesicular stomatitis virus and vaccine control.
- Methods:
 - RT-qPCR/RT-PCR and sequencing
 - ELISA SI (typing FMDV/VSV)
 - ELISA-3ABC/EITB (detection of antibodies against FMDV NSP)
 - ELISA LPBE (detection of antibodies against FMDV SP)
 - Viral neutralization (detection of anti-FMDV and -VSV antibodies)



WRLFMD

Phase XXXIV of the WRLFMD PTS has started. The exercise involves 33 laboratories in 28 countries.



Two panels (virology) and (serology) have been prepared to cover a plausible FMD outbreak scenario. After receiving the sample panels, laboratories were asked to use their national laboratory contingency plans (or similar document) to identify which tests were appropriate for use. Laboratories were also asked to use the scenario information as well as the information from the virological panel to select appropriate assays for use with the serological panel including what FMDV serotype(s) should be tested.

4.2 Supply of reagents

BVI, Botswana

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
ELISA reagents (SAT 1, 2 & 3)	150 ml each	BNVL (Botswana)
ELISA reagents (O and SAT1, 2 & 3)	300 ml each	Zimbabwe
		Linibabwo

ICAR-NIFMD, India

Type of reagent	Quantity	Recipient of the reagent (Laboratories / Countries)
DIVA NSP ELISA	For testing 120481 serum samples	State FMD regional and collaborating centres



SPCE SP ELISA	For testing 145000 serum samples	State FMD regional and collaborating centres
Sandwich Ag ELISA	For testing 1450 serum samples	State FMD regional and collaborating centres

IZSLER, Italy

Distribution 1029 kits in 53 countries:

Ту	Quantity	
FMDV antigen detection	ELISA; type O, A, C, Asia1, SAT1-2	144
NSP Ab	ELISA KIT (3ABC)	99
	FMDV O	476
	FMDV A	177
SP-Antibody ELISA Kit	FMDV Asia1	61
	FMDV SAT2	43
	FMDV SAT1	29



LVRI, China

Type of reagent	Quantity	Recipient of the reagent
		(Laboratories / Countries)
Guinea pig antisera	10 ml	China
(against FMDV type O and A)	10 111	Onna
FMDV immune sera (type O)	150 ml	China
FMDV infected sera	30 ml	China
FMDV cell culture	50 ml	China
(inactivated)	00 111	Onna
FMD LBP-ELISA kit	20883 kits	China
(type O, A, Asia-1)		on ind
FMDV-NSP 3ABC ELISA kit	1802 kits	China
SPCE	2358 kits	China
(type O)		China
Conventional MultiRT-PCR	82 kits	China
FMDV real time RT-PCR kit	1000 kits	China
Typing real-time RT-PCR	300 kits	China

FGBI ARRIAH, Russia

Type of reagent	Quantity	Recipient of the reagent (Laboratories / Countries)
FMDV antibody detection kit	30	Belarus
FMDV antibody detection kit	3	Bangladesh
FMDV antibody detection kit	579	Russia (regional veterinary laboratories)
FMDV NSP ELISA kit	1	Bangladesh
FMDV NSP ELISA kit	19	Russia (regional veterinary laboratories)



NCFAD, Canada

Type of reagent	Quantity	Recipient of the reagent
Pre-coated FMD-NSP ELISA plates and reagents to complete tests, includes panels for lab certifications	For 8 labs	Canadian Animal Health Surveillance Network laboratories
FMD primers, probes and controls for real-time RT-PCR; includes panels for lab certifications	For 10 labs	Canadian Animal Health Surveillance Network laboratories
FMDV antibody positive serum	24 mL	BioAssay Works LLC, MD, USA
FMD 3ABC recombinant antigen	~12 mg	BioAssay Works LLC, MD, USA
FMDV pan-serotype monoclonal antibodies	~40 mg	Mologics LTD, UK
FMDV primers, probes and lyophilized master mix for real-time RT-PCR along with pipettes and pipette tips	1000 reactions	National Veterinary Research Institute, Vom, Nigeria

PANAFTOSA/VPH, PAHO/WHO

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMD gIII ELISA kit	28	Brazil
ELISA 3ABC kit	297	Argentina, Bolívia, Brazil, Colômbia, Ecuador, Guyana, South Korea, Paraguay, Peru & Uruguay
EITB kit	186	Brazil, Canada, Colômbia, Ecuador, South Korea, Paraguay, Peru & Uruguay
CFL-O ELISA kit	129	Argentina, Brazil, Colômbia, Paraguay, Peru & Uruguay
CFL-A ELISA kit	129	Argentina, Brazil, Colômbia, Paraguay, Peru & Uruguay
Typing ELISA kit	17	Argentina, Brazil, Colômbia, Chile, Ecuador, Paraguay & Peru
Cell lines	8	Argentina & Brazil
FMDV strains	20	Canada & Paraguay
Viral RNA	103	Argentina, Colômbia, Chile, Ecuador & Peru
SP and NSP positive sera	21	Argentina, Colombia, Ecuador & Guyana



RRLSEA, Thailand

Type of reagent	Quantity	Recipient of the reagent (Laboratories / Countries)
Rabbit anti FMDV type O	13	National lab, Thailand
Rabbit anti FMDV type A	17	National lab, Thailand
Rabbit anti FMDV type Asia1	17	National lab, Thailand
Guinea pig anti FMDV type O	22	National lab, Thailand
Guinea pig anti FMDV type A	16	National lab, Thailand
Guinea pig anti FMDV type Asia1	17	National lab, Thailand
Concentrate Inactivated FMDV type O	59	National lab, Thailand
Concentrate Inactivated FMDV type A	85	National lab, Thailand
Concentrate Inactivated FMDV type Asia-1	68	National lab, Thailand
Control serum C++	14	National lab, Thailand
Control serum C+	12	National lab, Thailand
Control serum C-	11	National lab, Thailand

Sciensano, Belgium

Type of reagent	Quantity	Recipient of the reagent (Laboratories / Countries)
FMD positive serum	540 ml	joint EU-RL partner ANSES, France

SENASA, Argentina

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
Complement	362 ml	232 ml internal 130 ml delivered to other laboratories
Hemolisine	160 ml	150 ml internal 10 ml delivered to other international laboratories
Guinea Pig Hyperimmune Sera	289 ml	279 ml internal 20 ml delivered to other international laboratories
Inactivated Viral Antigen	29.8 ml	
Viral Suspension	2535 ml	
Hemolytic system production	4500 ml	
Positive controls for complement fix.	40 ml	


Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
Production of epithelia and vesicular liquid stocks	105 ml	
Panel of sera	304 ml	

WRLFMD

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antigens, FMDV antisera and serum controls	1015.5 ml	Egypt, Iraq, Italy, Korea (Rep. of), Namibia, Poland, Saudi Arabia, Thailand, United States of America, United Kingdom & Vietnam
FMDV-specific monoclonal antibodies	15.5 ml	France & Thailand
Cell lines for FMDV culture	18 ml	Austria
FMD virus isolates	414 ml	United Kingdom

4.3 Training courses organised by Network partners

ANSES, France

- Molecular Biology training, 18-22 July 2022.
 - 5 Countries: Montenegro, Slovenia (funded by EC, EURL), Kosovo, Moldova (funded by EuFMD, LoA), Albania (2 weeks funded by IAEA)
- Participation to EuFMD online training
 - Formation en ligne d'investigations sur la fièvre aphteuse pour l'Algérie, 4-29 July 2022.
 - Formation en ligne d'investigation sur la fièvre aphteuse pour la Tunisie, 8-29 March 2022.
 - FMD Laboratory Investigation Training Course, 15 November December 2022.

FGBI ARRIAH, Russia

Type of technical training provided	Country of origin of the expert(s) provided with training	No. participants from the corresponding country
Seminar	Pakistan	160
Seminar	Russia	25
Seminar	Russia	52



Type of technical training provided	Country of origin of the expert(s) provided with training	No. participants from the corresponding country
Hands-on training courses	Russia	3

FMD NRL, Kenya

• Biorisk implementers training by DETRA via Sandia National Laboratories.

ICAR-NIFMD, India

Seven laboratory training programs and workshops were organized by ICAR-NIFDM, as part of capacity building for state FMD regional and collaborating centres. A total 9 personnel were trained on FMD serosurveillance and hands on training on DIVA ELISA, FMD seromonitoring and hands on training on SPC-ELISA and Serotype detection by sandwich ELISA

IZSLER, Italy

- Virtual Workshop: Foot-and-mouth disease diagnostic methods
 - o 2nd March 2022
 - Training provided to staff of the two veterinary field laboratories in Northwest Syria.
 - Focused on enzyme-linked immunosorbent assays (ELISAs) and the basics of ELISAs in Northwest Syria.
 - Objectives:
 - update the staff of the field laboratories in Northwest Syria on FMD diagnostic methods, focused on ELISAs and the basics of ELISAs;
 - agree on the remote support and plan for testing the samples of FMD Post-Vaccination Monitoring in the Dairy Cattle Population in Northwest Syria.

LVRI, China

- 26th Meeting of the OIE Sub-Commission for Foot and Mouth Disease in South-East Asia, China and Mongolia
 - o 17th March 2022
- The 3rd Regional Expert Group Meeting on Foot-and-Mouth Disease
 2nd June 2022
- Special Meeting of the SEACFMD National Coordinators 'Focused on FMD Preparedness and Response'
 - o 9th June 2022
- 25th SEACFMD National Coordinators Meeting (2022.10.3-5)
 - o 3rd-5th October 2022
- Provincial training



NCFAD, Canada

• Foreign Animal Disease Recognition course for Canadian Veterinarians

PANAFTOSA/VPH, PAHO/WHO

- Simulation exercise: vesicular diseases in Brazil 9 events in several states in Brazil (Maranhão, Rondônia, Minas Gerais, among others). The simulation exercise was organised by the State Agency of Brazil, with the participation of MAPA and the Pan American Center for Foot-and-Mouth Disease (Panaftosa).
 - The exercise promoted theoretical review and practical training on clinical and epidemiological investigation, sample collection and submission to the laboratory, foot-and-mouth disease diagnosis, screening procedures, biosecurity, spread control, information system, and communication flow, and discussion and evaluation of strategies and methods to contain the spread of foot-and-mouth disease. This simulation exercise focused on the actions to be carried out regarding notifications of vesicular diseases.
 - This is part of the continuous training process of the Official Veterinarians of the State of Alagoas as well as compliance with the guidelines stated in the National Programme for the Eradication and Prevention of FMD.
- Simulated animal health emergency exercise took place in Juscimeira in the state of Mato Grosso, Brazil, from 30th July to 5th August 2022.
 - The exercise had national scope, with the purpose of training the members of the State Emergency Group (GEASE) and assessing the capacity of Official Veterinary Service to respond to a foot-and-mouth disease outbreak, as part of the activities of the Strategic Plan for the suspension of foot-and-mouth disease vaccination in the state.
- Simulated FMD emergency exercise with official veterinarians that took place in Quito, Ecuador, on 16-17th November 2022.
- Laboratory Training
 - The reference laboratory receive professionals for training in various techniques for the diagnosis of FMD and differentials (vaccine matching, RTqPCR, and RT-PCR, ELISA 3ABC / EITB).
 - 6 professionals from Paraguay (SENACSA; December 2021)
 - 1 professional from Argentina (INTA; July 2022)
- Sequencing emerging pathogens and bioinformatics analysis workshop
 - Organized the workshop with the objective of strengthening the diagnostic capacity of laboratories in South America
 - Professionals from 7 countries were invited in May 2022.

RRLSEA, Thailand

- One-step multiplex RT-PCR and ELISA Typing for National Laboratory in Thailand
- In house Training; Biosafety in RRL

Sciensano, Belgium

• Training course organised for 6 trainees from Kenya and Ethiopia within the framework of the JOINT international networking project



WRLFMD

- The WRLFMD has hosted delegates from Greece, Israel, Austria and Botswana for hands-on training in FMD diagnostic methods.
- The WRLFMD (with EuFMD/ANSES and Sciensano) has provided e-learning training for FMD diagnostics in November 2022

4.4 Collaborative projects

ANSES, France

Collaborators	Purpose of collaboration	Outcomes
FLI, CIRAD, CICbioGUNE, IDvet, BI, UNOTT, CISA-INIA, WBVR, UP, UoS, ISRA, LCV, ANSES	SPIDVAC : Improved control of priority animal diseases: Novel vaccines and companion diagnostic tests for African horse sickness, peste des petits ruminants and foot-and-mouth disease	
SLU, FLI, Sciensano, SAP institute, ANSES	FMDV_PersistOmics : From proteogenomic host response signatures of persistent foot- and-mouth disease virus (FMDV) infection to diagnostic markers and therapeutic control» Acronym	

APQA, Republic of Korea

Collaborators	Purpose of collaboration	Outcomes
Bangladesh (CDIL)	Genetic characterization of foot and mouth disease viruses in FMD Pool 2 countries	Data and materials (2020- 2024)
Cambodia (NAHPRI); Lao PDR (NAHL)	Genetic characterization of Foot-and-mouth disease viruses and avian influenza viruses in FMD and AI endemic countries	Data and materials (2018- 2022)
United Kingdom (WRLFMD)	Establishment of genetic interpretation technology of FMDV and NGS platform for molecular epidemiology	Data and materials (2020- 2022)
Viet Nam (NCVD)	The monitoring and genetic characterization of avian influenza and Foot-and-mouth disease viruses in Vietnam	Data and materials (2015- 2024)

ICAR-NIFMD, India

Collaborators	Purpose of collaboration	Outcomes



Wildlife Conservation Trust	Understanding FMD virus ecology in livestock wild life interface in buffer zone of Sanjay Tiger Reserve/Bandhavgarh Tiger Reserve	Testing of 1224 serum samples collected from cattle, buffaloes, and goats by 3AB3 NSP ELISA revealed 17.7%, 2.7%, and 9.8% of cattle, buffaloes, and goats, respectively, were positive for 3AB3 NSP antibody at the livestock-wild life interface.
ICAR-NRC on Pig	Kinetics of FMD virus serotype specific protective antibody response induced in pigs vaccinated with commercial FMD vaccine intended for use in cattle	Ongoing
WRL-FMD, UK; ICAR-IVRI, India	FMD Vaccine Quality Testing and Enhancing India's Animal Vaccine Testing Capabilities	

IZSLER, Italy

Collaborators	Purpose of collaboration	Outcomes
The Pirbright Institute	Research agreement aimed to continuous validation and improvement of diagnostic kits (ELISA), new developments	 Continued development of antigen-detection assays for FMDV and other vesicular diseases Development of assays for FMD vaccine quality Validation of a novel universal serology assay for diagnosis of FMD Research activities in the framework of AgResult project
University of Turin & In3Diagnostic (Italy); The Pirbright Institute; Friedrich-Loeffler-Institut (FLI); IZSAM – Teramo Italy	Validation of Lateral Flow Devices (LFD) for detection and serotyping of Foot and Mouth Disease Virus (FMDV) and antigenic detection of Lumpy Skin Disease Virus (LSDV). EuFMD-FAR-2022	Field validation of LFDs for:Detection of LSDDetection and serotyping of FMDV



FGBI ARRIAH, Russia

Collaborators	Purpose of collaboration	Outcomes
Assessment of immunity level in animals vaccinated against FMD and detection of possible virus circulation in zones here vaccination is practiced (at the stage of signing) MONGOLIA	Eradication of highly dangerous diseases including FMD in Mongolian livestock	continues to 2025
Joint CIS measures for FMD prevention and control	FMD prevention and control	continues to 2025
Agreement on crossborder trade and TADs risk reduction between China, Mongolia and Russia, P.R. of China and Mongolia.	Interactions in case of emergencies associated with angerous animal diseases including FMD	continues
Cooperation on the prevention and control of foot and mouth disease and other transboundary animal diseases between the countries of the Caucasus, Russia and Iran. GF-TADs: Armenia, Azerbaijan, Georgia, Iran, Turkey.	Exchange of information on outbreaks of diseases, vaccination of animals	continues

FMD NRL, Kenya

Collaborators	Purpose of collaboration	Outcomes
 FMD lab Embakasi WRL Pirbright WOAH 	Implement a Twinning Project for Lab Capacity building	Diagnostic capacity buildingReference capacity
 FMD lab Embakasi University of Minnesota USDA - PIADC KWS 	Research project on FMD Epidemiology at the Livestock-Wildlife interface	Understanding FMD Epidemiology at the wildlife-livestock interface
FMD Lab EmbakasiIZSLER	LFD Validation project	Validated LFDs

NCFAD, Canada

Collaborators	Purpose of collaboration	Outcomes
Biostone Animal Health	Evaluation of FMD SPCE for A, O and ASIA1	Inter-lab comparison of tests



Mologics, UK; Botswana Institute for Technology Research and Innovation, Botswana	Serotype specific lateral flow tests	Lateral flow strip test for FMDV serotypes A, O, SAT 1, 2, 3 and panserotype
BioAssay Works LLC, MD, USA; Botswana Institute for Technology Research and Innovation, Botswana	FMD-NSP lateral flow tests	Testing specificity
Shaddari Inc., Montreal, QC, Canada	Computational tool for foot- and-mouth disease vaccine matching	A vaccine matching tool that can rely on either VNT data or FMDV P1 sequences

PANAFTOSA/VPH, PAHO/WHO

Collaborators	Purpose of collaboration	Outcomes
Ministry of Agriculture, Livestock and Food Supply - Brazil	Performance of reagents in inactivating foot- and-mouth disease virus in field epithelium samples: a comparison between six commercial products. Increase the capillarity of diagnosis of foot-and-mouth disease in large countries.	In progress
Biological Institute of São Paulo - IBSP	Detection of 3ABC protein in various age groups and with multiple vaccinations. Evaluate vaccine purification (withdrawal of the FMDV nonstructural protein).	In progress
Biological Institute of São Paulo - IBSP	Post-vaccination immune response monitoring. Evaluate vaccine effectiveness at the field level in the different age groups in the vaccination schedule proposed by Brazilian legislation (350 animals).	In progress
Ministry of Agriculture, Livestock and Food Supply - Brazil	Validation and determination of sensitivity and specificity of rapid tests for FMD antigen detection.	In progress



Sciensano, Belgium

Collaborators	Purpose of collaboration	Outcomes
BVI, Botswana	bilateral collaboration	Participation of Sciensano in ILC organised by BVI in 2022
LNV, Burundi	bilateral collaboration	paper published in 2022 (DOI: <u>10.3390/v14051077</u>)
NVRI, Nigeria	bilateral collaboration	to be resumed in 2023
KULeuven, Belgium (promoter), Nairobi University, Kenya and Addis Ababa University, Ethiopia	JOINT international networking project	 training course organised paper published in 2022 (DOI: <u>10.3390/agriculture12010049</u>) co-supervisor of PhD obtained in 2022 (LIRIAS3677278)



RRLSEA, Thailand

Collaborators	Purpose of collaboration	Outcomes
SATREPS/JICA	Differential diagnosis systems of FMD and similar vesicular diseases as well as important infectious diseases affecting productivity in livestock using rapid diagnostic techniques and test kits are established.	 The development work of <u>FMD</u> rapid diagnostic test kit with the sensitivity and specificity required for practical use as Pen-side (PS) Testing is completed from the technical perspective. By the end of the project period, the development work of Standard Operating Procedures (SOPs) for the differential diagnosis of vesicular diseases using the FMD rapid diagnostic test kit and the multi-diagnostic kit is completed.
ACDP Collaboration	Development of serotype- specific real-time RT-PCR (ssRT-qPCR) assay for serotyping FMD viruses originating in Southeast Asia (SEA) and application of nucleotide sequencing and phylogenetic analysis to study the molecular epidemiology of FMD in SEA.	 Output: Serotype-specific real-time RT-PCR assays for SEA. Molecular epidemiology studies using P1 sequences. Outcome: Fully validated serotype-specific real-time RT-PCR assay(s) for direct serotyping of FMDV isolates in SEA. A better understanding of the genetic variability and evolution of FMDV in SEA.
Kodaira Research Station, NIAH, National Agriculture and Food Research Organization, Japan	Investigation study on persistent infection circumstances of foot-and- mouth disease virus in cattle in Thailand	The carrier status of foot and mouth disease in Thailand where there is a continuous outbreak.

SENASA, Argentina

Collaborators	Purpose of collaboration	Outcomes
USDA;	Understanding cross-reactive responses	In progress
INTA	between heterologous FMD virus strains in the bovine model	



Collaborators	Purpose of collaboration	Outcomes
	The main objective of this project is to carry out a rational study of heterologous protection between FMDV strains from the host (immune responses) and pathogen (antigenic determinants) perspectives.	
RAHO 6 DAH, Vietnam	FMDV circulating strains characterization in Vietnam: antigenic characterization and vaccine matching	In progress
	Cross protection assessment of circulating strains in Vietnam	

WRLFMD

Collaborators	Purpose of collaboration	Outcomes
DIC Wates and Pusvetma, Indonesia	Characterization of FMDV strains	Full genome sequencing
APQA , Republic of Korea	Molecular epidemiology of FMD in Asia	Collection of sequence data and phylogenetic analyses
IZSLER, Italy	IZSLER/Pirbright collaboration	Development of immunoassays for vesicular diseases
IZSLER, Italy; Sciensano, Belgium	Calibration of VNT methods	To compare VNT methods used in different laboratories

4.5 In vivo potency studies undertaken during 2021

APQA, Republic of Korea

Purpose of study	Study design	Vaccine strain used in Korea	Challenge strain	Result
Research study on pigs	Two doses (Vaccinated with one-week interval and challenged at 7 days after the booster vaccination)	O1 Manisa + O3039 O/RUS/Primorsky/2014 (O/SEA/Mya-98) O1 Campos	O/VN/08/2018 (O/PanAsia)	25% (1/4) protected 75% (3/4) protected 100% (4/4) protected



	A22 Iraq		100% (4/4)
One dose (Challenged at 28 dpv)	A/RUS/Zabaikalsky/2013 (A/ASIA/Sea-97)	A/TAI/10/2019* (A/ASIA/Sea- 97)	100% (4/4) protected
	A24 Cruzeiro + A/ARG/2001	,	100% (4/4) protected
	A22 Iraq		25% (1/4) protected
One dose (Challenged at 28	A/RUS/Zabaikalsky/2013 (A/ASIA/Sea-97)	A/PAK/1/2020 (A/ASIA/Iran-	75% (3/4) protected
dpv)	A24 Cruzeiro + A/ARG/2001	05)	100% (4/4) protected

FMD NRL, Kenya

Purpose of study	Study design (PD₅₀)	Name of Vaccine strain (Lots)	Name of Challenge strain	PD₅₀ Value
Vaccine Lot* potency test	PD50	O K77/78 (1 &2)	O K77/78	29.5 & 43.0
-d0-	PD50	A K5/80 (1 &2)	A K5/80	20.2 & 13.9
-d0-	PD50	SAT2 K52/84	SAT2 K52/84	43.0
-d0-	PD50	SAT2 K52/84	SAT2 K52/84	43.0

*Kenya Veterinary Vaccines Production Institute (KEVEVAPI) vaccine

ICAR-NIFMD, India

Purpose of study	Study design (i.e., PD50, PGP etc)	Name of Vaccine strain	Name of Challenge strain	Result
Vaccine QC	In-Vitro			

Five coded batches of FMD vaccines have been tested

- A group of 20 FMD sero-negative calves were selected for each batch of testing consisting of non-vaccinated control (02), safety testing (02) and potency test (16).
- From potency test group, the pre vaccination (0 day) as well as 28 days post vaccination serum collected and was evaluated for serotype specific FMD antibody titre using VNT for potency.



Şap Institute,Türkiye

Purpose of study	Study design	Name of Vaccine strain	Name of Challenge strain	Result
PD50/Adopted new Strain	PD50	A/TUR/2021 (A/ASIA /IRAN05 ^{FAR11})	Homology	7.42
Vaccine Efficacy (For per batch release)	PD50	O/ME-SA/PanAsia-2QOM15 A/ASIA/G-VII A/ASIA/IRAN05 ^{FAR11} ASIA1/ASIA/Sindh-08	Homology	Variable by strains and batch. But >6 PD50
Vaccine Efficacy (Exp)	PD50	O/ME-SA/PanAsia-2 ^{QOM15} A/ASIA/IRAN05 ^{FAR11}	Homology	7.12 8.36

SENASA, Argentina

Purpose of study	Study design	Name of Vaccine strain	Name of Challenge strain	Result
Vaccine control for certification	PD ₅₀	Trivalent Scheme (O ₁ Campos, A24 Cruzeiro, A Argentina 2001) reduced dose identification	O1/campos homo	12.58
Vaccine control for certification	PD ₅₀	Trivalent Scheme (O ₁ Campos, A24 Cruzeiro, A Argentina 2001) reduced dose identification	A24/Cruzeiro	16.00
Vaccine control for certification	PD ₅₀	Trivalent Scheme (O ₁ Campos, A24 Cruzeiro, A Argentina 2001) reduced dose identification	A/ARG/2001	12.70
Vaccine control for certification	PD ₅₀	Trivalent Scheme (O ₁ Campos, A24 Cruzeiro, A Argentina 2001) reduced dose identification	O/SKR/01/2017	9.00

WBVR-Lelystad, Netherlands

Purpose of study	Study design	Name of Vaccine strain	Name of Challenge strain	Result
Registration (n=3)	PD ₅₀	Various	Homologous	confidential
Vaccination (TPI)	Prime/boost	Multivalent	none	Under study



Appendix 1 Details of clinical samples from field cases from countries in FMDV endemic regions tested during 2021

Laboratory	Samples from	Total	0	A	ပ	Asia 1	Sat 1	Sat 2	Sat 3	Untyped	NVD	Comments
AHI	Ethiopia	181	67	33	-	-	-	22	-	-	59	
ANSES	Mali	10	-	-	-	-	-	8	-	-	2	
	Niger	60	5	2	-	-	-	-	-	37	16	
	Oman	149	74	13	-	-	-	-	-	44	18	
	Tunisia	15	15	-	-	-	-	-	-	-	-	
APQA	Cambodia	12	8	-	-	-	-	-	-	4	-	
	Vietnam	11	4	-	-	-	-	-	-	4	3	
ARC-OVI	South Africa	1175	-	-	-	-	-	11	55	-	1109	
BVI	Botswana	19	-	-	-	-	-	9	-	-	10	
	Malawi	5	3	-	-	-	-	-	-	-	2	
	Mozambique	25	8	-	-	-	-	12	-	-	5	
	Namibia	4	-	-	-	-	-	4	-	-	-	
	Zimbabwe	22	-	-	-	-	-	8	-	-	14	
	160 Karakhatar	32	-	-	11	-	-	-	-	117	160	
FGI-ARRIAH	Kazakhstah	2	2	-	-	-	-	-	-	-	-	
	Russia	3 152	3 2	-	-	-	-	-	-	-	- 150	
EMD	Russia	152	Z	-	-	-	-	-	-	-	150	
laboratory	Kenya	61	13	-	-	-	4	14	-	-	30	
LNERV	Senegal	3	-	-	-	-	-	-	-	-	3	
LVRI	China	14	9	-	-	-	-	-	-	-	5	
NCFAD	Ghana	20	8	-	-	-	-	-	-	12	-	
NVRI	Nigeria	31	20	-	-	-	-	-	-	-	11	
PANAFTOSA/ VPH	Chile	30	-	-	-	-	-	-	-	-	30	12 samples positive for Senecavirus A
PD-FMD	India	411	141	4	-	9	-	-	-	-	255	
RRLSEA	Thailand	313	142	36	-	-	-	-	-	-	135	
Şap Institute	Türkiye	148	81	-	-	-	-	-	-	2	65	
SENASA	Argentina	19	-	-	-	-	-	-	-	-	19	
WRLFMD	Algeria	5	4	-	-	-	-	-	-	1	-	
	Botswana	1	-	-	-	-	-	-	-	1	-	
	Egypt	34	3	13	-	-	-	-	-	16	2	
	Ethiopia	48	19	9	-	-	-	5	-	9	7	
	Indonesia	6	1	-	-	-	-	-	-	4	1	
	Israel	10	9	-	-	-	-	-	-	1	-	
	Malawi	2	_	-	-	-	-	_	-	2	-	
	Mongolia	17	13	_	-	-	-	_	-	4	-	
	Namihia	4	1	_	_	-	_	1	_	2	_	
	Dakietan	- 1 50	י 10	1	-	12	-	I I	-	ے 12	- ว	
	Delectinion	10	וש 10	4	-	12		-	-	15	2	
	State of	١Z	١Z	-	-	-	-	-	-	-	-	
	Sudan	40	10	9	-	-	-	-	-	15	6	



Laboratory	Samples from	Total	0	А	ပ	Asia 1	Sat 1	Sat 2	Sat 3	Untyped	NVD	Comments
	Thailand	16	8	5	-	-	-	-	-	3	-	
	Tunisia	3	3	-	-	-	-	-	-	-	-	
	UAE	15	7	-	-	-	-	-	-	3	5	
	Zambia	3	2	-	-	-	1	-	1	-	-	



Appendix 2 Vaccine matching studies undertaken by Network partners during 2021

Vaccine efficacy is influenced by both vaccine potency and vaccine match and it is possible that a poor match may to some extent be compensated by high potency vaccines and by administering more than one dose at suitable intervals. The use of oil adjuvant is also expected to improve efficacy. Thus, a vaccine with a weak antigenic match to a field isolate, as determined by serology, may nevertheless afford some protection if it is of sufficiently high potency. Therefore, in the absence of a good match, or where the match is unknown, vaccines of high potency should preferably be used. The r_1 values shown below, represent the one way serological match between vaccine strain and field isolate, calculated from the comparative reactivity of an antiserum, raised against the vaccine in question, to the vaccine virus and the field isolate.

Key:



For VNT:

 $r_1 \ge 0.3 -$ suggest that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection

 $r_1 \le 0.3$ - suggest that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect.

For LB-ELISA:

 $r_1 \ge 0.4 -$ suggest that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection

 $r_1 \le 0.4$ - suggest that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect.



APQA, Republic of Korea

Field virus	Vaccine strain					
Topotype/ Genotype	Country/Year (No. viruses)	O/3039	O/RUS/Primorsky/2014	O1/Campos	O/PanAsia2 (Korean Vaccine candidate)	O/SKR/BE/2017 (Korean Vaccine candidate, Ind2001)
O/ME-SA/PanAsia	O/LA/1/2019	М	Ν	Ν	М	М
	O/VN/24/2020	М	Ν	Ν	Ν	М
O/ME-SA/Ind-2001e	O/CAM/20/2019	М	N	Ν	N	М
	O/LA/10/2020	М	Ν	Ν	М	М

Field viru	us (type A)	Vaccine strain
Topotype/	Country/Year	A/SKR/YC/2017
Genotype	(No. viruses)	(Korean Vaccine candidate, SEA-97)
A/Asia/Sea-97	A/CAM/26/2019	N
	A/CAM/27/2019	М
	A/TUR/13/2017	Ν
	A/ISR/13/2017	Ν
A/Asia/G-VII	A/BHU/3/2017	Ν
	A/IRN/25/2018	Ν

FMD NRL, Kenya

Virus Isolate	Vaccine strain: OK77/78 r1 Value
K10/21	0.35
K80/20	0.80
K109/20	0.35
K13/20	0.45
K68/20	0.65
K95/21	0.40
K13/20	0.35



FGBI ARRIAH, Russia

Field Isolates	Vaccines				
	O ₁ Manisa <i>(ME-SA</i>)	O/Primorsky/2000 (O/PanAsia)	O/Zabaikalsky/2010 (O/Mya-98)	O/Kazakhstan/2010 (O/PanAsia 2)	O/Zabaikalsky/2016 (O/Ind-2001)
O/Orenburg (Russia)/2021	0.28	0.04	0.08	0.64	1.0
O/Kazakhstan/2022	0.23	0.22	0.05	0.58	1.0
O/Mongolia/2021	0.28	0.44	0.06	1.0	1.0

ICAR-NIFMD, India

Serotype	No of isolates tested	No of isolates showing r value more than 0.3	Percent Match
O (INDR2/1975)	4	4	100 %
A (IND40/2000)	3	0	0 %
A (IND27/2011)	3	3	100 %

Serotype	Strain	Genotype/Topotype	Lineage
0	INDR2/1975	ME-SA	Branch B
A	IND40/2000	Genotype 18	Non-deletion
Asia1	IND63/1972	Genotype 1	Lineage B

LVRI, China

Field isolate	Lineage	Animal	Vaccine strain		new candidate vaccine strain
			O/BY/2010	Re-O/JSCZ/2013	Re-O/17002
2022-031	CATHAY	Pig	Ν	Ν	М



NVRI, Nigeria

Field virus	r1 value per Vaccine virus strain							
isolate(s)	O-Manisa	0-3039	SAT 2035	SAT 251				
MAL 05/2022	0.85	0.22						
MOZ 09/2022	0.59	0.29						
ZIM 02/2022			0.65	0.16				
BOT 06/2022			0.57	0.17				
MOZ 54/2022			0.55	0.50				
NAM 66/2022			0.32	0.09				

NVRI, Nigeria

			VNT	r1 value /	' titre		
Sample Name	O/3039	O/Manisa	0/PanAsia-2	A/Eri98	A/Sau95	SAT2/Eri98	SAT2/Zim 7/83
O/Nig 38/2020	0.37 1.68	0.45 2.20	0.44 2.17				
O/Nig 8/2021	0.51 1.82	0.55 2.29	0.48 2.21				
A/Nig 100/2020				0.56 2.57	0.47 2.15		
A/Nig 16/2020				0.43 2.42	0.51 2.19		
SAT2/Nig 51/2020						1.00 2.09	0.36 2.08
SAT2/Nig 1/2021						0.70	0.35 2.08



RRLSEA, Thailand

Submitting country	Serotype O	Serotype A
Thailand	56	28

Şap Institute,Türkiye

		VNT r1 value	
Sample Name	O/TUR07 vaccine strain	A/IRN17	A/IRAN21
O/SAP/TUR/17/2022	0.49		
O/SAP/TUR/13/2022	0.39		
O/SAP/TUR/12/2022	>1		
A/IRAN17 vaccine strain virus		Matched	0.082
A/IRAN21 vaccine strain virus		0.105	Matched

WRLFMD

Se	erotype O		O 3 Boeh Inge	039 ringer lheim	O Ca Boeh Inge	mpos ringer lheim	O₁ Ca Bioge Ba	i mpos énesis agó	O M Boeh Inge	anisa pringer lheim	Pan/ Boeh Inge	Asia 2 pringer lheim	O/TU	R/5/09 SD
Isolate	Topotype	Lineage	r ₁	titre	r ₁	titre	r ₁	titre	r ₁	titre	r ₁	titre	r ₁	titre
COD/40/2021	EA-2	-	0.47	1.71	NT	-	0.68	2.62	0.18	1.88	0.3	1.95	0.63	2.08
COD/76/2021	EA-2	-	1	2.14	NT	-	0.76	2.67	0.46	2.28	1	2.47	0.91	2.24
NMB/01/2021	EA-2	-	0.49	1.76	NT	-	0.63	2.71	0.35	2.03	0.46	2.23	0.72	2.26
UGA/20/2020	EA-2	-	0.83	2.1	NT	-	0.76	2.55	0.45	2.22	0.59	2.29	0.79	2.21
UGA/25/2020	EA-2	-	0.68	2.01	NT	-	0.65	2.48	0.39	2.16	0.6	2.3	0.48	1.99
ZAM/12/2018	EA-2	-	0.98	2.08	NT	-	0.74	2.76	0.71	2.22	0.63	2.34	0.58	2.27
ZAM/13/2018	EA-2	-	1	2.11	NT	-	0.91	2.85	0.78	2.26	0.76	2.42	0.69	2.35
ALG/02/2022	EA-3	-	0.73	2.09	0.8	2.48	0.5	2.58	0.7	2.39	0.83	2.51	0.81	2.3
ALG/04/2022	EA-3	-	0.56	1.97	0.53	2.29	0.43	2.52	0.51	2.25	0.55	2.33	0.63	2.19
ETH/05/2020	EA-3	-	0.36	1.67	0.34	1.94	0.63	2.59	0.69	2.1	0.47	2.17	0.52	2.04
ETH/05/2021	EA-3	-	0.9	2.07	0.74	2.42	0.87	2.73	0.94	2.24	0.6	2.27	0.94	2.31
ETH/05/2022	EA-3	-	0.39	1.71	0.43	2.18	0.7	2.64	0.4	2.04	0.34	2.03	0.91	2.29
NIG/38/2020	EA-3	-	0.37	1.68	NT	-	0.63	2.65	0.45	2.2	0.44	2.17	0.54	0.21
NIG/46/2020	EA-3	-	0.35	1.65	NT	-	0.56	2.6	0.17	1.78	0.3	2	0.62	2.16
NIG/08/2021	EA-3	-	0.51	1.82	NT	-	1	2.88	0.55	2.29	0.48	2.21	0.85	2.3
NIG/12/2021	EA-3	-	0.69	2.07	NT	-	0.72	2.72	0.41	2.22	0.33	2.19	0.6	2.37
NIG/16/2021	EA-3	-	0.49	1.92	NT	-	0.66	2.68	0.38	2.19	0.4	2.27	0.48	2.27

54 | Page



Se	erotype O		O 3 Boeh	039 ringer	<mark>O Ca</mark> Boeh	mpos pringer	O₁ Ca Bioge	impos énesis	O M Boeh	anisa nringer	Pan/ Boeh	Asia 2 bringer	О/ТU М	R/5/09 SD
			Inge	lheim	Inge	lheim	Ba	agó	Inge	lheim	Inge	lheim		02
Isolate	Topotype	Lineage	r ₁	titre	r ₁	titre	r ₁	titre	r ₁	titre	r ₁	titre	r ₁	titre
NIG/18/2021	EA-3	-	0.59	2	NT	-	0.81	2.77	0.81	2.52	0.35	2.21	0.51	2.3
PAT/10/2021	EA-3	-	0.48	1.73	0.27	1.98	0.52	2.62	0.49	2.1	0.5	2.12	0.57	2.2
SUD/06/2020	EA-3	-	0.55	1.86	0.38	2.07	0.64	2.68	0.61	2.27	0.27	2.07	0.69	2.06
SUD/17/2020	EA-3	-	0.14	1.28	0.45	2.14	0.49	2.56	0.18	1.73	0.26	2.04	0.68	2.05
TUN/01/2022	EA-3	-	0.6	1.92	NT	-	0.56	2.65	0.71	2.35	0.46	2.33	0.91	2.29
TUN/03/2022	EA-3	-	0.65	1.95	NT	-	0.55	2.64	0.62	2.29	0.41	2.28	0.74	2.2
ETH/28/2019	EA-4	-	0.47	1.79	0.4	2.05	0.9	2.75	0.36	2.02	0.51	2.2	1	2.36
ISA/03/2022	ME-SA	Ind-2001	0.69	1.76	0.2	1.92	0.47	2.46	0.54	2.14	0.4	2.12	0.5	2.09
JOR/01/2017	ME-SA	Ind-2001	0.87	1.95	0.42	2.06	0.54	2.62	0.72	2.42	0.68	2.29	0.72	2.34
JOR/03/2017	ME-SA	Ind-2001	0.72	1.88	0.34	1.97	0.46	2.55	0.48	2.24	0.48	2.14	0.5	2.18
MOG/17/2021	ME-SA	Ind-2001	0.94	2.04	0.59	2.28	0.63	2.73	0.97	2.33	0.84	2.25	0.91	2.42
MOG/07/2022	ME-SA	Ind-2001	0.75	1.94	0.33	2.02	0.47	2.6	0.65	2.15	0.61	2.11	0.78	2.35
NEP/25/2021	ME-SA	Ind-2001	0.59	1.88	0.21	1.98	0.58	2.58	0.46	2.14	NT	-	1	2.39
NEP/55/2021	ME-SA	Ind-2001	0.54	1.84	0.15	1.82	0.43	2.45	0.45	2.13	NT	-	0.6	2.12
TAI/15/2020	ME-SA	Ind-2001	0.69	1.86	0.35	2.12	0.62	2.57	0.56	2.32	0.43	2.13	0.94	2.32
TAI/21/2020	ME-SA	Ind-2001	0.69	1.85	0.14	1.7	0.55	2.51	0.32	2.08	0.35	2.03	0.57	2.1
TAI/02/2021	ME-SA	Ind-2001	0.51	1.73	0.16	1.79	0.37	2.34	0.32	2.08	0.45	2.15	0.62	2.15
ISR/05/2022	ME-SA	PanAsia-2	0.48	1.69	0.18	1.78	0.42	2.37	0.33	1.97	0.32	2.09	0.57	2.18
ISR/09/2022	ME-SA	PanAsia-2	0.57	1.76	0.25	1.92	0.58	2.51	0.33	1.97	0.39	2.18	0.54	2.16
JOR/06/2021	ME-SA	PanAsia-2	0.38	1.54	0.17	1.73	0.25	2.24	0.19	1.82	0.3	1.95	0.56	2.12
JOR/10/2021	ME-SA	PanAsia-2	0.37	1.53	0.22	1.85	0.18	2.09	0.11	1.61	0.23	1.84	0.35	1.92
PAK/78/2019	ME-SA	PanAsia-2	0.33	1.56	0.36	1.97	0.4	2.24	0.32	2.03	0.41	2.14	0.49	1.99
PAK/04/2020	ME-SA	PanAsia-2	0.11	1.1	0.26	1.83	0.39	2.41	0.07	1.41	0.34	2.06	0.59	2.07
PAK/09/2021	ME-SA	PanAsia-2	0.45	1.61	0.15	1.95	0.47	2.58	0.19	1.94	0.32	2.19	0.3	1.92
PAK/12/2021	ME-SA	PanAsia-2	0.81	1.87	0.25	1.72	0.42	2.53	0.25	2.06	0.32	2.19	0.78	2.34
PAT/01/2021	ME-SA	PanAsia-2	0.53	1.78	0.29	2.01	0.36	2.46	0.4	2.01	0.53	2.15	0.72	2.31
PAT/01/2022	ME-SA	PanAsia-2	0.56	1.79	0.26	1.95	0.51	2.61	0.5	2.1	0.64	2.23	0.6	2.23
UAE/01/2021	ME-SA	PanAsia-2	0.38	1.64	0.19	2.02	0.43	2.56	0.48	2.08	0.32	2.14	0.44	2.13
UAE/09/2021	ME-SA	SA-2018	0.59	1.83	0.23	2.1	0.6	2.7	0.44	2.04	0.32	2.13	0.68	2.32
UAE/15/2021	ME-SA	SA-2018	0.75	1.94	0.28	2.19	0.51	2.63	0.56	2.15	0.47	2.3	0.69	2.32

Se	rotype A		A22 Boeh Inge	A22 Iraq Boehringer Ingelheim		A Iran 2005 Boehringer Ingelheim		A GVII 2015 Boehringer Ingelheim		A/TUR/20/ 06 <i>MSD</i>		A aysia 97 hringer elheim	A Eritrea 98 Boehringer Ingelheim		A Saudi 95 Boehringe Ingelheim	
Isolate	Topotype	Lineage	r 1	titre	r 1	titre	r 1	titre	r 1	titre	r 1	titre	r 1	titre	r 1	titre
ETH/25/2019	AFRICA	G-IV	0.27	2.01	0.43	2.21	0.04	0.59	0.13	0.97	NT	-	0.23	2.11	0.11	1.67
ETH/01/2020	AFRICA	G-IV	0.22	1.93	0.45	2.23	0.04	0.53	0.03	0.57	NT	-	0.25	2.14	0.06	1.37
ETH/04/2022	AFRICA	G-IV	0.13	1.68	0.05	1.31	0.07	0.83	0.13	0.95	NT	-	0.29	2.21	0.06	1.37

55 | Page



Se	rotype A		A22	Iraq	A I 20	ran 05	A (20	GVII)15	A/TU C	R/20/ 6	ر Mala ç	A aysia 97	A Er 9	itrea 8	A S g	audi)5
			Boeh Inge	ringer Iheim	Boeh Inge	ringer Iheim	Boeh Inge	ringer Iheim	М	SD	Boeh Inge	ringer Iheim	Boeh Inge	ringer Iheim	Boeh Inge	ringer Iheim
Isolate	Topotype	Lineage	r ₁	titre	r ₁	titre	r 1	titre	r 1	titre	r 1	titre	r 1	titre	r ₁	titre
NIG/16/2020	AFRICA	G-IV	0.55	2.34	NT	-	0.19	1.35	0.09	1.04	NT	-	0.43	2.42	0.51	2.19
NIG/86/2020	AFRICA	G-IV	0.13	1.72	NT	-	0	0	0.08	0.97	NT	-	0.22	2.13	0.37	2.05
NIG/100/2020	AFRICA	G-IV	0.35	2.14	NT	-	0	0	0.13	1.19	NT	-	0.56	2.54	0.47	2.15
SUD/04/2019	AFRICA	G-IV	0.19	1.99	0.14	1.72	0.06	0.75	0.11	1.1	NT	-	0.26	2.09	0.66	2.19
SUD/01/2021	AFRICA	G-IV	0.07	1.56	0.13	1.71	0	0	0.19	1.34	NT	-	0.15	1.85	0.63	2.18
SUD/02/2022	AFRICA	G-IV	0.14	1.84	0.37	2.05	0	0	0.01	0.21	NT	-	0.13	1.78	0.33	1.89
NEP/05/2021	ASIA	G-VII	0.38	2.28	NT	-	0.2	1.47	0.41	1.72	0.15	1.77	NT	-	NT	-
PAK/28/2021	ASIA	Iran-05	0.2	1.95	0.31	2.03	0.61	1.61	0.2	1.27	0.2	1.75	NT	-	NT	-
PAK/29/2021	ASIA	Iran-05	0.14	1.81	0.35	2.08	0.51	1.53	0.21	1.29	0.16	1.66	NT	-	NT	-
TAI/05/2021	ASIA	Sea-97	0.39	1.94	0.07	1.48	0.46	1.49	0.11	0.9	0.33	1.82	NT	-	NT	-
TAI/06/2021	ASIA	Sea-97	0.32	1.85	0.07	1.52	0.5	1.52	0.08	0.75	0.39	1.88	NT	-	NT	-

Sero	type Asia-	1	Asia 1 Shamir Boehringer Ingelheii						
Isolate	Topotype	Lineage	<i>r</i> ₁	titre					
PAK/76/2019	ASIA	Sindh-08	0.45	2.26					
PAK/77/2019	ASIA	Sindh-08	0.48	2.29					
PAK/31/2021	ASIA	Sindh-08	0.44	2.15					
PAK/48/2021	ASIA	Sindh-08	0.38	2.09					

Serot	ype SAT 2		SAT2 Boehringe	Zim 83 er Ingelheim	SAT2 Eritrea 98 Boehringer Ingelheim				
Isolate	Topotype	Lineage	r ₁	titre	r 1	titre			
NIG/14/2020	VII	-	0.32	2.03	0.6	1.8			
NIG/51/2020	VII	-	0.35	2.08	1	2.09			
NIG/01/2021	VII	Lib-12	0.35	2.03	0.71	1.87			
NMB/01/2020	III	-	0.09	1.37	0.1	1.05			



Appendix 3 Nucleotide sequence analysis

FMDV nucleotide sequence data for phylogenetic analysis

Testing Laboratory	Sample Country	Region Sequenced	Total	0	А	C	ASIA-1	SAT 1	SAT 2	SAT 3	FMDV GD	Notes
AHI	Ethiopia	VP1	33	19	9	-	-	-	5	-	-	
	Mali	VP1	2	-	-	-	-	-	2	-	-	
ANSES	Niger	VP1	7	5	2	-	-	-	-	-	-	
ANJEJ	Oman	VP1	87	74	13	-	-	-	-	-	-	
	Tunisia	VP1	13	13	-	-	-	-	-	-	-	
ΑΡΟΑ	Cambodia	VP1	8	8	-	-	-	-	-	-	-	
711 0,71	Vietnam	VP1	4	4	-	-	-	-	-	-	-	
	South Africa	VP1	51	-	-	-	-	-	11	40	-	
ARC-OVI	South Africa	Complete Genome	60	-	-	-	-	30	20	10	-	
	Botswana	VP1	9	-	-	-	-	-	9	-	-	
	Malawi	VP1	3	3	-	-	-	-	-	-	-	
BVI	Mozambique	VP1	20	8	-	-	-	-	12	-	-	
	Namibia	VP1	4	-	-	-	-	-	4	-	-	
	Zimbabwe	VP1	8	-	-	-	-	-	8	-	-	
	Kazakhstan	VP1	2	2	-	-	-	-	-	-	-	
FGI-ARRIAH	Mongolia	VP1	3	3	-	-	-	-	-	-	-	
	Russia	VP1	2	2	-	-	-	-	-	-	-	Orenburg, Russia
LVRI	China	VP1	39	39	-	-	-	-	-	-	-	
	Ghana	VP1	3	3	-	-	-	-	-	-	-	
NCFAD	Ghana	Complete Genome	5	5	-	-	-	-	-	-	-	
PANAFTOSA / VPH	South America	-	6	3	3	-	-	-	-	-	-	historical samples
PD-FMD	India	VP1	56	52	2	-	2	-	-	-	-	
RRL SEA	Thailand	VP1	80	64	16	-	-	-	-	-	-	
	Türkiye	VP1	30	30	-	-	-	-	-	-	-	
ŞAP IIIstitute		Capsid	5	5	-	-	-	-	-	-	-	
	France	VP1	3	3	-	-	-	-	-	-	-	Samples from PTS &
Sciensano	Botswana	VP1	9	3	-	-	-	1	3	1	1	
	United Kingdom	VP1	5	3	-	-	-	-	-	2	-	schemes
	United Kingdom	VP1	18	4	2	-	10	-	2	-	-	All
SENASA	Interlaboratory	VP1	3	2	-	-	-	-	-	1	-	Historical
SEIWISH	SENASA	VP1	3	3	-	-	-	-	-	-	-	samples
	Algeria	\/D1	Λ	Л	-						_	
	Fount	VP1	- 1 12	+ 2	15	-	_	-	-	-	-	
WRLFMD	Ethionia	VP1	33	ر 19	9	_	_	-	5	-	_	
	Indonesia	VP1	35 २		2	_	_	_	-	_	_	
	maonesia	VI 1	5	5								

57 | Page



Testing Laboratory	Sample Country	Region Sequenced	Total	0	А	J	ASIA-1	SAT 1	SAT 2	SAT 3	FMDV GD	Notes
	Israel	VP1	9	9	-	-	-	-	-	-	-	
	Mongolia	VP1	13	13	-	-	-	-	-	-	-	
	Pakistan	VP1	35	19	4	-	12	-	-	-	-	
	Palestine	VP1	12	12	-	-	-	-	-	-	-	
	Sudan	VP1	20	11	9	-	-	-	-	-	-	
	Thailand	VP1	13	8	5	-	-	-	-	-	-	
	Tunisia	VP1	3	3	-	-	-	-	-	-	-	
	United Arab Emirates	VP1	7	7	-	-	-	-	-	-	-	



Appendix 4 Selected phylogenetic trees for 2022

A4.1: Sequencing of viruses associated with outbreaks in Indonesia (O/ME-SA/Ind-2001e lineage)

Data from WRLFMD, MNFMDL, Malaysia and PUSVETMA, Indonesia





A4.2: Sequencing of viruses associated with outbreaks in Thailand

Data from RRLSEA, Thailand





A4.3: Sequencing of viruses associated with outbreaks in China (2020-22)

Data from LVRI, China





A4.4: Sequencing of viruses associated with outbreaks in India

Data from ICAR Directorate of Foot and Mouth Disease, International Centre for Foot and Mouth Disease, India





A4.5: Sequencing of viruses associated with outbreaks in Kazakhstan and Russia

Data from FGBI, ARRIAH, and WRLFMD

Further information is presented in: Tyulegenov et al., (2022) Foot-and-mouth disease in Kazakhstan. Transbound Emerg Dis. 69(4):1712-1714.





A4.6: Sequencing of FMD viruses representing the emerging O/ME-SA/PanAsia-2^{ANT10} lineage in Pool 3

Data from JUST, Jordan, KVRI, Israel and WRLFMD





A4.7: Introduction of O/EA-3 into Tunisia

Data from Laboratoire de Virologie, Institut de la Recherche Vétérinaire de Tunisie, Tunisia, ANSES, France, WRLFMD





A4.8: Diverse serotype SAT2 lineages detected in Ethiopia

Data from AHI, Ethiopia, WRLFMD





A4.9: Detection of the O/EA-3 topotype in Niger

Data from ANSES, France, WRLFMD









Data from OVI, South Africa





A4.11: Serotype SAT3 outbreaks in South Africa (2022)

Data from OVI, South Africa





A4.12: Continued spread of the O/EA-2 topotype in Southern Africa (2022)

Data from BVI Botswana, WRLFMD



*, not a WRLFMD Reference Number

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Appendix 5 The 17th Annual Meeting of the WOAH/FAO FMD Reference Laboratory Network

29th November to the 1st December 2022

Core Members

	WOAH Reference Laboratory for Foot and Mouth Disease, Dirección de Laboratorio
•	Animal, SENASA, Argentina
	Speaker: Sabrina Galdo; Participant: Galdo Novo
	WOAH collaborating Centre for validation, quality assessment and quality control of
	diagnostic assays and vaccine testing for vesicular diseases in Europe, and FAO
	Reference Centre for Vesicular Diseases
	Sciensano, Belgium
	Speaker: David Lefebvre; Participant: Floris Breman
	Retewana Vassina Institute (RVI). Retewana
	DUISWAIIA VACCIIIE IIISIIIUIE (DVI), DUISWAIIA Speaker: Joseph Hyera
	Centro Panamericano de Fiebre Aftosa (PANAFTOSA) and PAHO (WHO and WOAH
OPS OMS	Reference Laboratory for FMD Brazil
PANAFTOSA Salud Pública Veterinaria	Speaker: Edviges Maristela Pituco
	FAO and WOAH FMD Reference Laboratory, National Centre for Foreign Animal
	Disease National Centres for Animal Disease, Canadian Food Inspection Agency,
	Canada
	Speaker: Charles Nfon
	WOAH and China National FMD Reference Laboratory, Lanzhou Veterinary
24	Research Institute (LVRI), CAAS, People's Republic of China
	Speaker: Wen Dang
	WOAH FMD Reference Laboratory, French Agency for Food and, Environmental and
	Occupational Health & Safety (ANSES), France
	FAO Reference Centre for FMD in South Asia, ICAR – Directorate of Foot-and-Mouth
_	Disease Indian Council for Agricultural Research, Mukteswar, Nainital (Uttarakhand)
۲	India
	Speaker: Rabindra Prasad Singh: Participants: Sarayanan Participant: Jaiati Mohapatra
	WOAH/FAO FMD Reference Laboratory, Istituto Zooprofilattico Sperimentale della
	Lombardia e dell'Emilia Romagna (IZSLER). Italy
	Speaker: Santina Grazioli; Participant: Maccabiana Giampietro
	WOAH Reference laboratory for Foot and Mouth Disease, Animal and Plant
	Quarantine Agency (QIA), Republic of Korea
	Speaker: Jong-Hyeon Park; Participant: Sang Ho Cha
	FAO FMD Reference Laboratory, Wageningen Bioveterinary Research, Lelystad,
	Netherlands
	Speaker: Aldo Dekker; participant: Phaedra Eble
	Reference Laboratory for FMD. Federal Covernmental Institute. Centre for Animal
	Health (FGLARRIAH) Vladimir Russian Federation
	Speaker the


FAO Reference Laboratory for FMD in Africa and WOAH FMD Reference Laboratory, Transboundary Animal Diseases Programme, ARC-Onderstepoort Veterinary Institute (ARC-OVI), South Africa Speaker: Livio Heath
Department of Livestock Development, Pakchong, Thailand Speaker: Kingkarn Boonsuya Seeyo
FAO World Reference Laboratory (WRLFMD) and WOAH FMD Reference Laboratory The Pirbright Institute Pirbright, United Kingdom Speakers: Donald King, Anna Ludi, Antonello Di Nardo; Participant: David Paton
WOAH FMD Reference Laboratory, Foreign Animal Disease Diagnostic Lab, Plum Island Animal Disease Center (PIADC), United States of America Speaker: Modou Moustapha, Participant: Jamie Barnabei, Muhamed Fawzi, Robin Holland

Affiliates

* XK	Australian Centre for Disease Preparedness (ACDP), Australia Speaker: Nagendra Singanallur
***	Animal Health Institute (AHI), Ethiopia Speaker: Daniel Gizaw
	Foot and Mouth Disease Laboratory, Kenya Speaker: Abraham Sangula
	National Veterinary Research Institute, Vom, Plateau State, Nigeria Speaker: Hussaini Ularamu
C*	Şap Institute (and WELNET FMD), Ankara, Turkey Speaker: Naci Bulut; Participants: Sena Inel Turgut, Ünal Parlak, Can Çokçalışkan, Beyhan Sareyyüpoğlu
*	ISRA/LNERV, Senegal Speaker: Modou Moustapha

WOAH/FAO Representatives

eofmd	The European Commission for the Control for Foot-and-Mouth Disease
Food and Agriculture Organization of the United Nations Speakers: Melissa McLaws, Samia Metwally: Participant: Ibrahim WoraSalami	
World Organisation WOAH – World Organisation for Animal Health More Animal Health Speakers: Bolortuya Purevsuren, Min-Kyung Park	



PCP Support Officers (PSOs) & Heads of Regional Laboratory Networks/Epi/Lab leaders

Lab Leader, Egypt Participant: Ahmed Refaat Ahmed Habashi	
Epi Leader, West Eurasia Participant: Satenik Kharatyan	
Lab Leader, SAARC, India Participant: Rajeev Ranjan	
PSO, South Sudan, Sudan, Palestine Participant: Kees Van Maanen	

Invited Speakers

USDA	USDA, Fort Collins USA
	Speaker: Sarah Mielke
	FAO FMD Reference Laboratory, Wageningen Bioveterinary Research, Lelystad, Netherlands Speaker: Michiel Harmsen

Vaccine Producers

Boehringer	Boehringer-Ingelheim, VPH Veterinary Public Health
Ingelheim	Participants: Pascal Hudelet
Biogénesis Bagó	Biogenesis-Bago
	Participants: Rodolfo Bellinzoni



TUESDAY 29th NOVEMBER 2022, DAY 1

Opening of the 17th annual meeting and adoption of agenda (Don King)

Opening remarks from Dr King outlined the core activities of the Network: (1) collation/exchange of laboratory epidemiology data, (2) diagnostic test improvement and harmonization, (3) understanding FMD epidemiology and the changing patterns of risk and (4) quality of FMD vaccines

Actions from last year were reviewed.

Action	Progress
Action 021-01 coordinate contributions from the Network to the WOAH Code and Manual – Led by DL, CN, LB-K and SG. The harmonisation of heterologous post- vaccination responses (Paragraph "D. Vaccine matching tests" of Chapter 3.01.08 of the Manual) will be reviewed by the new working group	David is currently working to update these chapters and is currently focusing on the PCR section. It is planned that the revised text will be distributed to the Network for comments and approval.
Action 021-02 Plan to improve ongoing connectivity of the Network to regional laboratories (e.g. regional roadmaps) and the inclusion of more laboratories in the proficiency testing schemes	Hybrid/virtual format of the Network allows for wider representation and contribution to the Annual meeting. Furthermore, additional countries were invited to the 2022 PT schemes organised by the reference laboratories.
Action 021-03 Organise a shipment of samples to WRLFMD to further investigate the re-identification of SAT 1 in East Africa for the first time since 2007.	SAT 1 was not confirmed: samples from ETH tested at WRLFMD during 2022 and no viruses from the SAT 1 serotype were detected.
Action 021-04 Samples to be shipped from NVRI, Nigeria for sequence analysis as soon as possible.	Batches of Nigerian samples have been recently analysed at NCFAD and WRLFMD.
Action 021-05 WRLFMD or Sciensano to provide virus for monoclonal antibody screening to IZSLER so that the antigen ELISA kit can be upgraded.	Open – taken forward in 2022
Action 021-06 Potency tests are expensive with ethical constraints and are being undertaken by a number of partner organisations. From a network perspective, we should consider how we can coordinate	Open – this information will be placed on the website in 2022



these studies and ensure that data are rapidly communicated to support FMD control initiatives. WRLFMD to explore whether this information can be included as a new webpage on the Network website.	
Action 021-07 Please complete a survey to share your opinions on the EuFMD FAST Report: https//www.surveymonkey.com/r/XHVLHNS.	Completed
Action 021-08: FAO will also explore whether larger volumes of post-vaccination sera might be supplied to Network laboratories for use as reference sera.	To be discussed at this meeting and be taken forward by serology/vaccine QA/QC working group.
Action 021-09: It is proposed that the Network re-establish a working-group to cover vaccine selection and quality and the harmonisation of heterologous post-vaccination responses. Proposed members include: Aldo, Charles, Livio, Maristela, Phaedra, Sabrina, Santina, Samia.	Will be taken forward in 2022 with Anna Ludi leading the group as she is now back from maternity leave.

Action 022-01 – WRLFMD to review actions from previous meetings to ensure that they have been closed.

Action 022-02 – WRLFMD to put together a short survey (excel sheet) to list kits used and to the extend they are validated to international standard. Results will be presented next year.

Update from WOAH (Min Kyung Park and Bolortuya Purevsuren)

This presentation reviewed the WOAH global status of FMD where 5 new applications from countries have been evaluated during the 2021-2022 evaluation cycle. Out of the 5 applications, 2 received a positive outcome, which include a new zone recognised as FMD-free with vaccination in Russia and the endorsement of the official control programme in Botswana, which focuses on the northern part of the country that does not have an official FMD-free status. However, FMD outbreaks in Botswana during August 2022 have led to suspension of Zone 6b, which was previously free from FMD without vaccination. Elsewhere, FMD outbreaks in Kazakhstan (zone 5) has led to suspension of the FMD-free status in the zones of the northern part of the country, due to the outbreak in zone 5 and due to implementation of vaccination since June 2022 in the neighbouring zones 1 to 4 previously having and FMD-free status without vaccination. FMD outbreaks which started in April have led to the suspension of FMD-free status in Indonesia.



The presentation also outlined changes to the WOAH Terrestrial Code and Manual, where the latest version of the FMD Chapter (potentially proposed for adoption in May 2023) includes the following changes:

- 1. Provision on introduction of vaccinated animals into countries/zones free from FMD where vaccinated is not practised (only from countries/zones free with vaccination)
- 2. Harmonisation of requirements for official recognition and maintenance of official FMD-free status and endorsement of official control programme by WOAH
- 3. Elaborated provisions regarding the establishment of a protection zone in face of threat
- 4. Recommendations for importation of fresh meat of small ruminants from FMDinfected countries/zone

Changes to the Terrestrial Manual Chapter 3.1.8 on FMD adopted in 2022 included: (1) addition of SVV infection to list of vesicular diseases that cannot be differentiated from FMD and (2) amendment of Table 1 test methods available for FMD diagnostics to qualify that it is essential to perform a confirmatory test (Ag-ELISA or RT-PCR) when virus isolation positive results are obtained.

Dr Purevsuren provided a brief update on the GF-TADs FMD Working Group including the work of the SEACFMD Campaign in Southeast Asia which is current under review.

Update from FAO (Samia Metwally)

This update from the FAO reviewed the FAO-WOAH global FMD control strategy and the work of the regional epidemiology and laboratory networks to combat zoonotic transboundary animal diseases. During the presentation, Dr Metwally requested support from the Network laboratories to review a new document that provides practical surveillance guidelines that are tailored for endemic countries at different/lower stages of the PCP.

Action 022-03 – Network has agreed to review this document.

Global and regional epi and lab networks for zoonotic TADs and emerging pathogen threats have new objectives including preparation of a global action plan to strengthen cooperation, collaboration and information sharing in Africa, Middle East and West Eurasia. FMD Roadmap meetings have been recently conducted for West, Central and East Africa (http://www.gf-tads.org/fmd/events/en/). Country level changes to PCP status were also presented where Georgia has advanced to stage 3, Jordan, Saudi Arabia and Tanzania have advanced to stage 2 and Gambia, Mali and Nigeria have advanced to stage 1.

A new initiative from the FAO and WOAH aims to compile a body of evidence that FMD Serotype C is no longer circulating in livestock populations. A taskforce has been established with members from FAO, WOAH and WRLFMD with 2 phases (1) gathering evidence and measuring risk and (2) reducing risk and maintaining preparedness.

EuFMD update (Kees van Maanen)

Dr van Maanen provided an overview of the work of EuFMD including recent achievements to improve training infrastructure, and national lab capacity for FAST diagnosis. The EuFMD supports the work of the WRLFMD and has also recently contributed to enhanced global surveillance via funding to ANSES and IZSLER for sample collection, shipment, data analysis, as well as PT schemes. Small scale vaccine immunogenicity studies have been



recently completed in Jordan, Palestine and Uganda where the results will be published shortly. Research projects supported under the 10th Fund for Applied Research (FAR) call included: (1) emergency vaccination against FAST disease in disease free countries, (2) enhancing laboratories capacity for FAST diseases, (3) evaluating vaccination approaches strategies and vaccine types for FAST diseases, and (4) digital support tools for optimization of surveillance and other control activities for FAST diseases.

Other topics for discussion:

Nagoya Protocol – impacts and actions (All)

As discussed in previous closed sessions of the Network, the implementation of the Nagoya Protocol (https://www.cbd.int/abs/about/) continues to have relevance for international reference laboratories. It was noted by the Network that Nagoya is already having an impact on our work as the protocol needs to be addressed in any formal MTAs that cover shipping of materials between laboratories. The recent presentation by Dr Hudelet at the EuFMD OS22 highlighted important issues relating to the Protocol on the development of new vaccine strains – that are essential for the control of FMD.

Network partners agree to prepare a position paper with input from the vaccine companies to clearly outline the difficulties that the Nagoya Protocol is causing. Two forms of the document are imagined: (i) a formal review that might be submitted for peer-reviewed publications and (ii) a short summary document to summarise the main issues that might be circulated by WOAH and FAO to CVOs and other government officials. Dr Metwally mentioned that the FAO works with both ministers and CVOs and a summary of the impact could be distributed to them. It was also noted that Nagoya is not just an issue for FMD but also other disease such as ASFV.

Action 22-04 – WRLFMD to draft a Nagoya position paper (and short summary) with contribution from the vaccine companies.

Nomenclature Group Update (Antonello Di Nardo)

Following discussion at last year's Network meeting, a survey was distributed to the Network partners to gauge opinions on the nomenclature that should be recommended for FMDV positive samples and isolates (with 15 responses). Five items were considered important in naming the viruses: serotype, country, year, sequential number of registry and reference laboratory. Three options were presented: (i) continue with the current system where there is inconsistent naming of viruses by different laboratories but perhaps include a laboratory code in the sample ID (ii) follow the results of the survey and use a format that follows Serotype/Country/Sequential no/year lab and (C) using a centralised system to assign sequential names for FMDV samples collected by the Network but this approach would require coordination and resources to maintain such a system, and would also mean that names would be disconnected from the local LIMS used in each of the labs . After discussion, it was agreed that the simplest option would be (ii) and the Network working group will now work to prepare a formal recommendation that accommodates these points.

Action 22-13 – Should the management section on the first day be confidential? Next year there will be no management session. If you disagree, please contact WRLFMD.

Action 22-14 – The working groups: Nomenclature, Serology/vaccine QA/QC, Manual and Code working group could be put on website







The meeting was opened with a welcome address from Dr Matthijn de Boer on behalf of Prof. dr. Annamarie Rebel (Director of Wageningen Bioveterinary Research). The delegates expressed thanks to the meeting hosts, WBVR, and to WOAH, FAO and EuFMD for supporting the meeting. A vote of thanks was also given to Jacqueline Wijbenga at WBVR, and Sarah Belgrave and Julie Maryan at WRLFMD for assistance with the meeting logistics. Sponsorship for the meeting was obtained from Biogenesis Bago, Boehringer Ingelheim and MSD Animal Health.

Update from WRLFMD (Don King)

During 2022, 252 samples from 12 countries have been tested at the WRLFMD. This is in addition to genotyping reports where only sequences were submitted and analysed. These sample numbers are lower than in 2021 and the probably reflect the increased costs and logistics associated with international shipments. Other Network partners confirmed similar observations – which indicate that costs and logistics to receive samples into the Network are more challenging post-COVID.

The presentation focussed on headline epidemiological events that have occurred during 2022:

- A new clade within O/ME-SA/PANASIA-2^{ANT-10} has caused outbreaks in Eastern Mediterranean countries (Jordan, Palestine and Israel). These FMD viruses are most closely related to those found in Pakistan and UAE and this lineage appears to have become more dominant than sub-lineage O/ME-SA/PANASIA-2^{QOM-15} that was previously found in this location.
- There continues to be increased dominance of O/ME-SA/Ind-2001e over other serotype O lineages. For example, in SEACFMD countries there were previously four lineages of serotype O; however, since 2020/2021 only O/ME-SA/2001e has been detected. Indonesia, which has previously been free from FMD (since 1990) has reported its first FMD cases duef O/ME-SA/Ind-2001e. This is a difficult outbreak to control because there are 17.7 million head of cattle in addition to an even larger population of small ruminants. It is anticipated that Indonesia will use vaccine from different manufacturers and will require support from the Network to monitor the performance of these vaccines.
- For Pools 2 and 3, an emerging lineage called O/ME-SA/SA-2018 has been detected in India, Sri Lanka and UAE. There is an increased number of reports for this lineage; however, vaccine matching suggests there is good antigenic match.
- FMD outbreaks in the Maghreb in North Africa have been due to the O/EA-3 topotype and sequence data shared within the Network shows that this is a new introduction that is distinct to cases that occurred in 2018.
- For Southern Africa (Pool 6), the O/EA-2 topotype continues to cause more outbreaks and has now been reported in Zambezi, Namibia, Malawi and Mozambique. Together with cases in Zambia (2018-2021) this is the first detection of serotype O in southern Africa for ~20yrs. These findings are important because serotype O vaccines are not widely used in the region.
- Published reports of FMD cases in Egypt have been characterised as O/EURO-SA and A/EURO-SA: South American viruses. These unexpected outbreaks need to be monitored closely since there is potential for onward spread in North Africa and the Eastern Mediterranean



Pool 1: Southeast Asia (Kingkarn Boonsuya Seeyo)

An increasing number of samples are characterised as from the lineage O/ME-SA/Ind-2001e. Training of scientists from other regional labs is continuing, and this includes biosafety training activities. Research activities include validation of ELISA (specificity and sensitivity). Also, studies are ongoing looking at the antigenic comparison of O/ME-SA/2001 and the locally produced vaccine strains; since there is discussion to switch to using a tailored O/ME-SA/2001 vaccine strain.

Pool 1: East Asia and China (Wen Dang)

Three serotype O lineages of FMDV have been detected since 2020: O/SEA/Mya-98, O/CATHAY and O/ME-SA/Ind-2001, while the last case of serotype A was seen in 2019. During 2022, there has been only one official FMD outbreak reported in China due to O/CATHAY although surveillance has identified positive samples comprising O/SEA/Mya-98 (n=3), O/ME-SA/Ind-2001e (n=12) as well as O/CATHAY (n=24). It is believed that O/Mya-98 is circulating in pigs however no clinical cases have been reported since 2021. The total number of clinical cases is decreasing which could be due to a decrease in illegal animal movement from southeast Asia due to the COVID pandemic.

Pool 1: East Asia and South Korea (Jong-Hyeon Park)

No FMD outbreaks have been reported in South Korea. Samples have been collected for quarantine inspection: RT-PCR (385) and SP ELISA (501,112) and NSP ELISA (505,641). In 2022, three different commercial vaccines were used in cattle and pigs in the country. The sero-positivity using the SP ELISA is increasing, with 97.9% cattle having FMDV-specific antibodies. Testing has continued for NSP antibodies; however, none have been detected during this year. Samples which were typed as O/ME-SA/Ind-2001e have been collected from Vietnam and Cambodia as part of research collaborations. Serotype O vaccine matching was performed on four samples: Laos (2), Vietnam (1) and Cambodia (1) where antigenic match was seen against O-3039 and O/SKR/BE/2017. For A/ASIA/SEA-97 two samples from Cambodia were tested with one being matched against A/SKR/YC/2017. A/ASIA/G-VII (strains received from WRLFMD) did not match against A/SKR/YC/2017. Small scale heterologous *in-vivo* challenge studies using challenge strains of O PanAsia, A Sea-97 and A Iran-05 have been recently carried out. Encouraging data was presented for vaccines from different manufacturers (Boehringer Ingelheim, Biogenesis Bago and ARRIAH).

Question: What is the testing algorithm used for NSP surveillance? Two ELISA kits are used as well as the EITP in very some instances which allow false positives to be excluded.

Pool 1: Russia (tbc)

In December 2021, there was an FMD outbreak in Orenburg Oblast due to a O/ME-SA/Ind-2001e lineage virus. Samples have been tested from Russia (152), Kazakhstan (2) and Mongolia (3); which all represent closely related viruses in the O/ME-SA/Ind-2001e lineage. Vaccine matching for three of these strains confirms an antigenic match to O/Kazakhstan/2010 (O/Pan Asia 2) and O/Zabaikalsky 2016 (O/Ind-2001). 40,000+ serological samples have been submitted from Russia as part of surveillance, and additionally cattle and buffalo serological samples from Pakistan have also been tested for VNT and LPBE SP. During 2022, Russia has supplied kits to Belarus, Bangladesh and Russia.



Pool 2: India (Rabindra Prasad Singh)

Serotype O, A and Asia 1 FMD viruses were detected in 2021 and 2022. Lineage O/ME-SA/Ind-2001d has not been seen since 2018 and appears to have been replaced with O/ME-SA/Ind-2001e. After only being identified in a few states in 2019/2020, the emerging O/ME-SA/SA-2018 lineage has now been detected in many Indian states and there is almost an equal number of Ind-2001e and O/SA-2018 outbreaks. In addition, FMD viruses related to O/ME-SA/PanAsia have been detected Jammu and Kashmir. For serotype A, the dominant lineage is G-18/non-deletion/2019. For Asia 1, it is Group IX, which was first reported in Bangladesh. Overall, there has been an increase in number of outbreaks (almost 8-fold) compared to last year and there has been an increased in number of outbreaks due to serotype A. The percent match for vaccine matching against serotype A is 40%, with a 100% match for serotype O and Asia 1. The laboratory has recommended to change the serotype A vaccine strain used in the country. The laboratory also carried out within country serological PTS with 10 laboratories.

Action 22-05 – ICAR-DFMD to send sequences of PanAsia related isolates from Jammu and Kashmir to WRLFMD.

Pool 3: Turkey (Naci Bulut)

Only serotype O FMD outbreaks have been reported in Turkey during 2022. The Thrace region remains free from FMD with the used of vaccination since 2010. The laboratory has tested 148 samples from the Anatolia region which were from 86 field outbreaks. Most samples have been characterised as O/ME-SA/PanAsia-2^{QOM-15} and the remainder are O/ME-SA/PanAsia-2^{ANT-10}. Vaccine matching suggests that there is a good match with the locally produced vaccines. No serotype A viruses have been detected since 2018 and no Asia 1 since 2015. Sera is routinely collected 30 days post-vaccination. Under this scheme, over 107,000 samples have been tested by LPBE and NSP ELISA. There has been a sharp decline in prevalence by NSP in young animals (4-11months) which correlates with a decrease in the number of outbreaks in Anatolia. Elsewhere in Pool 3, for Pakistan, Iran, and Afghanistan there is very low vaccination coverage achieved (less than 50% coverage). There is a big gap on the sample submission to regional lab as no regional submissions have been received to the Sap Institute during this period. During 2022, three potency invivo studies have been performed with new potential vaccine strains. A study has also been carried out to investigate the duration of immunity conferred by the Sap Institute FMD vaccine. The best results were seen when a $6PD_{50}$ vaccine was used with a booster and no maternal antibodies were present.

Pool 4: Kenya – East Africa (Abraham Sangula)

In Kenya there have been reports of FMD outbreaks due to serotype O (n=13), serotype SAT 1 (n=4) and serotype SAT 2 (n=14). SAT 2 is becoming more dominant in the country, which is a change from past years where serotype O was dominant. However, additional samples (n=49) have not yet been serotyped and all samples collected during 2022 need to be sequenced. Surveillance carried out for suspect outbreaks includes VNTs and NSP ELISAs. Vaccine matching for serotype O (by VNT) shows a match which OK77/78. Four homologous *in-vivo* potency studies have taken place with >6 PD₅₀ values.

Action 22-06 – Send the latest batch of samples to WRLFMD.



Pool 4: Ethiopia – East Africa (Daniel Gizaw)

The name of the laboratory has changed to the Animal Health Institute (AHI), to combine responsibility for national animal health diagnostics with the National control and eradication of tsetse fly and trypanosomosis. Outbreaks for FMD have been reported in most of the country where the following serotypes have been identified: O (n=67), A (n=33) and SAT 2 (n=22). Based on sequencing completed by WRLFMD, the current lineages circulating are: A/AFRICA/G-IV, O/EA-3, O/EA-4, SAT 2 XIV, SAT 2 XIII and SAT 2 VII^{Lib-12}. Serotype SAT 1 was last seen in 2007.

Pool 5: Nigeria – West Africa (Hussaini Ularamu)

Recent samples tested by NVRI comprise serotype O (n=10), serotype A (n=5) and serotype SAT 2 (n=5). SAT 1 has not been seen since 2015. Surveillance samples have also been submitted for 3ABC NSP ELISA; approximately 50% of sera were positive. A new risk to the area is an increase in the number of animal movements from the Central African Republic. ISO17025 accreditation has been obtained for NSP ELISA.

Pool 4-6: Sub-Saharan Africa (Livio Heath)

This presentation covered the recent FMD outbreaks that have been reported in South Africa. The SAT 2 outbreaks have been going on for almost two years; with 119 outbreaks in KwaZulu-Natal caused by viruses that are closely related to those recovered from cases in 2021. SAT 3 outbreaks have occurred in Limpolo and the central provinces of North-West, Gauteng, Mpumalnga and Free State. A total of 1,175 clinical samples have been tested by OVI, with 11 samples typing as SAT 2 and 55 typing as SAT 3. Currently South Africa is using BVI vaccine, where the original plan was not to deploy vaccines outside of the buffer zone; however, vaccination outside of this zone has now started. Buffalo have not been implicated in all outbreaks and anecdotal evidence suggests that the viruses are being maintained within the cattle population. Since illegal animal movements have been implicated in some of the outbreaks, a new identification system for cattle is being implemented.

Surveillance has results in the testing of >200,000 samples for SPCE and >7,000 samples for NSP. For tracking outbreaks, SP-ELISA has been implemented as the first test followed by NSP ELISA. OVI has also performed serological testing in support of regional surveillance and trade purposes for samples from: Eswatini, Malawi, Lesotho, Mozambique and Zimbabwe.

Discussion – at this stage vaccination is only a single vaccine dose is administered since the policy is vaccination to slaughter. However, this may change to vaccinating animals twice.

The outbreaks are mostly in cattle but have also been seen in small ruminants (particularly sheep). There are some reports of FMDV circulation in buffalo, but this is only for serotype SAT 2 in the North of the country. Wildlife has not been tested since they are not considered important maintenance hosts.

Pool 4-6: Sub Saharan Africa (Joseph Hyera)



Submissions have been received from five countries with the following lineages: O/EA-2 found in Malawi and Mozambique and SAT 2 topotype 2 in Botswana, Zimbabwe, Mozambique and Namibia. Serological surveillance took place in Malawi, Mozambique and Botswana. Recent data highlights that the O/EA-2 topotype has moved from pool 4 to pool 6 and is currently considered as a high threat. Vaccine matching suggests that O1 Manisa is a good match for representative O/EA-2 field isolates.

Pool 5: Update Senegal (Modou Moustapha)

There have been no submissions from suspect FMD cases during 2022 because field veterinarians are on strike and will not send samples for laboratory testing.



WEDNESDAY 30th NOVEMBER 2022, DAY 1

Pool 7: South America (Sabrina Galdo)

During 2022, suspect FMD samples (n=18) were submitted to SENASA but no FMD virus was detected and these were diagnosed as poxvirus cases. Active surveillance occurred for 4,000 samples, with 134 positives on the 3ABC ELISA which were all subsequently negative on EITB (i.e., false positives). Ninety samples were tested by VIAA antigen AGID for export; these were all negative. Samples from Pirbright were sequenced and these will later be used for vaccine matching.

Serotype C3 Indaial is currently included in the vaccine formulation as it is believed that additional virus strains in the formulation may improve the performance of high potency monovalent FMD vaccines (see: Di Giacomo et al., 2022). A decision on whether to continue to use serotype C has not yet been decided. Two potency studies (PD₅₀) using trivalent vaccine and challenging with homologous strains have occurred; in both cases the results were above 6PD₅₀.

Pool 7: South America (Edviges Maristela Pituco)

In 2022, no samples of suspected FMD were received. Support has been given to Chile to identify Seneca virus A (manuscript has been published) where the incursion of the virus appears to be from the south and not connected to the USA. Venezuela is greatest concern for vesicular disease; between 2011-2017 seventy-two epithelial tissues were sent and these were all VSV.

The outbreak of the FMDV serotype O/EURO-SA in Egypt has been characterised and the closest sequence is O/Auauca/Colombia/2017 although currently there are no outbreaks in Colombia. The serotype A found in Egypt has a closest genetic relative to isolates collected in Venezuela. Phylogenetic trees were presented highlighting a evolutionary gap in sampling that could represent virus replication in Venezuela or Egypt.

Discussion: Seneca Valley vaccines are being developed. These are promising and show good performance. For vesicular stomatitis, vaccines against the New Jersey serotype already exist but are restricted to the Andean region.

Action 22-07 – The risk assessment, which concludes that serotype C poses an insignificant risk, will be shared with the network.

Update from SCIENSANO (David Lefebvre)

No FMD suspect cases have been received. A WOAH Twinning project between SCIENSANO and the National Veterinary Laboratory in Burundi has been accepted. This project will start when funding becomes available (date to be confirmed).

Update from ANSES (Labib Bakkali-Kassimi)

Samples received by ANSES from Tunisia were characterised as serotype O/EA-3 and represent a new incursion of this topotype into North Africa. Additional samples were received from Niger (serotype O/EA-3, A/G-IV), Mali (SAT 2/VII) and Oman (O/ME-SA/SA-2018, O/ME-SA/Ind-2001e, A/Africa/G-I, O/EA-3, and O/ME-SA/PanASIA-2^{Ant-10}). ANSES have also carried out NSP surveillance for Niger and Oman. As the EURL for FMD, ANSES organises a PTS that is distributed to 46 laboratories (40 countries).



Discussion: The A/AFRICA/G-I strains in Oman are closely related to isolates from the Bahrain quarantine station (originally from East Africa) and it is not clear how the virus entered Oman. It could be that two different incursions have occurred from East Africa. Suggestion was made to make contact with the laboratories in Eritrea, and Somalia to seek further samples for characterisation.

Update from IZSLER (Santina Grazioli)

No clinical samples for field cases of FMD have been received.

During 2022, there has been close collaboration with EuFMD to carry out post-vaccination trials and improve laboratory preparedness. No in-person training has been carried out; however virtual training to update field laboratories in Northwest Syria has occurred. Five percent of samples in Syria were negative for both SP and NSP; all others (app. 1200 samples) were positive for FMD antibodies. Twenty sera from Mauritania were tested, and all were FMDV negative. Compared to 2021, supply volumes for the IZSLER kits has increased, but the levels are still not back to pre-COVID pandemic levels. The requests for kits are mostly for SP-ELISA type O. The current kits don't recognize SAT 3 but work to find new monoclonal is underway and can be anticipated to replace serotype C in the kit. IZSLER hosts the reagent bank for improved emergency diagnostic response in Southeast European countries (includes PCR reagents).

Discussion: For the LFDs the panFMD detects serotype C. There is no market to make an LFD that just detects serotype C. Lateral flow for SAT 3 is more important as panFMD covers serotype C. LFD works well on clinical sign (epithelial or fluid); however, sensitivity is lower than PCR.

Action 22-08 – The network should keep track of the LFDS that are being developed and validated.

Update from FADDL/APHIS, Plum Island (Muzafar Makhdoomi)

During 2022, FADDL has tested 2,537 suspect samples but none were positive for FMD. No vaccine matching has taken place but carried out one PD₅₀ (serotype O homologous challenge). Currently there are two vaccine banks managed by FADDL: the North American Foot and Mouth Disease Vaccine Bank (NAFMDVB, Canada and USA) and the National Vaccine and Veterinary Countermeasures Bank (NAVVCB). The Foreign Animal Disease Diagnostic Course has been held this year, which may be supplemented with virtual training content in the future. The laboratory carried out a site visit to Columbia to improve biosecurity, surveillance and movement control. During mid to end of 2024, all FMD activities will move to NBAF in Kansas; however, there will be duplication of capacity at both sites for a certain amount of time. The laboratory would also like to host the FMD Network Meeting at NBAF once they have moved.

Discussion – If possible, in the future, it would be great to include results from endemic areas (from the research group).

Introduction from WBVR, The Netherlands (Aldo Dekker)

No suspicious samples were submitted to WBVR during 2022. The laboratory has carried out one *in-vivo* potency studies for commercial reasons – with confidential results. WBVR have also carried out a prime/boost multivalent study for WRLFMD (as part of the on-going



twinning project with AU-PANVAC). In regard to standardizing serology, sera are available from potency tests for various strains however there are limitation on how these could be shared (due to commercial restrictions). The lab is working with IZSLER to look at standardising sera that could be used to calibrate the results for ELISA.

Discussion: Should animals be kept separately after challenge to prevent transmission of FMD between the study animals? Currently there is no legal document to stipulate this and there are ethical difficulties in housing animals separately.

Action 22-09 – WBR (Aldo Dekker) to review animal studies and prepare a report highlighting the evidence for keeping animals separate after infection.

Update from NCFAD (Charles Nfon)

During 2022, samples have been submitted from Canada and Ghana. The samples from Ghana were characterised as belonging to the O/EA-3 topotype. The vaccine matching test is up and running and the laboratory would like to harmonise their methods with other Network laboratories. NCFAD currently have an ongoing project looking at a machine-learning approach to predict vaccine matching results using only sequence data – initial results for serotype O and A indicate that the tool can predict vaccine matching status for up to 90% of field isolates.

Update from CSIRO (Nagendrakumar Singanallur Balasubramanian)

No suspect cases were submitted to CSIRO. Coordinated projects include a regional Southeast Asia proficiency testing program, which includes 8 specific pathogens (FMD is one of these). This includes 23 countries: South Asia (6), Southeast Asia (10), East Asia (6) and Pacific (1). Publications from the laboratory include the validation of assay (specifically on sensitivity/specificity) and system-based approach to assess host response.

General topics for discussion

Review of Serotype C project (Sarah Mielke)

Serotypes C FMD viruses have not been detected anywhere in the world since 2004 and a previous publication co-authored by the Network has proposed that this serotype may now be extinct. This presentation described the results from a study conducted by USDA to understand whether data from the Network can be used to substantiate a claim of serotype C extinction. The analysis uses surveillance data from the WRLFMD (1942-2021) and the Network (2012-2020) for regional pools 1-6 to build a framework to analyse the data grouped by pool at three levels of data summary, (a) by year and country, (b) combined over years for each country, and (c) combined over years and countries within a pool. This work supports claims of freedom from FMD serotype C at different scales with varying degrees of certainty by combining data with explicit epidemiological assumptions. Assumptions were (1) risk of introduction for serotype C is equal across years and (2) outbreak data in key countries represents the entire RVP. Three detection prevalence thresholds were used (1%, 2% and 5%) where the analysis tested the 95% probability of detecting serotype C. Using an unstratified approach (year and country) results support serotype extinction in all 6 regional pools, but when looking specific countries (not year) the evidence become less well supported where many countries do not reach 95% probability (at the different prevalence thresholds). The purpose of the talk was to present these data to the Network and to request



for feedback on the assumptions that were made, and to review the specific data for the endemic pools.

Action 22-10 –Share document with network – with the request that Network partners provide feedback - at least for one endemic setting

Opportunities for enhanced surveillance using LFDs - review/feedback on inactivation protocol (Aurore Romey)

It is widely recognised that global surveillance of FMD could be enhanced by using lateral flow devices (LFDs) to collect FMDV genomic material that can be further analysed when these devices are sent to a laboratory. Shipping FMDV-positive LFDs requires careful consideration to ensure that biosafety risks are minimised. From previous studies it has been found that LFDs soaked in 0.2% citric acid for 15 minutes inactivated FMDV, but diagnostic assays can still be carried out. For further validation this approach, LFDs and inactivation protocols were implemented in the field (Nigeria, Turkey and Pakistan). Virus could not be isolated using cell culture after citric acid inactivation; however, infectious virus could be recovered via transfection in some of these samples (using ZZR cells). *In vivo* studies at FLI show that RNA can be infectious when injection but not by non-invasive exposure. A protocol to describe this method has been approved by EuFMD STC. To ensure application of inactivation protocol in the field three actions could be implemented: (1) certificate stamped and signed by the veterinary services (2) sending directly the tube containing LFD in the citric acid solution and (3) adding a pH indicator on the LFD.

Discussion: In certain countries (Italy, UK and USA), full length RNA is considered an infectious pathogen and therefore shipments will still need to come under IATA regulations. However, shipping of these LFDs without dry ice is still a huge advantage and cost saving. It was agreed that the Network should provide opinion on the inactivation protocol and highlight any local/national restrictions that might have impacts on the international shipment of LFDs.

Action 22-10 - ANSES to prepare a survey that will summarise the different national restrictions and opinions on the specific controls that should be adopted to minimise the risk of sending LFD shipments

Thursday 1st December 2022, DAY 3

General topics for discussion (cont.):

FMD Vaccine Quality Control

Alternative tools for FMD vaccine QA/QC (Michiel Harmsen)

This presentation summarised the use of llama heavy-chain antibodies (VHHs) to directly assess the integrity of FMDV capsids using reagents that recognise epitopes that are present on 146S and 12S components. This direct immunoassay approach addresses the ethical and costs concerns associated with FMD vaccine batch testing via immunisation studies animals. A range of VHHs are now available for FMDV which offer (1) low limit of detection, (2) higher throughput (3) serotype and often strain specific and (4) and ability to assess the quality of VLP vaccines as well as conventional vaccines. Some of these



serotype-specific reagents are broadly reactive while others are highly strain specific and therefore a different VHH may be required for each vaccine. The presentation also highlighted VHHs that could be used to discriminate between 75S (empty particles, no RNA) and 146S. The current format of these tests uses a double antibody sandwich (DAS) ELISA and the use of heat treatment can used to qualify 12S and 146S components. Beyond their use of vaccine QC, the VHHs could also be used for epitope mapping. In the future, it is anticipated that secondary phage libraries will be used to improve strain recognition.

Heterologous cut-offs and inter-lab variability (Anna Ludi)

This talk described results from a recently published collaborative paper involving Network partners: "Predicting cross-protection against foot-and-mouth disease virus strains by serology after vaccination" (Gubbins, 2022). The aim of this paper is to understand the correlation between heterologous *in-vivo* potency studies and virus neutralisation tests. Using data generated from 17 vaccine heterologous potency studies, the average heterologous neutralising antibody titre associated with 75% protection ranged from 1.17 to 2.46 log₁₀. Although it was not possible to define a common threshold, it was noted that the data were more consistent if data from two outlier O Manisa studies was removed. Further cross-protection data are needed to understand the factors that underpin this variability and to develop more robust antibody thresholds.

The presentation also described results from a project funded by EuFMD which studied the reproducibility of the FMD VNT in European laboratories. Variable results were observed when the same sera were tested against the same viruses in different FMD reference laboratories. Harmonisation of methodology and re-calibration of results based on the use of reference sera will be explored to try to reduce these differences.

Action 22-11 – The Network Working Group on vaccines/serology will look at standardised sera, as well as other options to calibrate and harmonise the data across laboratories.

Do FMD vaccines cover regional risks? (Don King)

FMD vaccines provided from different suppliers often contain different vaccine strains (with different potencies and formulation). Vaccine matching studies undertaken by Network partners assess the antigenic suitability of vaccine strains to cover genetically diverse field strains. However, the extent of vaccine matching is very limited due to difficulties to access BVS and vaccine viruses and therefore many FMD vaccines used in endemic settings are usually not tested. The Network meeting in 2019 endorsed the concept of reference antigen panels that might be used to test vaccines by assessment of heterologous VNT titres. This presentation summarised work from the WRLFMD where an antigen panel has been implemented for Eastern Africa as part of a twinning project with AU-PANVAC. This approach can be used to highlights poor quality vaccines and gaps where current vaccines do not cover key FMDV lineages in the area.

PRAGMATIST for antigen bank managers has now been developed (Ludi et al., 2022). Work is now underway to modify this tool for endemic settings using an approach that will adopt regionally relevant reference antigens.



Discussion: The Network should agree on virus reference antigens for the global pools and share these viruses within the Network. Work to continue to collect representative post-vaccination sera is also a priority.

Informatic tools for FMD

Updates on FMD Dashboard (Antonello Di Nardo)

WRLFMD (with support from EuFMD) has developed a range of dashboards for FMD. The system currently hosts 3 applications: FMDbase, FMDtype and PRAGMATIST. These will be pulled together into an openFMD App in 2023. In 2023, a FMD Surveillance Dashboard will be developed, to present data on FMD outbreaks (contemporary and historical) with the possibility to link to this other tools.

Action 22-12 Feedback needed on the nomenclature options 1, 2 or 3

SEACFMD dashboard (Bolortuya Purevsuren)

A demonstration of the SEACFMD dashboard was provided which shows information on FMD outbreaks in Southeast Asia (per year, etc). The system has different streams that can be adjusted to fit the background of the user (example policy maker, animal worker, etc.), and also displays upcoming events and a toolbox that includes communication material (in local languages).



Review of regional and FMDV lineage distribution information (Notes for Annual Report)

Suggested changes per serotype are highlighted below:

Serotype O

- For O/EA-3 include Gulf States of the Middle East on the map
- Add ME-SA/2018
- Show movement of O/EA-3 out of Africa

Serotype A

Add A/AFRICA-GIV

Changes per pools are highlighted below:

Pool 1

- Ind-2001e two new arrows: (1) Indonesia story (risk area further east/south), (2) Mongolia into Kazakhstan and Russia
- Antigenic variability within serotype A has led to switch in vaccine stain for Packchong
- Asia 1 is absent from the region

Pool 2

- Increased number of outbreaks caused by O/SA-2018 (40%) vs Ind-2001e (60%)
- Risk of O/SA-2018 moving into Southeast-Asia
- Highlight spread to pool 3
- Group IX of Asia 1 is causing recent outbreaks
- 95% of outbreak are from serotype O; however, A also recently detected.

Pool 3

- G-VII not detected by any laboratory since 2018; should importance be decreased?
- A IRN-05 has had a switch in antigenicity with a decrease in A IRN-05^{FAR 13} cases and an increase in A IRN-05^{FAR 11}
- Potential introduction of East African viruses into the region (serotype O and A through trade with Gulf States).
- Asia 1 circulating in Pakistan (60% serotype Asia 1 but the last time more balanced between the 3 serotypes). We may see an increase in Asia 1 outbreaks as the current immunity will be low due to only a few outbreaks being seen
- Possibility of South American strains in Eastern Mediterranean countries from Egypt (serotype O and A)

Pool 4/5

- Serotype O is predominant serotype followed by SAT 2 then A (serotype O 50%, serotype A 25%, serotype SAT 2 25%)
- O-EA-3 is dominant over O-WA (2015/2017 last detected)
- O/EA-2 big arrow into Southern Africa has a potential route
- SAT 1 south of Nairobi
- SAT 1 topotype X geographic restricted and little evidence it is circulating
- SAT 2 could potentially spread North
- For serotype A, A/Africa-G-IV is the most dominant
- Gap in surveillance in West and Central Africa also towards the East (difficulties collecting the samples and shipment)

Pool 6a

- Increase risk of O/EA-2
- Risk of SAT 2 and SAT 3; Botswana has a different lineage of SAT 2
- SAT 2 outbreak appears to be spreading from domestic animal to domestic animal rather than involvement of buffalo

Pool 7

• Serotype O and A in Egypt at the same time, may help to give light with what is happening in Venezuela (serotype O and A). No new risk for pool 7.

General Comments

- Gap that we don't have coordinates for the WRL data excel sheet will help to collect more of this data.
- Maybe these maps should go on website