



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

Annual Report 2016

Editors:

Dr Donald King and Dr Mark Henstock,
The Pirbright Institute, UK



OIE/FAO FMD Reference Laboratory Network



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1 OIE/FMD Reference Laboratories Network

1.1 Principle Goals

The Network of OIE/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 2016 - 31st December 2016

1.3 Collated input from

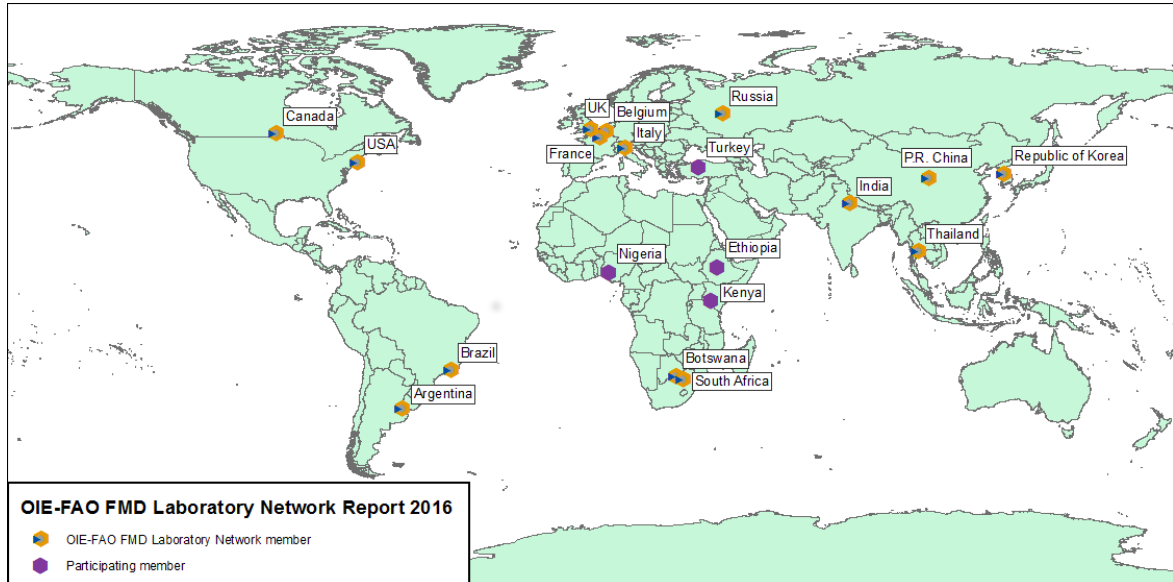


Figure 1-1: Participating laboratories



OIE Reference Laboratory for Foot and Mouth Disease, Dirección de Laboratorio Animal

SENASA, Argentina



OIE 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

CODA-CERVA, Ukkel, Belgium



OIE Regional Reference Laboratory for Sub-Saharan Africa (RRLSSA)

BVI, Gabarone, Botswana



Centro Panamericano de Fiebre Aftosa (PANAFTOSA) and OIE Reference Laboratory for FMD

Rio de Janeiro, Brazil



FAO FMD Reference Laboratory

National Centre for Foreign Animal Disease National Centres for Animal Disease, Canadian Food Inspection Agency, Winnipeg, Manitoba, Canada



OIE and China National FMD Reference Laboratory

Lanzhou Veterinary Research Institute (LVRI), CAAS, Gansu, People's Republic of China



OIE FMD Reference Laboratory

French Agency for Food and, Environmental and Occupational Health & Safety (ANSES), Maisons-Alfort, Paris, France



FAO Reference Centre for FMD in South Asia

Project Directorate on FMD (PDFMD), Indian Council for Agricultural Research, Mukteswar, Nainital (Uttarakhand), India



OIE/FAO FMD Reference Laboratory

Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER), Italy



OIE Reference laboratory for Foot and Mouth Disease

Animal and Plant Quarantine Agency (QIA), Anyang city, Gyeonggi-do, Republic of Korea

FAO Reference Centre for FMD for
Central Asia and West Eurasia and OIE
Reference Laboratory for FMD



Federal Governmental Institute, Centre for Animal
Health (FGI ARRIAH), Vladimir, Russian Federation

OIE Regional Reference Laboratory for
Foot and Mouth Disease in the South
East (RRLSEA)



Department of Livestock Development, Pakchong,
Thailand

FAO Reference Centre for FMD and other
vesicular diseases for the Americas and
the Caribbean and OIE FMD Reference
Laboratory



Foreign Animal Disease Diagnostic Lab, Plum Island
Animal Disease Center (PIADC), Greenport, United
States of America

FAO Reference Laboratory for FMD in
Africa and OIE FMD Reference
Laboratory



Transboundary Animal Diseases Programme, ARC-
Onderstepoort Veterinary Institute (ARC-OVI), South
Africa

FAO World Reference Laboratory and
OIE FMD Reference Laboratory



The Pirbright Institute Pirbright, Surrey, United
Kingdom

Additional input kindly supplied by:

NATIONAL Animal Health Diagnostic &
Investigation Center (NAHDIC)



Sebeta, Ethiopia

National Veterinary Research Institute



Vom, Plateau State, Nigeria

Foot and Mouth Disease Laboratory



Embakasi, Kenya

ŞAP INSTITUTE (and WELNET FMD)



Ankara, Turkey

2 Genetic and antigen diversity and global distribution of foot-and-mouth disease viruses

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. 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 viruses to 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 **OIE/FAO FMD Laboratory Network** along with commercial vaccine and diagnostic providers. The worldwide distribution of the different serotypes and variants of FMD virus (as compiled in 2016) and the associated activities of the Network laboratories are presented in this report.

2.1 Introduction

Global surveillance undertaken by the OIE/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	EurAsia including the Middle East
Pool 4	Eastern Africa
Pool 5	Western Africa
Pool 6	Southern Africa
Pool 7	South America

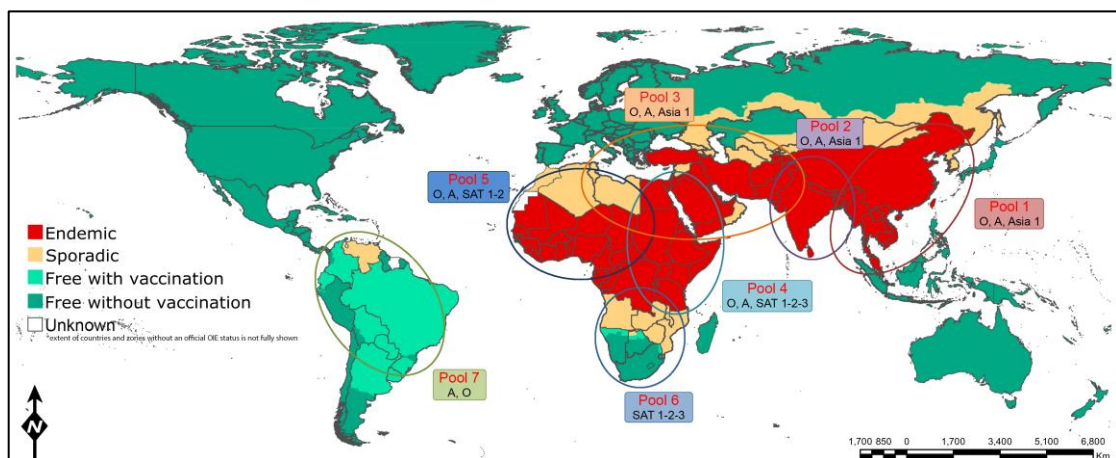


Figure 2-1: Distribution of the seven endemic pools of FMD showing conjectured status of FMD in countries during 2016. Virus circulation and evolution within these regional virus pools results in changing priorities for appropriately adapted vaccines. Periodically, viruses spread between pools and to 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). There is some overlap between pools 4 and 5.

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 the Americas, is now enabling a targeted approach to be applied to the 'Progressive Global Control of FMD' initiative overseen by the OIE and FAO and for which the Network laboratories will play a pivotal role.

Overview of the Global situation in 2016

Information regarding contemporary FMD outbreaks can be found on the World Animal Health Information Database (WAHID) located on the OIE website (http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home), as well as the EMPRES Global Animal Disease Information System (<http://empres-i.fao.org/>)

provided by FAO. Further supplementary data and updates are generated on a monthly basis by EuFMD

(<http://www.fao.org/ag/againfo/commissions/eufmd/commissions/eufmd-home/fmd-surveillance/situation-reports/en/>).

During 2016, 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 OIE WAHIS Interface: http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home/indexcontent/newlang/en, summarised in Figure 2-2 and described elsewhere in this report). *Additional disease outbreaks in countries in the FMD endemic pools have also been reported to OIE during 2016 (data collated in Table 2-1).*

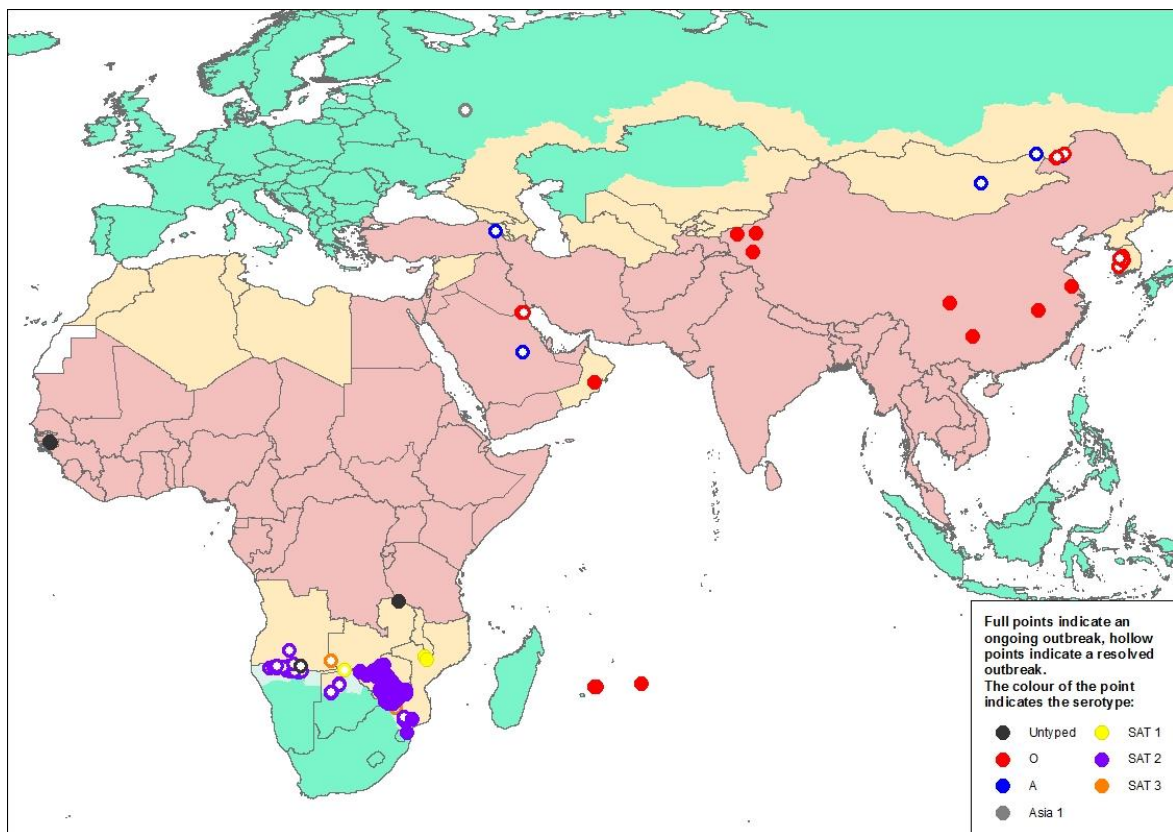


Figure 2-2: Map indicating the location of significant epidemiological events and disease outbreaks reported to OIE in immediate notifications or follow-up reports in 2016 (data available from: http://www.oie.int/wahis_2/public/wahid.php/Diseaseinformation/Immsummary).

Table 2-1: New FMD outbreaks reported to OIE during 2016 (data retrieved from WAHID on www.oie.int on 23rd March 2017). Note: not all outbreaks shown in Figure 2-2 are collated in this table and data may be incomplete

Country	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Total
Afghanistan			1	7	17	13				...			38
Angola			1										1
Bhutan			11							...			11
Burkina Faso	7		1	2	1		12	13	8	1	5	5	55
Cambodia	7	6	5	1	3	8	11	16	17	5	6	14	99
Central African Republic			+..							+..			+..
Chad			0					1					1
Congo (Dem. Rep. of the)			3							...			3
Cote D'Ivoire	3	9								...			12
Egypt	17	8	10	1	6					...			42
Eritrea			0								1		1
Ethiopia			8							...			8
Ghana			2							...			2
Guinea-Bissau			?							...			?
Iran			4697							343			5040
Iraq	60	153	187	67	107	45	39	5	3	14	1	4	685
Kenya		3			7	7	14	4	13		5		53
Kuwait	11	1								...			12
Malaysia	1	2	2	2	5	8				...			20
Mali			0					8		1			9
Mauritania			?							?			?
Mauritius			0				158	4	1				163
Myanmar			1				1	2	2	3	2	1	12
Nepal	9	4	4	6	7	6				...			36
Niger			+..							...			+..
Nigeria			+..					1	1			1	3
Palestinian Auton. Territories		1									1		2
Saudi Arabia			+							...			+
Senegal			2							0			2
Somalia			15							...			15
South Africa	2	0	0	0						...			2
Sudan	2	2								...			4
Tanzania	2	4	5	4	2	4				...			21
Thailand	19	11	9	8	5	3				...			55
United Arab Emirates	1		1						1				3
Vietnam	4	9	10	1	6	1			1	3		1	36
Zimbabwe						1				...			1

Legend for Table 2-1

0	Continuing previous outbreak (s)
...	No information available for this disease
0	Disease absent
?	Disease suspected but not confirmed
+?	Confirmed infection/infestation without clinical signs
+..	Disease present but without quantitative data
+	Disease present with quantitative data but with an unknown number of outbreaks
+()	Disease limited to one or more zones
+?()	Infection/Infestation in one or more zones
?()	Disease suspected but not confirmed limited to one or more zones

Further details of many of the characterisation of viruses retrieved from these outbreaks are provided later in this report.

In South America, there continues to be tangible progress of the regional control programme to achieve FMD-free status since no clinical cases due to FMD have been reported in 2016, and it is now several years since any outbreaks have been reported across the entire continent (the last reported outbreaks were serotype A in Venezuela in March 2013 and serotype O in Paraguay in December 2011).

Long distance trans-pool viral movements

The **OIE/FAO FMD Laboratory Network** has recently detected a number of viral lineages that have emerged from their established endemic pools to cause field outbreaks in geographically distant locations (the main events are summarised in Figure 2-3). There is probably no single factor that underpins these changes, but these dynamic transboundary patterns are probably influenced by the migration of people in North Africa and the Middle East due to the escalation of regional political crises, as well as new trading patterns and demand for animal protein that arise due to increased prosperity in East Asian countries. These unexpected outbreaks caused by emerging viral lineages reinforce the importance of surveillance activities undertaken by the Network.

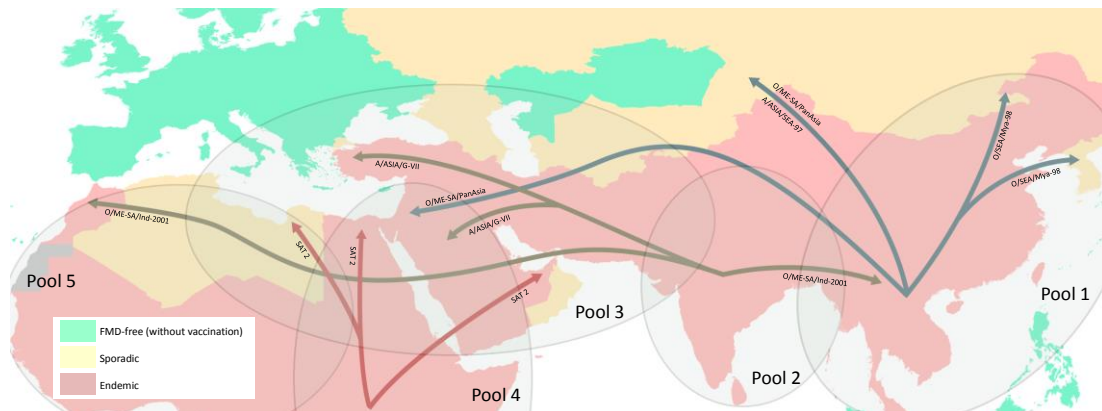


Figure 2-3: Long distance FMD virus movements within Asia and Africa (2009-2016). The different coloured arrows represent viruses from sub-Saharan Africa (red), Indian sub-continent (brown), and Southeast/East Asia (blue) that have moved into new geographical locations outside of the endemic pools (represented by shaded ovals) where they usually circulate.

2.1.1 Official status of countries and zones during 2016

The official status of OIE member countries is shown in Figure 2-4

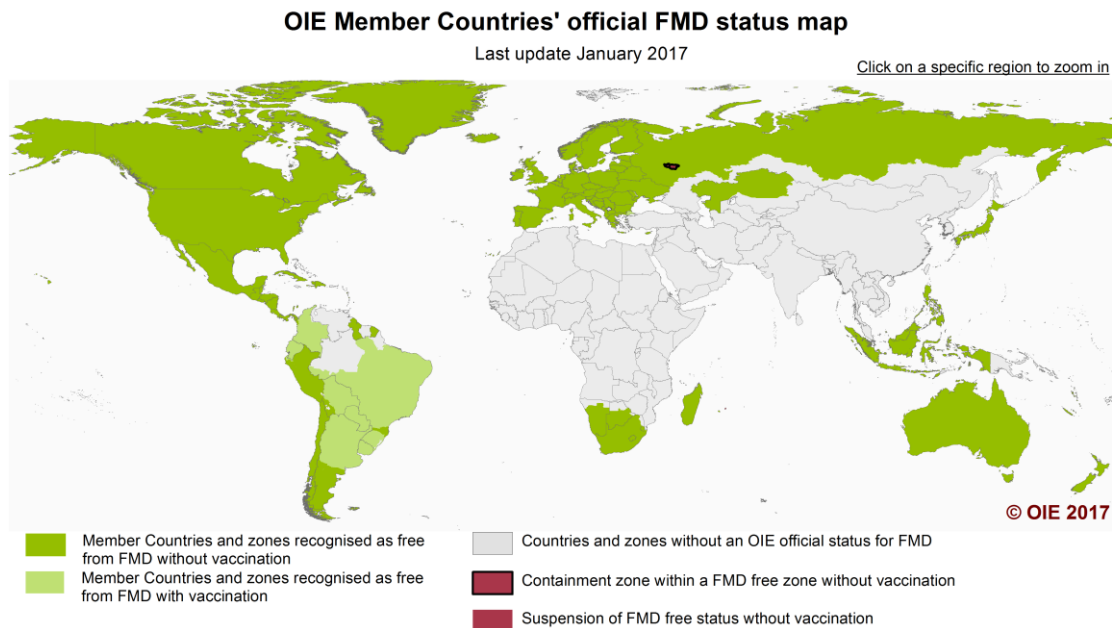


Figure 2-4: Official FMD status for OIE member countries. Data provided from the OIE: <http://www.oie.int/en/animal-health-in-the-world/official-disease-status/fmd/en-fmd-carte/>

2.2 Overview of the activities of the OIE/FAO FMD Laboratory Network during 2016

The OIE/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.

Over three thousand clinical samples from suspect cases of FMD were tested by laboratories in the Network (and associated laboratories) during 2016. These samples were collected from 40 countries from all FMD endemic pools 1 to 6 (Figure 2-8). **However, sampling within these pools is not equivalent: surveillance within West Africa (Pool 5) is particularly sparse and efforts are currently underway with the network to improve sample collection and testing in this region.**

Serotype C has not been detected since 2004 when the last cases due to the serotype were recognised in Kenya and Brazil. The Annual Network Meeting in November 2015 considered the difficulties of interpreting serotype-specific serological data and other epidemiological approaches that might be adopted to substantiate the “extinction” of this serotype. Recommendations arising from these discussions have been submitted to the OIE for consideration [expected at General Session 2017].

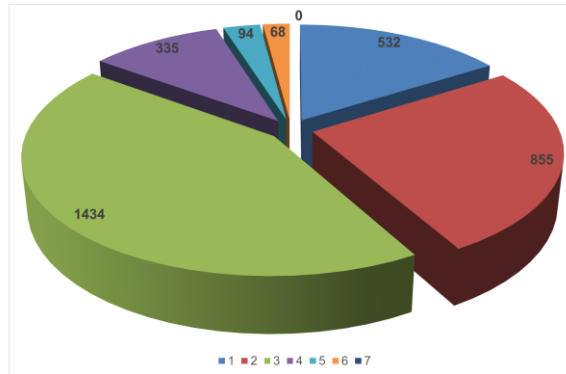


Figure 2-5: Samples (n=3318) tested for FMD investigation (virology) by the OIE/FAO FMD Laboratory Network from FMD endemic countries only during 2016 and their distribution across the seven FMD endemic pools (see Figure 2-1)

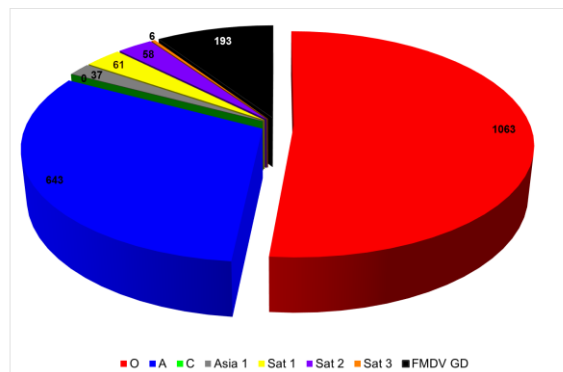


Figure 2-6: Summary of results for characterised isolates (n=1960) from FMD endemic countries were reported by the Network during 2016. FMDV GD denotes samples that were only positive using molecular (RT-PCR methods), while a further 5832 samples were tested but found to be negative for FMDV using all diagnostic methods.

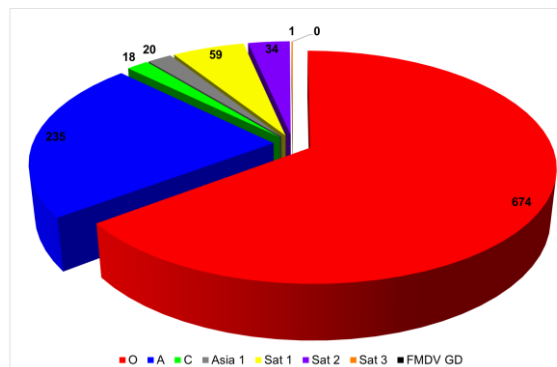


Figure 2-7: Summary of 1041 samples (viruses and field isolates) that were sequenced (VP1/capsid/complete genome) during 2016 (see Appendix 3).

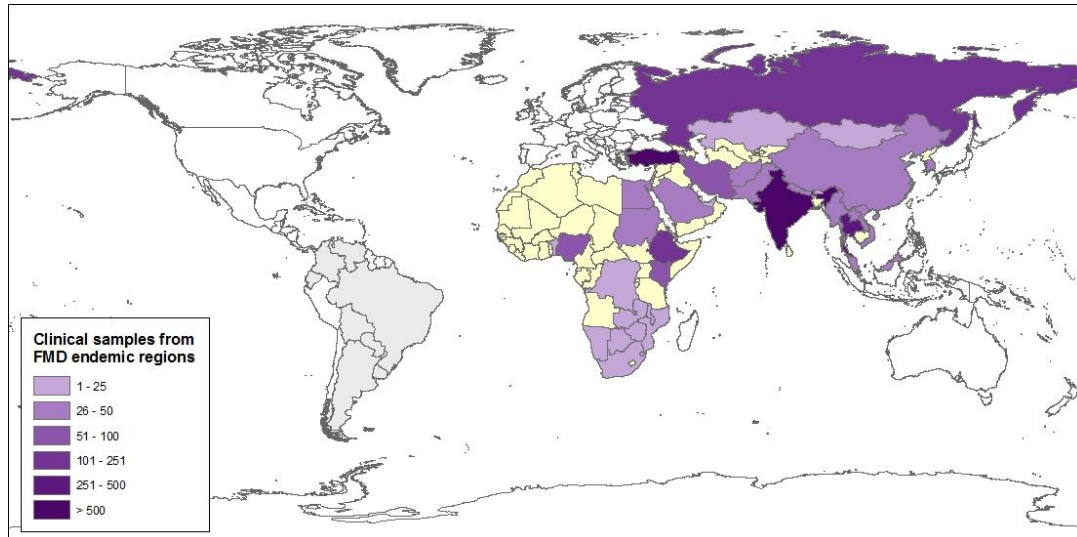


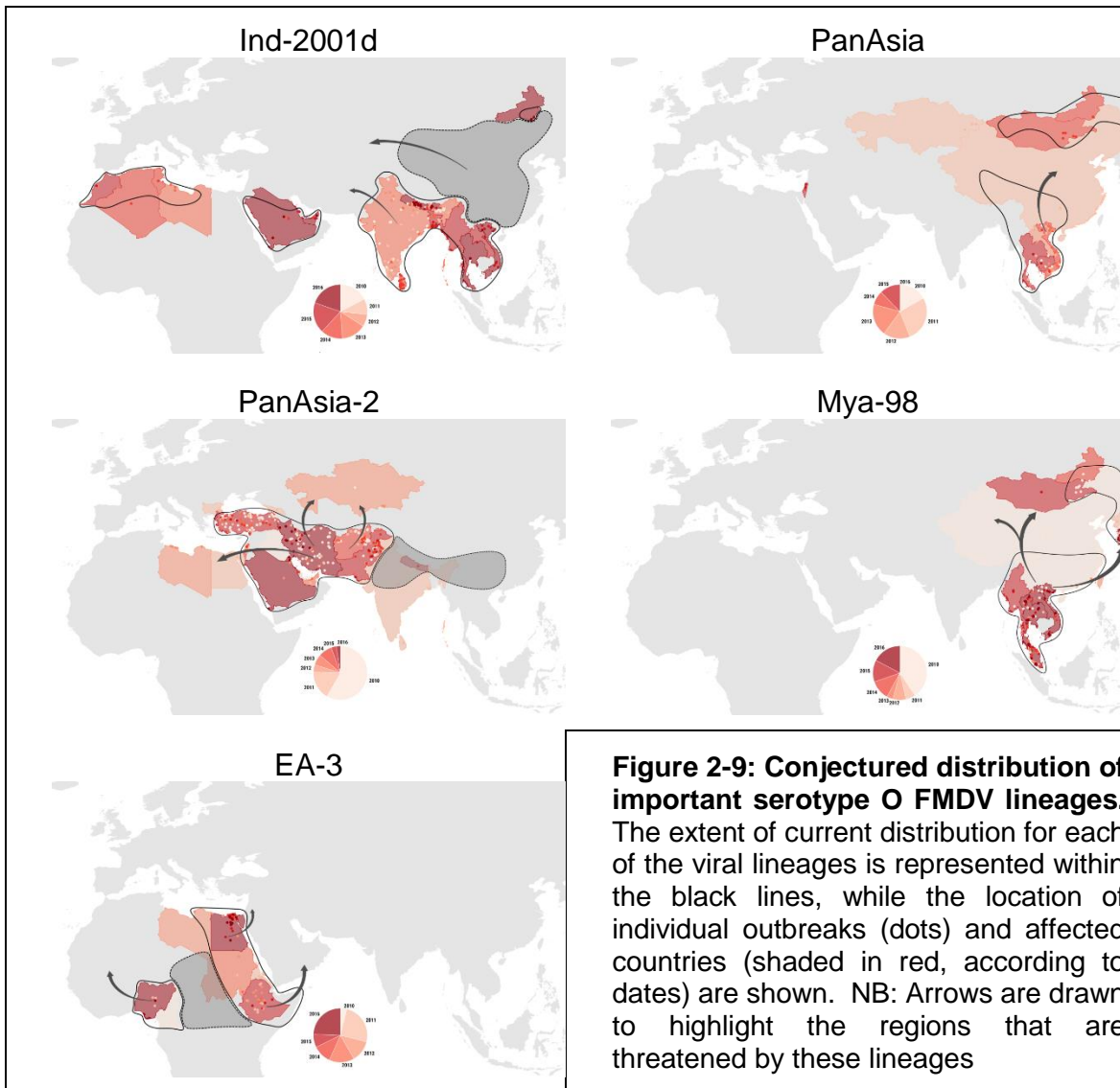
Figure 2-8: Distribution of samples collected from suspect cases of FMD (highlighted in purple) and tested by the OIE/FAO FMD Laboratory network during 2016. FMD endemic countries where no samples have been tested are highlighted in pale yellow. NB: No clinical cases have been reported in South America since 2013; countries having zones that are not FMD-free (without vaccination) are represented in grey.

The results for the individual samples are reported later in this report. It is also important to note that a much larger number of samples (such as sera, OPF and lymph node samples) were also received and tested by laboratories within the network during this period for surveillance activities: these numbers are also summarised in the tables for each of the individual endemic pools. Characterization results obtained on samples received by WRLFMD and PANAF-TOSA can also be found respectively at: <http://www.wrlfmd.org/> and at: <http://new.paho.org/panaftosa>.

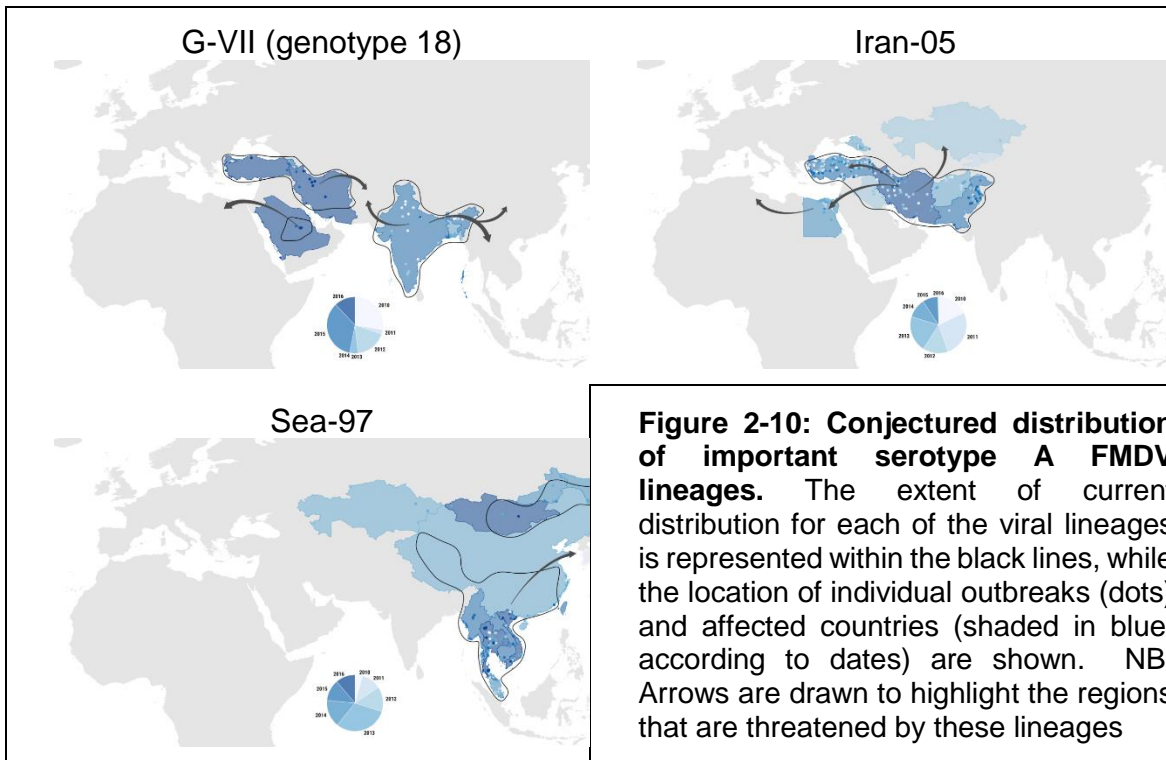
2.3 Distribution of different FMD viral lineages

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 this underlying complexity of FMDV virus distribution in the different pools (at serotype, toptype and lineage levels). In order to help visualise the changing patterns in FMDV distribution (see Figure 2-3) and recognise risks for the emergence of new lineages, the Network has reviewed available intelligence for epidemiologically important FMDV lineages. The “top-ten” virus lineages selected (see figures below) represent those that have already demonstrated a potential for long-distance trans-pool spread: O/ME-SA/Ind-2001d, 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.

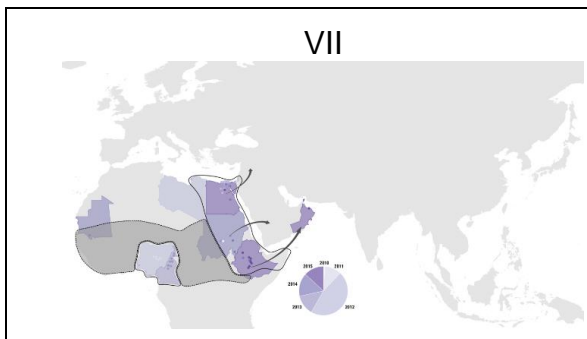
FMDV O



FMDV A



FMDV SAT 2



samples for laboratory analyses. NB: Arrows are drawn to highlight the regions that are threatened by this lineage

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 Table 2-2 below. Details of vaccine matching work undertaken by the OIE/FAO FMD Laboratory Network are summarised in Appendix 2.

Table 2-2: Recommendations from WRLFMD on FMD virus strains to be included in FMDV vaccine antigen banks.

High Priority	<p>A/ASIA/G-VII(G-18)* O Manisa O PanAsia-2 (or equivalent) O BFS or Campos A24 Cruzeiro Asia 1 Shamir A Iran-05 (or A TUR 06) A22 Iraq SAT 2 Saudi Arabia (or equivalent i.e. SAT 2 Eritrea)</p>
Medium Priority	<p>A Eritrea SAT 2 Zimbabwe SAT 1 South Africa A Malaysia 97 (or Thai equivalent such as A/Sakolnakorn/97) A Argentina 2001 O Taiwan 97 (pig-adapted strain or Philippine equivalent)</p>
Low Priority	<p>A Iran '96 A Iran '99 A Iran 87 or A Saudi Arabia 23/86 (or equivalent) A15 Bangkok related strain A87 Argentina related strain C Noville SAT 2 Kenya SAT 1 Kenya SAT 3 Zimbabwe</p>

Note: Discussions are currently underway to adopt a risk-based approach for different FMD viral lineages to identify priority vaccines for use in Europe and other FMD-free settings.

* Recent *in vitro* data from WRLFMD for serotype A viruses from Saudi Arabia and Iran highlights an apparent gap in coverage in vaccines provided by some manufacturers.

2.5 *Senecavirus A*

Senecavirus A (genus *Senecavirus*, family *Picornaviridae*) is an emerging virus that has been recently detected in pigs sampled in the Americas (Brazil, Canada and USA) and China. The clinical signs associated with *Senecavirus A* infection can be indistinguishable from those caused by other vesicular disease causing viruses, including FMDV, with pigs presenting with vesicles on the snouts and coronary bands, lameness, anorexia, lethargy, and fever. Thus it is important to test outbreaks of vesicular disease to exclude FMD.

During 2016 a total of 4401 samples were tested in USA and 500 in Canada for reasons of differential diagnosis (all negative for FMDV).

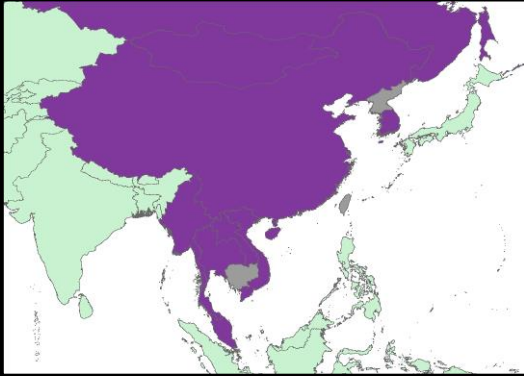
3 Overview of Network surveillance activities in each of the regional endemic pools

3.1.1 Pool 1 Regional synopsis

Conjectured circulating FMD viral lineages in Pool 1 during 2016

- Serotype O (4 viral strains):
 - SEA/Mya-98
 - ME-SA/PanAsia
 - ME-SA/Ind2001d
 - CATHAY
- Serotype A:
 - ASIA/Sea-97
- Serotype Asia-1:
 - Not detected in the region since 2005 (Myanmar) and 2006 (Vietnam, P.R. China)

Table 3-1: Overview of samples collected and tested from pool 1 during 2016



Countries within Pool 1 that have provided samples to FMD reference centres during 2016 (in purple).

Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	Surveillance Activities
LVRI, Lanzhou, China	China	34	13250
QIA, Republic of Korea	Republic of Korea	21	
FGBI ARRIAH, Russia	Mongolia	5	
RRL SEA Pakchong, Thailand	Lao PDR, Myanmar, Thailand	322	
WRLFMD, UK	Hong Kong, P.D.R. Laos, Malaysia, Myanmar, Republic of Korea, Thailand, Vietnam	150	

Pool 1 headlines: Changes to FMD status in 2016:

- The O/ME-SA/Ind-2001 lineage has **rapidly** spread from the Indian sub-continent through Southeast Asia. Field cases of this FMDV strain were first detected in Laos and Vietnam in 2015, and during 2016 cases were detected in Myanmar and Thailand (in June and September, respectively). At the end of 2016 (November), this lineage was also detected in the Russia Federation, close to the Chinese border
- O/CATHAY toptotype has been reported for the first time in mainland China.
- Endemic strains normally found in southeast Asia continue to cause FMD outbreaks in the area:
 - Continued FMD cases in China, Lao PDR, Malaysia, Republic of Korea, Thailand and Vietnam due to the O/SEA/Mya-98 lineage.
 - Outbreaks in China, Mongolia, Thailand and Vietnam due to the A/ASIA/Sea-97 viral lineage
 - Field cases in Mongolia and Russia due to the O/ME-SA/PanAsia viral lineage

Vaccine recommendations for Pool 1

- Internationally produced vaccines:
 - O: Campos, Manisa, Primosky, Taiwan & 3039
 - O-PanAsia (or suitable alternative)
 - A: Malaysia/97 & Iraq/64
 - A22-IRQ,
 - Asia 1: Shamir
- Locally produced vaccines (at RRL SEA):
 - O: 189/87 (Udonthani/87)
 - A: Sakolnakorn/97 & Lopburi/2012
 - Asia1: Petchaburi/85
- Locally produced vaccines (at FGBI ARRIAH):
 - A/Zabaikalsky/RUS/2013
 - O PanAsia-2
 - Asia-1 Shamir/89
- Locally used vaccine strains (by Chinese manufactures):
 - O/Mya-98 (O/Mya98/BY/2010)
 - O/PanAsia (O/China99)
 - Re-A/Sea-97 (Re-A/WH/09)
 - Asia1/GV (Asia1/JSL/06).

These are produced as: Type O and Type A (monovalent vaccines), Type O-A and Type O-Asia1 (bivalent vaccine), Type O-A-Asia1 (multi-valent vaccine) and a synthetic peptide vaccine (Type O for use in pigs only). In China vaccination

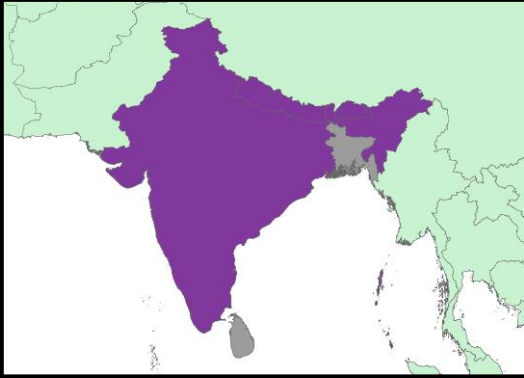
occurs 2 times a year (in spring and autumn). More than 1 billion doses are produced and administered in China per year

3.1.2 Pool 2 Regional synopsis

Conjectured circulating FMD viral lineages in Pool 2 during 2016

- Serotype O:
 - ME-SA/Ind-2001
 - ME-SA/PanAsia-2 (last detected in 2011 in Sri Lanka)
- Serotype A:
 - ASIA/IND (genotype VII also known as genotype 18)
- Serotype Asia-1:
 - lineage C subdivided into Eastern and Western clusters

Table 3-2: Overview of samples collected and tested from pool 2 during 2016



Countries within Pool 2 that have provided samples to FMD reference centres during 2016 (in purple).

Laboratory	Countries of Origin	Number of Samples	
		<i>Clinical Field Cases</i>	<i>Surveillance Activities</i>
ARC-OVI, South Africa	Mauritius	64	92
ANSES, France	Mauritius	13	15
RRLSS, BVI, Botswana	Mauritius	18	
PDFMD, India	India	672	
WRLFMD, UK	Bhutan, Mauritius, Nepal	88	

Pool 2 headlines: Changes to FMD status in 2016:

- FMDV serotype O (O/ME-SA/Ind-2001d) is now dominant in the region accounting for 97% of the total specimen submissions into the Indian FMD Reference Laboratory (PD-FMD, Mukteswar) in recent years.
- Two viral lineages that are endemic in Pool 2 have spread beyond this pool to cause FMD outbreaks in other regions
 - O/ME-SA/Ind-2001 in the Gulf States, North Africa and Southeast Asia
 - A/ASIA/G-VII in the Middle East (Saudi Arabia, Turkey) and Armenia
 - Precise routes by which these viruses are being spread need to be defined
- An outbreak of O/ME-SA/Ind2001d occurred in Mauritius in the Indian Ocean during July 2016 (previously FMD free – without vaccination)

Vaccine recommendations for Pool 2

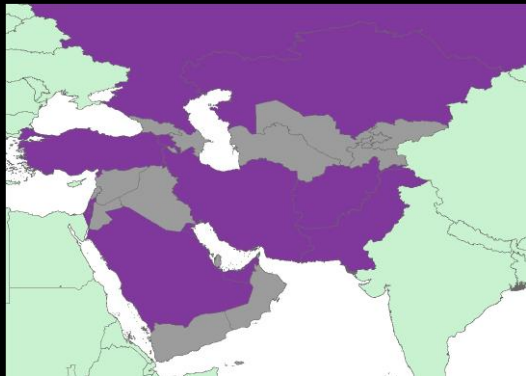
- Internationally produced vaccines:
 - O/ME-SA/PanAsia-2 (or suitable alternative). *In vitro* vaccine matching data for O/ME-SA/Ind2001 provides evidence for an antigenic match with O/TUR/09 vaccine (MSD) and O-3039 (Merial).
- Locally produced vaccines (by Indian suppliers):
 - O/IND/R2/1975
 - A/IND/40/2000
 - Asia1/IND/63/1972

3.1.3 Pool 3 Regional synopsis

Conjectured circulating FMD viral lineages in Pool 3 during 2016

- Serotype O:
 - ME-SA/PanAsia-2 (predominantly from ANT-10 and FAR-09 sub-lineage with QOM-15 in Iran and BAL-09 in Kuwait).
 - ME-SA/Ind-2001d (recent incursion during 2013/14 from the Indian sub-continent)
- Serotype A:
 - ASIA/Iran-05 (from SIS-12, SIS-10, FAR-11 and BAR-08 sub-lineages)
 - ASIA/G-VII
- Serotype Asia-1: (Sindh-08 lineage)

Table 3-3: Overview of samples collected and tested from pool 3 during 2016



Countries within Pool 3 that have provided samples to FMD reference centres during 2016 (in purple).

Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	Surveillance Activities
FGBI ARRIAH, Russia	Armenia, Kazakhstan, Russia	128	
SAP Institute, Ankara, Turkey	Turkey	1128	
ARC OVI, South Africa	UAE		1
WRLFMD, UK	Afghanistan, Iran, Israel, Kuwait, Pakistan, Palestine, Saudi Arabia, UAE	178	

Pool 3 headlines: Changes to FMD status in 2016:

- New FMD-free (without vaccination) zone established in Russia (apart from southern border buffer) and northern Kazakhstan
- Established viral lineages (O/ME-SA/PanAsia-2, A/ASIA/Iran-05 and Asia-1) continue to cause FMD outbreaks across the region
- The A/ASIA/G-VII (aka G-18) FMD viral lineage from the Indian sub-continent is spreading through the region
 - During 2016 this lineage was detected for the first time in Armenia and Iran, and was re-isolated in Saudi Arabia.
 - *in-vitro* (vaccine-matching) and *in-vivo* data indicate that vaccines (based on the A/ASIA/Iran-05 strain) that are currently used in the region are unlikely to provide protection
 - New wave of infection has occurred in Turkey during 2016, which may be due to a novel antigenic variant
- O/ME-SA/Ind2001d lineage continues to cause outbreaks
 - Sequence data provides evidence for multiple introductions of this viral lineage from the Indian sub-continent
- Asia 1 outbreak in Vladimir Oblast in the Russian Federation in October 2016

Vaccine recommendations for Pool 3

Internationally produced vaccines

- MSD and Merial*:
 - O/ME-SA/PanAsia-2 (or suitable alternative)
 - O/Manisa
 - A Iran-05 (or A TUR 06)
 - A22/Iraq
 - Asia-1 Shamir
- ARRIAH:
 - O/PanAsia-2
 - A/ASIA/G-VII
 - Asia-1 Shamir/89
 - A/ASIA/Iran-05 (from the Russian isolate /Krasnodarsky/RUS/2013)
- Other suppliers in the region:
 - SAP FMD Institute, Ankara, Turkey (including A/ASIA/G-VII lineage)
 - Vetal
 - JOVAC and MEVAC Jordan, Iran and Egypt

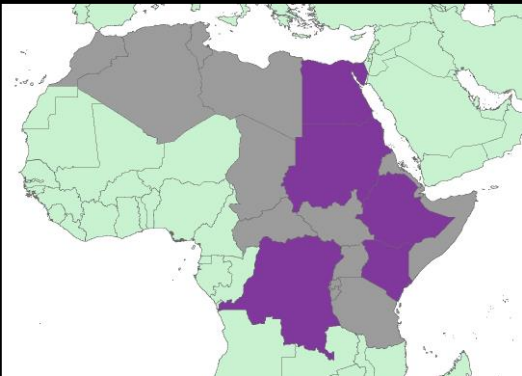
* Merial (BI) and MSD do not currently provide a vaccine tailored to the A/ASIA/G-VII lineage

3.1.4 Pool 4 Regional synopsis

Conjectured circulating FMD viral lineages in Pool 4 during 2016

- Serotype O:
 - EA-2 (Kenya, Tanzania, DR Congo, Uganda)
 - EA-3 (Egypt, Ethiopia, Eritrea, Sudan)
 - EA-4 (Ethiopia, Kenya, Uganda)
 - ME-SA/Sharqia-72 (detected in samples collected in Egypt in 2009)
 - ME-SA/Ind2001 (in Libya, Tunisia, Algeria and Morocco)
- Serotype A
 - AFRICA/I (Kenya, Tanzania, D.R. Congo)
 - AFRICA/IV (Sudan, Eritrea, Egypt)
 - AFRICA/VII (Ethiopia, Egypt)
 - ASIA/Iran-05^{BAR-08} (Egypt)
- Serotype SAT 1
 - I (Kenya, Tanzania)
 - IX (Ethiopia)
- Serotype SAT 2:
 - IV (Kenya, Tanzania)
 - VII (Sudan, Egypt, Mauritania)
 - XIII (Ethiopia, Sudan)
- Serotype SAT 3
 - Only detected in African buffalo in the south of the Queen Elizabeth National Park, Uganda in 1970, 1997 and 2014)

Table 3-4: Overview of samples collected and tested from pool 4 during 2016



Countries within Pool 4 that have provided samples to FMD reference centres during 2016 (in purple).

Laboratory	Countries of Origin	Number of Samples	
		Clinical Cases	Field Surveillance Activities
RRLSS, BVI, Botswana	Democratic Republic of Congo	3	
NAHDIC, Ethiopia	Ethiopia	165	
FMD Laboratory, Kenya	Kenya	79	
WRLFMD, UK	Egypt, Ethiopia, Sudan	88	

Pool 4 headlines: Changes to FMD status in 2016:

- O/ME-SA/Ind-2001 viral lineage has not spread further in North Africa during 2016
 - Most recent outbreaks have occurred in Morocco (November 2015)
 - No evidence for spread in Egypt or elsewhere in the region
- Elsewhere, serotypes O, A, SAT 1, SAT 2 outbreaks circulate

Vaccine recommendations for Pool 4

- Internationally produced vaccines:
 - O/Manisa
 - O/PanAsia-2 (or equivalent)
 - A/Eritrea
 - SAT2/Eritrea
- Locally produced vaccines from KEVIVAPI (Kenya):
 - O: K 77/78 – EA1
 - A: K5/80 –G1
 - SAT1: T155/71- NWZ
 - SAT2: K52/84 – IV
- Locally produced vaccines from NVI (Ethiopia):
 - Topo type O 3, EA 3

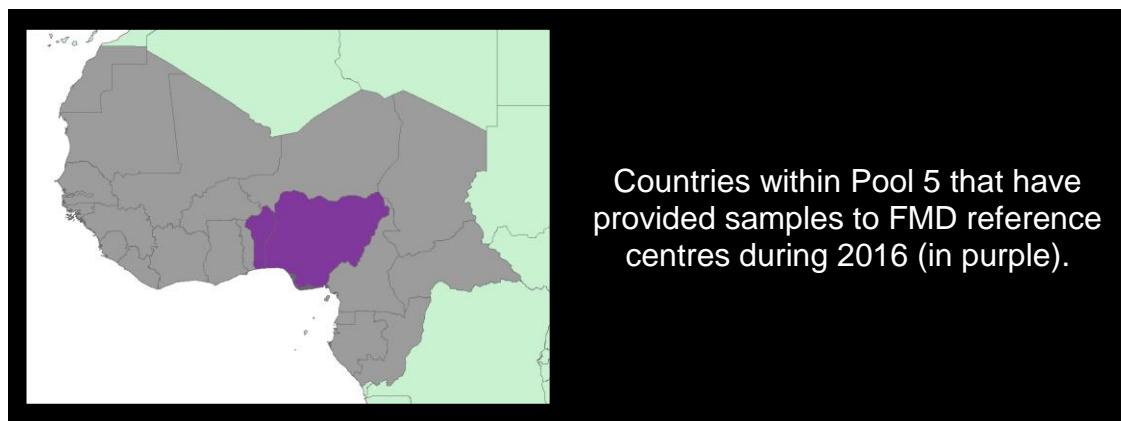
- Topo type A , Africa 3
- Topo type SAT 2, XIII
- Locally produced vaccines from BVI (Botswana)

3.1.5 Pool 5 Regional synopsis

Conjectured circulating FMD viral lineages in Pool 5 during 2016

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

Table 3-5: Overview of samples collected and tested from pool 5 during 2016



Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	Surveillance Activities
NVRI, Nigeria	Nigeria	37	
CODA-CERVA, Belgium	Nigeria	10	37
RRLSS, BVI, Botswana	Benin	22	
WRLFMD, UK	Nigeria	25	

Pool 5 headlines: Changes to FMD status in 2016:

- First meeting of the West Africa Road Map for FMD held in Lomé, Togo during September 2016
- New topotype of SAT1 was isolated from Nigeria*
 - First isolation of SAT 1 from West Africa in approx. 40 years

* see Ehizibolo et al., 2017

Vaccine recommendations for Pool 5

- Internationally produced vaccines:

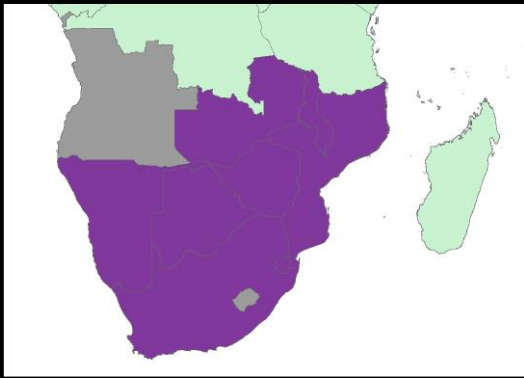
- O/Manisa
- O/Maghreb
- O/PanAsia-2 (or equivalent)
- O: 3039
- A: Eritrea
- SAT2: Eritrea & Zimbabwe
- Locally produced vaccines
 - O: Nigeria 03/14
 - A: Nigeria 07/13
 - SAT2: Nigeria 03/12

3.1.6 Pool 6 Regional synopsis

Conjectured circulating FMD viral lineages in pool 6 during 2016

- Serotype SAT 1:
 - Topotypes I, II and III
- Serotype SAT 2:
 - Topotypes I, II and III
- Serotype SAT 3:
 - Topotypes I, II and III)

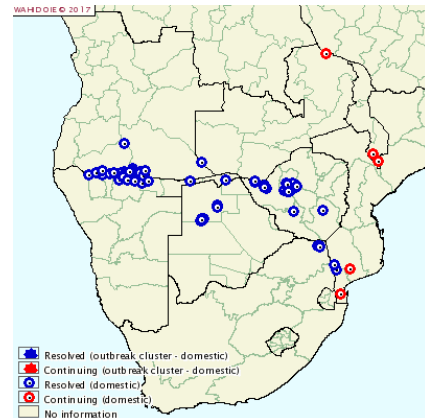
Table 3-6: Overview of samples collected and tested from pool 6 during 2016



Countries within Pool 1 that have provided samples to FMD reference centres during 2016 (in purple).

Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	Surveillance Activities
RRLSS, BVI, Botswana	Botswana, Malawi, Zambia, Zimbabwe	22	
ARC-OVI, South Africa	Mozambique, Namibia, South Africa, Swaziland, Zambia, Zimbabwe	26	18934
WRLFMD, UK	Botswana, Malawi, Mozambique, Namibia, Zambia, Zimbabwe	20	

Figure 3-1: An overview of FMD outbreaks from southern African countries for events reported to the OIE during 2016 (some of these field cases were initially reported during 2015). These outbreaks represent cases due to SAT 1 (Malawi), SAT 2 (Angola, Botswana, Mozambique and Zimbabwe), SAT 3 (in a protection zone in South Africa and in Zambia). NB: Some outbreaks (Angola and Namibia) were not typed.



Pool 6 headlines: Changes to FMD status in 2016:

- Drought has led to increased cattle movements, with resultant spread of FMD over wider geographical areas
 - Outbreaks due to three serotypes (SAT 1, SAT 2 and SAT 3)
 - SAT 1 (topotype I) cases in southern Malawi
 - SAT 2 cases in southern Mozambique appear to be related to cases from previous years (2014/15),
 - SAT 2 cases on the border between Namibia and Angola
 - SAT 3 in South Africa (in a control zone in Limpopo)

Vaccine recommendations for Pool 6

- Internationally produced vaccines:
 - SAT 1: SAT105, BVI vaccine
 - SAT 2: SAT251, BVI vaccine
 - SAT 3: SAT306, BVI vaccine
- Locally produced vaccines
 - SAT 1: SAT105, SAT109, A South African and a Botswana isolate
 - SAT 2: SAT251, SAT2035, South African isolate from Kruger National Park
 - SAT 3: SAT306, SAT309, South African isolate from Kruger National Park

3.1.7 Pool 7 Regional synopsis

FMD status of countries of South America (downloaded from the OIE website:
http://www.oie.int/fileadmin/Home/js/images/fmd/FMD_SouthAmerica_EN G.png).

Laboratory	Countries of Origin	Number of Samples	
		<i>Clinical Field Cases</i>	<i>Surveillance Activities</i>
SENASA, Argentina	Argentina		40326

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
 - O: O₁ Campos
 - A: A₂₄ Cruzeiro, A/Arg/2001
 - C: C₃ Indaial

4 Improving the quality of laboratory tests from international and international reference laboratories

4.1 Proficiency testing (PT) schemes organised by the OIE/FAO FMD Laboratory Network Partners

Brazil

1. Proficiency test organized – 2015
 - a. FMDV/VSV typing by PCR.
 - b. 13 lab participants – 10 labs have returned results.
2. Ongoing 2016 proficiency test:
 - a. FMD/VSV typing by ELISA (13 lab participants).

Canada

Type of test or trial	Number of participants	Results
Annual proficiency testing for FMD 3ABC ELISA	11 CAHSN Labs in Canada	28 analysts (in total) successfully completed PT panels
FMDV 3D RRT-PCR proficiency testing	10 CAHSN Labs in Canada	29 analysts (in total) successfully completed PT panels

China

1. Organized by CADC and FMDRL
 - i. 31 provincial veterinary labs invited
 - ii. Results reported in 2 days
- b. Materials and Methods
 - i. 6 coded cell culture samples per panel prepared by FMDRL
2*A+2*O+1*As1+1*Neg
 - ii. Samples collected along with the reagents
 - iii. Typing real-time RT- PCR
- c. Results: All 31/31 are up to standard

Italy

1. Organized for ten Balkan countries in the framework of an FMD simulation exercise planned and supported by EuFMD
 - a. The three main goals of the Laboratory simulation exercise were:
 - i. To test capacity to rapidly import diagnostic materials
 - ii. To test capacity to rapidly generate accurate results in the laboratory
 - iii. To test capacity to interpret results in the context of an epidemiological scenario

- b. Samples provided:
 - i. N. 6 epithelium homogenate, some spiked with inactivated FMDV, to be tested by RT-PCR and by Antigen ELISA
 - ii. N. 10 sera (cattle and sheep), to be analyzed by SP-ELISAs and NSP-ELISA
- c. Participants: Montenegro, Bosnia Herzegovina, Macedonia, Moldova, Albania, Republic of Kosovo, Romania, Greece, Bulgaria, Croatia
- d. Conclusions:
 - i. All laboratories demonstrated ability to use ELISA test
 - 1. ELISA kit for anti-SP Ab detection (serotypes O, A, Asia1)
 - 2. ELISA kit for Ag Detection and serotyping
 - ii. Nine laboratories had real-time PCR facilities
 - 1. seven produced results
 - 2. five produced accurate real-time RT-PCR results
 - iii. Speed of testing:
 - 1. Testing and reporting of six countries were done within three days
 - 2. Four countries were late in testing or reporting due to various reasons, in particular LSD emergency.
 - iv. The simulation exercise design, based on a “real-life” scenario, highlighted a weakness in the ability to interpret results (in particular serological results) in relation to an epidemiological scenario.

Republic of Korea

- 1. QIA organised the national proficiency tests in South Korea (2016)
 - a. 45 Provincial Veterinary Service Laboratories for diagnosis of FMD

Thailand

- 1. Inter-laboratory comparison round 4/2015 organized by RRLFMD, Pakchong, Thailand. Participating laboratories (17 laboratories):
 - a. 9 FMD laboratories within Thailand
 - b. 8 SEAFMD laboratories (Cambodia, Lao PDR, Philippines, Malaysia, Myanmar, Vietnam (Hanoi), Vietnam (Ho Chi Minh), Singapore, Thailand)

United Kingdom

	2015	2016		
Total invited laboratories ¹	91	94		
Total number of shipments ¹	66	70		
Participants from European Union (funded by EURL for FMD)	27 (EU member states)	28 (EU member states)		
% of labs meeting target performance ⁴	Cat-1 0 % Cat-2 0 % Cat-3 67 % Cat-4 33 %	Cat-1 0 % Cat-2 0 % Cat-3 60.71 % Cat-4 39.29 %		
EUFMD funded participants				
Participants from Global Network Labs ²	Panaftosa Brazil, Pakchong Thailand, BVI Botswana, OVI South Africa, ARRIAH Russia, NVRT Nigeria, LNERV Senegal, Emabakasi FMD laboratory Kenya, NAHDIC Ethiopia, USDA USA ³	BVI Botswana, Brazil, China, Ethiopia, Kenya, Nepal, Nigeria, Russia, South Africa, Thailand.		
% of labs meeting target performance ⁴	Cat-1 0 % Cat-2 10 % Cat-3 60 % Cat-4 30 %	Cat-1 0 % Cat-2 0 % Cat-3 60 % Cat-4 40 %		
Participants from EuFMD Member states (non-EU)	Serbia, Albania, FYRO Macedonia, Turkey, Georgia, Switzerland, Norway, Israel	Albania, Georgia, Macedonia, Norway, Serbia, Switzerland, Turkey		
% of labs meeting target performance ⁴	Cat-1 0 % Cat-2 0 % Cat-3 88 % Cat-4 13 %	Cat-1 0 % Cat-2 0 % Cat-3 66.6 % Cat-4 33.3 %		
Participants from neighbourhood countries	Montenegro, Armenia, Azerbaijan, Ukraine, Egypt, Lebanon, Morocco, Algeria	Algeria, Armenia, Azerbaijan, Iran, Lebanon, Moldova, Montenegro, Morocco, Tunisia		
% of labs meeting target performance ⁴	Cat-1 0 % Cat-2 0 % Cat-3 63 % Cat-4 38 %	Cat-1 0 % Cat-2 0 % Cat-3 77.7 % Cat-4 22.2 %		
Summary of EUFMD funded participants				
Invited				
Panels shipped	Panel 1	7	Panel 1	23
	Panel 2	23	Panel 2	23
	Panel 3	25	Panel 3	26
	Panel 4	-	Panel 4	14
Total number of participants funded by EUFMD	26	26		

¹ Additional countries participate in the PTS at their own expense (not funded via the EURL for FMD or EuFMD)

² Not including IZSLER and CODA-CERVA who participate as European NRLs

³ USA are self-funded

⁴ Scored according criteria agreed by the NRLs within Europe, each laboratory receives a personalized anonymous feedback letter to highlight areas in which they could improve, and performance of each laboratory is broadly categorized into one of four groups: (**Category 1**) to emphasize critical issues where immediate action is required that impact upon the laboratory to correctly identify FMD virus (virology tests) or FMDV infected animals (serological tests), (**Category 2**) laboratories with serious issues with the performance of individual tests that need to be addressed, (**Category 3**) to record additional observations which may need to be considered by the laboratory to improve the local performance of individual tests and (**Category 4**) laboratories whose tests which are fit for purpose and where no further action is required.

United States of America

1. NALHN (1,920 samples and 540 positive controls)
 - a. PTS sent to all State National Laboratory Network in US.

4.2 Supply of reagents

Argentina

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
Hyper immune guinea pig sera A24 Cruzeiro-A Arg2001-O1 Campos-C3 Indaial	235 vials x 1 ml	Argentina, Paraguay
FMD challenge viral suspension for PPG test A24 Cruzeiro-Arg2001-O1 Campos	440 vials x 1 ml	Argentina
Viral Inactivated Antigen	40000 ml	Argentina
Typing ELISA	16 x 5 plates	Argentina, Uruguay and Paraguay
3 ABC ELISA	4 x 100 plates	Argentina

Botswana

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	400 ml	CVRL - Zimbabwe
FMDV antigen kits	300 ml	CVRL - Zimbabwe
FMDV antigen kit	60 ml	BNVL - Botswana

Brazil

	Type of reagent	Quantity
Kits & Sets (NCPanaftosa)	3ABC-ELISA + EITB	18957
	ELISA-IS Typing	6300
	Lp-ELISA FMD Seroepidemiology	2600
	Lp-ELISA FMD Vaccine quality control	541000
Other biologicals	Positive control PCR (FMDV, BT, VSV)	
	VS viral strains	
	Cell Lines	

Canada

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	120 plates	CAHSN/Canada
FMDV real-time RT-PCR kits	29 panels	CAHSN/Canada

China

Type of reagent		Quantity	Recipient of the reagent (Laboratories/Countries)
Antibody kit	LPBE-O	7521 kits	Mainly provincial level veterinary labs in China
	LPBE-Asia1	3366 kits	
	LPBE-A	3351 kits	
	NSP-3ABC-ELISA	2028 kits	
Antigen kit	Multi-RT-PCR	228 kits	
	Real-time PCR	476 kits	

France

Type of reagent		Quantity	Recipient of the reagent (Laboratories/Countries)
Master mix rtRT-PCR pan-FMDV		24ml	12 countries
Positive control serum for NSP		6ml	France
Positive control serum for Type O		6ml	France

India

Type of reagent		Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits (LPBE)		1,65,520	FMD regional centers/network unit of DFMD, Other stake holders
FMDV antibody kit (3ABC-NSP ELISA)		50, 380	FMD regional centers/network unit of DFMD, Other stake holders
FMDV antigen kits (S-ELISA for antigen detection)		7,500	FMD regional centers/network units, SAARC Countries

Italy

Country		FMDV Ag detection ELISA			NSP Ab ELISA	SP Ab ELISA				
		O, A, SAT1, SAT2	O, A, C, Asia1	NEW FORMAT O, A, C, Asia1, SAT1-2		3ABC	O	A	Asia1	SAT1
EU/FMD/Rome						8	10	3	1	
Asia	Taiwan			2		4	3	2		
	South Korea	3	3	2		2				
	Vietnam		5	6						
	Hong Kong		1							
	Japan			3						
	Nepal			7						
	Mongolia		12							
	Myanmar			11	4	7	1	1		1
	China		14		6	443	277	86		
Central Asia & West	Pakistan					11	10	10		
	Balkan Countries		6			6	6	6		
	Russia			1		3	3	2		
	Turkey					1	1	1		
	Georgia			1		5	5	20		
	Afghanistan		3	10	5	4	4	4		
Middle East	Oman			5	3					5
	UAE					1	1			
	Israel	3	3		2	2	2	2		2
	Lebanon			2						
	Saudi Arabia			6						
	Kuwait		3							
Africa	Egypt	15	4		10	9	9			9
	Kenya	7			3					
	Cameroon			4						
	Morocco	7								
	Ethiopia			4		1	1		1	1
	Uganda			2						
FMD-free countries	Cyprus	2	2							
	New Zealand	1	1	1	1	1	1			2
	Bulgaria		1			1	1	1		
	Romania			2		1	1	1		
	Spain			1			1			
	Estonia	2	2							
	Slovenia					1	1	1		
	Greece		1			1	1	1		
	Latvia			1		1	1	1		1
	Switzerland	1	1							
Total		41	62	71	34	513	340	142	2	21

Republic of Korea

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits (FMDV NSP ELISA kits: 2 types)	Each 440T	National Animal health Laboratory, LAO PDR
FMDV antigen kits (FMDV Rapid diagnostic kits)	105T	National Animal health Laboratory, LAO PDR

Russian Federation

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	5219	Russia, Kazakhstan, Kyrgyzstan, Armenia, Moldova, Belarus, Tajikistan, Azerbaijan
FMDV antigen kits	35	Russia, Kazakhstan, Kyrgyzstan, Armenia, Moldova, Belarus, Tajikistan

Thailand

Type of reagents	Supplied nationally and own lab	Supplied to OIE Country Members in SEA	Remarks
Rabbit trapping antibody for type O, A and Asia1	Type O = 50 sets Type A = 54 sets Type Asia1 = 38 sets	Type O = 2 sets Type A = 5 sets (Laos, Myanmar, Vietnam)	Special purpose: One set of FMDV reagent was provided to WRL , Pirbright and QIA Korea for special testing of Cambodian samples:
Guinea pig detecting antibody for type O, A and Asia1	Type O = 50 sets Type A = 49 sets Type Asia1 = 40 sets	Type O = 2 sets Type A = 5 sets	① Rabbit trap.: Asia1 = 0.6 ml A/sakol/97 = 0.6 ml A/Lop/2012 = 0.6 ml
Inactivated & concentrated antigen (50X) for type O, A and Asia1	Type O = 125 ml Type A = 112 ml Type Asia1 = 106 ml	Type O = 4 ml Type A = 16 ml	② GP detect.: Asia1 = 1.0 ml A/sakol/97 = 1.0 ml A/Lop/2012 = 1.0 ml
Control serum for C++, C+ and C-	C++ = 360 ml C+ = 345 ml C- = 375 ml	C++ = 28 ml C+ = 28 ml C- = 20 ml	③ Inact. Conc. Antigen: Asia1 = 2 ml A/sakol/97 = 2 ml A/lop/2012 = 2 ml

United Kingdom

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
Ab LPBE kit (O, A, Asia1)	3	Afghanistan
Ab LPBE kit (O, A, Asia1 mixed)	1	Bangladesh
Ab LPBE kit (O, A, C, SAT1, SAT3 mixed)	1	Botswana
Reagents (O & negative)	12	China
Ab LPBE kit (6 serotype)	1	Czech Republic
Reagents (O, A, C, Asia1, SAT1, SAT3)	39	Czech Republic
Ab LPBE kit (6 serotype)	1	Estonia
Ab LPBE kit (O, A)	1	Indonesia
Ab LPBE kit (O, A, Asia1 mixed)	1	Iran
Ab LPBE kit (O, Asia1)	1	Iraq
Ab LPBE kit (O, A, Asia1 mixed)	10	Malaysia
Ab LPBE kit (O, A, Asia1 mixed)	2	Mongolia
Reagents (O, A, Asia1)	10	New Zealand
Ab LPBE kit (O, A, Asia1, SAT1, SAT3 mixed)	1	Oman
Ab LPBE kit (O, A, C, Asia1 mixed)	3	Poland
Reagents (SAT1, Asia1)	3	Romania
Ab LPBE kit (O, A)	2	Saudi Arabia
Ab LPBE kit (O)	2	South Korea
Ab LPBE kit (Single kits, 6 serotypes)	8	South Korea
Reagents (O)	20	South Korea
Reagents (Various)	28	South Korea
Ab LPBE kit (O, A, C, SAT1, SAT3 , Asia1 mixed)	1	UAE
Reagents (O)	1	UK Internal
Reagents (O, A, Asia1)	14	UK Internal
Reagents (SAT1, SAT2, SAT3, O, A, Asia1)	24	UK Internal
Ab LPBE kit (O, A, Asia1- singles and mixed)	26	Vietnam

United States of America

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
Antibodies	VSV	Canada
Antigens	VSV	Costa Rica
Ag ELISA kit	FMD/VSV	Panama
PCR reagents	FMD/VSV	Panama

4.3 Training courses organised by Network partners

Argentina

1. Training to vesicular disease diagnosis laboratory (LADIVES) of Central America - April 2016
 - a. Isolation, typing and viral characterization
 - b. Genetic characterization; PCR, q-PCR, sequencing.
 - c. Cell Culture
 - d. ELISA and VNT
2. Training in FMD vaccine quality control - Republic of Kenya – August 2016
 - a. Safety (residual active virus)
 - b. Sterility
 - c. Potency/ Performance
 - d. Purity (induction of antibodies against NSP)
 - e. Security (tolerance)

Botswana

1. Two Scientists (BNVL) - FMD diagnostics
2. Three BITRI scientists - FMD diagnostics
3. Two Scientist from Zimbabwe (CVL) - LPBE testing and troubleshooting
4. One technician from Uganda (NVI) - FMD diagnostics

Brazil

1. Training offered during 2016:
 - a. Laboratory Risk Management
 - b. Cell Culture
 - c. Virus Neutralization Test

Canada

1. FMD 3ABC ELISA and FMDV real-time RT-PCR proficiency panels administered to Canadian Animal Health Surveillance Network (CAHSN)
2. An analyst from a CAHSN lab on real-time RT-PCR
3. Scientist from Botswana Institute of Technology, Research and Innovation (BITRI) trained on monoclonal antibody production and FMD serology

China

1. National training
 - a. Seminars at the training courses organized by the provincial labs
 - b. Field training (sampling)
 - c. Biosecurity training staff from 4 provincial and other labs (15 people)
2. International training
 - a. 2 trainees from Myanmar, each for 3 months

Ethiopia

1. Workshop FMD carried for NADIC staff in January 2016.
2. Training on FMD outbreak investigation was carried in October 2016.

France

1. Training on FMD diagnostic for one trainee from Morocco

India

1. Training on FMD diagnosis (DIVA-ELISA) (n=3)
2. Training on FMD Decision Support System (n=2)

Italy

1. 25th - 28th January & 12th - 14th September: three-day technical visits of two EUFMD short term professionals, based in FAO Rome, finalized to design, discuss and elaborate the results of the Lab Proficiency Test organized for 10 Balkan countries and to familiarize with FMDV ELISA kits for antigen and antibodies serotyping and interpretation of serosurveillance results

2. 1st March - 15th April: Study visit of 1.5 months of an Egyptian researcher, in the framework of the Italy-Egypt cooperation project “Development of Nano-based Biosensor for FMDV”.
3. 14th November - 7th December: four-week hands-on training on reagents production and evaluation, ELISA assays development and calibration, cell cultures, theory and practice of FMD ELISAs for antigen and antibody detection and serotyping with results interpretation. Attendees: two scientists from UAE.
4. 17th - 22nd April: One week technical visit of two IZSLER scientists at Algeri and Tlemcen labs (Algeria), to verify technical and organizational progress in FMD lab diagnosis in the framework of an EU supported twinning, aimed at “Mise à niveau des laboratoires de l’Institut national de la médecine vétérinaire aux standards européens et internationaux”

Kenya

1. Three FMD real-time training courses
 - a. At: Nakuru (NTC)
 - b. Trainees: 36 German, 42 other EU & 12 Kenyan

Republic of Korea

1. 5th workshop for Scientific and Technical Training for Rabies, JEV, CWD, Brucellosis, ND, FMD
 - a. 9 participants from 4 Asian countries (10th October 2016 to 21st October 2016)

Russian Federation

1. Proficiency tests for the countries covered by the ARRIAH: Armenia, Azerbaijan, Belarus, Moldavia, Tajikistan, Kirgizstan (2 laboratories). FGBI ARRIAH is going to send the 6 samples of inactivated FMDV antigens and 8 sera from recovered and vaccinated animals in November 2016
2. Seminar on diagnostics, monitoring and prevention of highly dangerous animal diseases in Khabarovsk on 8th-9th June 2016 (58 attendees).
3. Seminar on FMD epidemiology, diagnosis, prevention and control under modern conditions for veterinary specialists of the Vladimir Oblast was held on 1st November 2016, housed by the FGBI “ARRIAH”, Vladimir (61 attendees).

Thailand

1. FMD antigen detection training course during 4th – 8th July 2016

- a. Participant from 9 Veterinary Research and Development Centres (VRDC) within Thailand and National Institute of Animal Health
2. AAHL, Australia: Dr.Singanallur, Nagendrakumar, Research collaborative work on vaccine matching, 29th July - 11th August 2016.
3. Dr.Sandar Lwin, Myanmar; Laboratory Training for FMD Diagnostics Capacity, 24th October 2016 – 13th January 2017, under IAEA support.
4. Follow up the research collaborative work and scientific discussion Dr Kenichi Sakamoto, NIAH Director, Japan, 18th May 2016.
5. FAO LMT and BLMT visit and assessment the biosafety system of the BSL3 Lab and staff 10th May 2016.
6. Dr Kriistina Boyd, Scientific visit and implement the PACS to RRL staff, 10th October 2016.
7. Scientific visit and research collaboration work with RRLSEA; the three officers from QIA, Korea, during 14th – 16th December 2016.

Turkey

1. Azerbaijan (PCR Diagnosis)
2. Pakistan (FMD vaccine control)
3. Regular training activities for veterinary services of Turkey

United Kingdom

1. Two week residential training course for FMD diagnostics provided to scientists from Sweden, Malta and Albania
2. Kenya – training in RT-PCR provided via a visit of two WRLFMD scientists to Embakasi (funded by EuFMD)
3. Thailand -Visit RRLSEA (Pakchong) for training in Ag-ELISA.
4. Botswana -training provided for RT-PCR and sequencing
5. Ethiopia - (as part of OIE twinning project)
 - a. Workshop FMD carried for NADIC staff in January 2016.
 - b. Training on FMD outbreak investigation was carried in October 2016
6. Tanzania -training provided for FMD sequencing via a visit of two scientists from WRLFMD to Sokoine University of Agriculture

United States of America

1. FAD Diagnostician refresher in Minnesota
2. FAD Diagnostician refresher in North Carolina
3. FAD Veterinary Pathologist Course
4. FADD Course only 1 course
5. Smith-Kilborne Course for FADs Washington, D.C
6. Palo Duro FMD Outbreak Scenario training
7. Courses for Department of Defence Veterinary Support to Stability Operations
8. LADIVES-Panama (Vesicular Diseases)

4.4 Collaborative projects

Argentina

Collaborators	Collaborative project
SENACSA Paraguay laboratories, SENASA Argentina	Bilateral agreement in diagnosis and control of zoonoses, and Biosecurity and Biosafety
Vietnam, Argentina	FO-AR Cooperation Project Southern-Southern countries: FMD vaccines quality control and FMD viral characterization
Dr. Cesar Milstein at PROCC-FioCruz-Brazil-ICT	FMDV proteins modelling studies
University of San Pablo, Dr. Cesar Milstein at Brazil-ICT	Activity Assessment of FMD antiviral compounds

Belgium

Collaborators	Collaborative project	Outcomes
NVRI, Nigeria CODA-CERVA, Belgium	OIE Laboratory Twinning Program for capacity building	<ul style="list-style-type: none"> • Personnel training • Implementation of SOPs • Sample characterization including phylogenetic analysis
BVI, Botswana CODA-CERVA	Bilateral collaboration	<ul style="list-style-type: none"> • Personnel training • Implementation of SOPs • Sample characterization including phylogenetic analysis

Botswana

Collaborators	Collaborative project	Outcomes
The Pirbright Institute, UK	ILC, PTs, and Genotyping	Improve capacity
CODA-CERVA	ILC	Improved capacity
Botswana National Veterinary Laboratory	Monitoring & maintenance of ISO17025 accreditation	Successful – 3 accredited test by retained SANAS accreditation status
BITRI	Development of a rapid test for FMD	At the product validation stage
Sokoine University of Agriculture Tanzania	Research Capacity building	MSc qualification
University of Botswana	Research Capacity building	PhD qualification

Brazil

Collaborators	Collaborative project	Outcomes
INSAI-Venezuela - PANAFTOSA	Post vaccination monitoring	4,000 sera samples (approx) analysed by Lp-ELISA Serotype O and A
COSALFA countries *	FMDV Regional Antigen Bank	Constitutive Agreement under revision by PAHO Legal Department
COSALFA countries *	Updating document of Minimum Standards for biorisk management in laboratories handling FMDV and/or its derivatives	Documents (two) for final approval of next COSALFA meeting (April 2017)

* COSALFA countries: all South America and Panama

Canada

Collaborators	Collaborative project	Outcomes
Botswana Institute for Technology Research and Innovation (BITRI)	Development of FMD pen side tests for antigen and antibody detection	Lateral flow devices for NSP antibody and SAT2 antigen detection
Australian Animal Health Laboratory	Evaluation of emergency and improved vaccines for FMD	In vivo “vaccine matching”
Plum Island Animal Disease Center/ARS and SENASICA Mexico	Survey of vesicular stomatitis in Mexico	Understand the epidemiology of VSV in the region
Iowa State University College of Veterinary Medicine	Diagnostic assays for FMDV in swine oral fluids	Molecular and serological assays for swine oral fluids
BioVet Inc, Canada	Luminex assays for FMDV antibody detection	Luminex assays for detection and serotyping of FMDV

China

Collaborators	Collaborative project	Outcomes
Korea Atomic Energy Research Institute/Prof. Seo HoSeong	Research and development of an attenuated edible FMD vaccine using salmonella as the vector	Korea collaborators visited LVRI in June , September and October, in total of 12 people
Pirbright Institute, UK/Don King	Engineering Foot-and-Mouth Disease vaccine with increased antigenic match and broadened coverage of antigen for the development of effective vaccine	<ul style="list-style-type: none"> ① Developed and transferred recombinant high-efficient type A vaccine , PD50≥9.0. It is currently used in the field ② Developed multi-epitope type O vaccine , it is now under the field trial ③ Established the platform of engineering vaccine using reverse-transgenic technology
Pirbright Institute, UK/Don King	Introduction and application of the related diagnosis materials from the FMDV circulating in surrounding countries	Established multi-qRT-PCR to detect O/PanAsia-2,A/Iran/05 and A/Asia/GVII and other virus strains
University of East Anglia/Professor Tom Wileman	Exchange of vaccine technology for the delivery of oral vaccines to mucosal	Prof. Tom Wileman and other 3 scientists visited LVRI in September
National Microbiology Laboratory-Public Health Agency of Canada/University of Manitoba/Dr Binghua Liang	Genetic variation in Foot-and-mouth Disease Virus A/HUBWH strain under selective pressures of antibody and its correlation with vaccine potency	<ul style="list-style-type: none"> ① Sequenced the FMDV A/HUBWH and compared it with the reference strains ② Prepared the antibody against type A virus and found that type A IgG and IgM could provide the selection pressure for the homologous virus

Ethiopia

Collaborators	Collaborative project	Outcomes
The Pirbright Institute	OIE twinning project	Building the capacity of NAHDIC in different areas: <ul style="list-style-type: none"> • FMD antigen detection • Molecular test • Serotyping • Vaccine matching

France

Collaborators	Collaborative project	Outcomes
DGSV Tunis, EuFMD, ANSES	Capacity analysis and scenarios for pooling resources in case of an outbreak of foot-and-mouth disease in Tunisia	Report, Publication
SLU, FLI, CODA-CERVA, INRA, Merial, ANSES	Host response gene signatures associated with FMDV infection, vaccination and persistence	Reports, Publication

India

Collaborators	Collaborative project	Outcomes
Department of Animal Husbandry, Dairying and Fisheries (DAH&DF), Govt. of India	Providing scientific inputs to the vaccination based FMD-CP, Supply of FMD-Diagnostic kits, Training, Scientific inputs and data analysis of FMD epidemiology and serology	FMD Epidemiology and Serology
ARS-USDA	“Understanding FMD viral ecology and landscape epidemiology towards control and eradication”	Designing effective control strategies

Italy

Collaborators	Collaborative project	Outcomes
IZSLER, The Pirbright Institute	Continuous validation and improvement of new diagnostic kits (ELISA)	Continuous improvement and validation of new generation ELISAs (ready-to-use kits) - Ongoing
IZSLER, USDA ARS PADC	Study of interaction between FMDV and host proteins during infection	Characterization and selection of mAbs (anti-SP and anti-NSP) suited for the study
IZSLER-Italy, ANSES-France, Institut de la Recherche Vétérinaire de Tunisie-Tunisia, Institut national de la Médecine vétérinaire, Algiers - Algeria	Evolutionary analysis of FMDV isolates from North Africa 2014-2015 epidemic	genetic and antigenic characterization of FMD isolates from the 2014-2015 FMD epidemic in Maghreb by full genome sequencing and monoclonal antibodies profiling
IZSLER, AHRI-Egypt	Development of Nano-based Biosensor for FMDV	Evaluation of nanogold particles conjugated with oligonucleotides to improve diagnostic performances of FMDV realtime RT-PC

Kenya

Collaborators	Collaborative project	Outcomes
FMD Lab Kenya & EUFMD	FMD Real-Time Training Courses - Nakuru (NTCs)	EU and Kenyan Vets capacity for FMD outbreak investigation
Kenya Wildlife Service, Olpejeta Conservancy, University of Minnesota & USDA- ARS	US National Academy of Sciences Partnership for Enhanced Engagement in Research (PEER) Project on FMD livestock-wildlife transmission	Understanding FMD livestock-wildlife transmission dynamics

Nigeria

Collaborators	Collaborative project	Outcomes
CODA-CERVA, Belgium	OIE-twinning	Building capacity and technology transfer
WRLFMD	Sample analyses and sequencing	Analyses of samples

Republic of Korea

Collaborators	Collaborative project	Outcomes
National Center for Veterinary Diagnosis, Department of Animal Health, Hanoi, Vietnam	To carry out Comparative studies of Avian influenza virus and Foot and mouth disease virus between Korea and Vietnam	Data and materials including the biological strains and clones (2016~2024)
Investigation and diagnostic center and response (IDCR), MPI New Zealand,	Collaboration on the Epidemiology of Current Animal Diseases (FMD, AI etc)	Attending collaborative FTA workshop a year
Regional Reference laboratory for FMD in SEA, Pakchong, Thailand	To differentiate the serotype of FMD samples collected in 2015	Diagnostic results

1. Establishment of the collaborative network with National Institute of Animal Health (NIAH) of Thailand and the Regional Reference Laboratory for FMD in South East Asia (RRLFMD), Department of Livestock Development
 - a. Dr Wilai Linchongsabongkoch
 - b. 18th – 22nd October

Russian Federation

1. Adopted at 40th Meeting of Intergovernmental Council for Cooperation in Veterinary Medicine on 5th April 2013 in Vladimir, Russia
 - a. Approved by the Council of the CIS Government Executives On 30th May 2014 in Minsk
 - b. Republics of Azerbaijan, Armenia, Belarus, Kazakhstan, Kyrgyzstan, Moldova, Russian Federation, Tajikistan, Uzbekistan
2. Sixth Meeting on Strengthening the Collaboration on Transboundary Animal Diseases and Emerging Infectious Diseases by Mongolia, China and the Russian Federation 12th – 13th October 2016, Vladimir, Russia.

- a. Heads of the Competent Veterinary Authorities from China, Mongolia and Russia, representatives of FAO and international organizations dealing with transboundary animal diseases. The major topic of the meeting was the strengthening of trilateral cooperation and data exchange on such dangerous animal diseases as FMD, ASF, HPAI, PPR and LSD participated in the meeting held on 12th - 13th October, housed by ARRIAH.

South Africa

Collaborators	Collaborative project	Outcomes
Dr B. Charleston (The Pirbright Institute), Oxford University	NSF-EID funded project investigating Persistence of FMD in African buffalo	Maree <i>et al.</i> (2016). <i>Journal of Virology</i> , 90 (10), 5132-40. Scott <i>et al.</i> (2017). <i>Journal of Virology</i> , DOI: 10.1128/JVI.02312-16.
Dr R. Reeve (University of Glasgow)	Tracking the antigenic evolution of foot-and-mouth disease virus	Reeve <i>et al.</i> (2016). <i>PLOS ONE</i> , 11 (7), e0159360.
Drs E. Rieder & TT. De los Santos (PIADC, USDA, ARS), Oxford University	USDA funded project to develop antigenically improved vaccines and adenovirus vaccines for FMD control	Ramulongo <i>et al.</i> (in preparation).
Dr A. Capozzo (INTA)	Implementation of novel in vitro assays to assess protection	Scott <i>et al.</i> (2017). <i>Vaccine</i> (in publication).
Dr K. de Clercq (CODA-CERVA-VAR), Dr E. Brocchi (IZSLER)	3ABC ELISA for southern Africa	Chitray <i>et al.</i> (in preparation).

Thailand

Collaborators	Collaborative project	Outcomes
National Institute of Animal Health (NIAH), Kodaira lab, Japan	<ul style="list-style-type: none"> ① Collaborating projects on Technology transfer on Sequencing ② Research topic: FMDV Whole Genome Sequencing ③ The recovery of FMD virus in probang (O/P) samples in positive NSP animals 	<ul style="list-style-type: none"> ① Two trainees from RRL were trained in NIAH, Japan for FMDV whole genome sequencing. ② Scientific information on Molecular epidemiology of FMDV and genomic variation information. ③ Information for FMD carrier animals to support the epidemiology and FMD control in Thailand
Department of National Park wildlife and Plants Conservation, Thailand	Sero-surveillance study in Wild life (One Health approach)	Information of FMDV serology in wildlife animals, zoo and national parks
World Reference Laboratory (WRLFMD), Pirbright Institute, UK (with the kind assistance from Dr. Valerie Mioulet)	Development of molecular serotyping of foot and mouth disease virus by real time RT-PCR.	Rapid and new technology for FMDV genotyping in field specimens
Animal and Plant Quarantine Agency (QIA), Republic of Korea	<ul style="list-style-type: none"> ① Validation of developed rapid diagnostic kit for FMD serotype ② Technology transfer to QIA staff on vaccine matching technique 	<ul style="list-style-type: none"> ① New diagnostic test kit for rapid test to be applied in FMD control measures ② Update and sharing information on FMD antigenic variation in the region

United Kingdom

Collaborators	Collaborative project	Outcomes
Malaysian Government	Development of vaccine matching tests for Southeast Asia	Improvement of serological tests for vaccine matching
CODA-CERVA (Belgium), FLI (Germany), SLU (Sweden), IZSVe (Italy) and University of Glasgow (UK)	Molecular epidemiology of epizootic diseases using next generation sequencing technology	Apply new technologies for molecular epidemiology
IZSLER (Italy)	Development of FMD ELISA tests	New ELISA tests for FMD diagnosis
SUA (Tanzania) and TVLA (Tanzania)	Improved tools for the surveillance and diagnosis of FMD	Understanding the epidemiology of FMD in endemic settings
NAHDIC (Ethiopia)	OIE Twinning Project	Improved diagnostic capacity for Ethiopia
Miyazaki University (Japan)	Validation of field tests for FMDV	Generate validation data for field tests
National Institute for Animal Health (Japan)	Development of new FMDV antigen field assays	Evaluation of new antigen ELISA formats

United States of America

Collaborators	Collaborative project	Outcomes
NAFMDVB	NSP serological confirmatory test	Protein Expression and His-tag Purification of: 2C, 3A, 3B, 3C, 3ABC and 3D
VDL-Central America	Differential diagnostic and enhance FMD surveillance	VSV IgG/IgM ELISA test validation
NAFMDVB	FMD Vaccine Matching Development	Standardization and optimization of SOP
RVSS-NAFMDVB	Development of in-house OIE standard LBPE and SPCE	Is now in validation phase

Appendix 1 - Details of clinical samples from field cases from countries in FMDV endemic regions tested during 2016

Laboratory	Samples from	Total	O	A	C	Asia 1	Sat 1	Sat 2	Sat 3	Untyped	NVD	Comments
Belgium	Nigeria	10	-	-	-	-	10	-	-	-	-	
	Benin	22	-	-	-	-	-	-	-	-	22	
	Botswana	6	-	-	-	-	-	-	-	-	6	
	D.R. Congo	3	-	-	-	-	-	-	-	-	3	
	Malawi	1	-	-	-	-	1	-	-	-	-	
	Mauritius	18	10	-	-	-	-	-	-	-	8	
	Zambia	10	-	-	-	-	-	-	-	-	10	
Botswana	Zimbabwe	5	-	-	-	-	-	2	-	-	3	
	Canada	500	-	-	-	-	-	-	-	-	500	Testing for differential diagnosis: 144 of the samples tested positive for Senecavirus A
China	China	34	17	-	-	-	-	-	-	10	17	
Ethiopia	Ethiopia	165	69	24	-	-	8	33	-	-	34	
France	Mauritius	13	10	-	-	-	-	-	-	-	3	
India	India	672	110	11	-	3	-	-	-	-	209	
Kenya	Kenya	79	5	20	-	-	25	1	-	-	28	
Nigeria	Nigeria	37	17	2	-	-	10	-	-	-	8	
Russia	Armenia	4	-	4	-	-	-	-	-	-	-	
	Mongolia	5	-	5	-	-	-	-	-	-	-	
	Kazakhstan	16	-	-	-	-	-	-	-	-	16	
	Russia	108	-	-	-	18	-	-	-	-	90	
South Africa	South Africa	23	-	-	-	-	-	-	5	-	18	
	Mauritius	64	6	-	-	-	-	-	-	-	58	
	Mozambique	2	-	-	-	-	-	1	-	-	1	
South Korea	Swaziland	1	-	-	-	-	-	-	-	-	1	
	South Korea	21	18	-	-	-	-	-	-	-	3	
Thailand	Thailand	253	137	51	-	-	-	-	-	-	65	
	Lao P.D.R.	47	-	-	-	-	-	-	-	-	47	All negative due to small volume and sample quality
	Myanmar	22	19	-	-	-	-	-	-	-	3	
Turkey	Turkey	1128	399	444	-	-	-	-	-	74	211	
	Afghanistan	27	10	1	-	3	-	-	-	10	3	
	Bhutan	14	1	-	-	-	-	-	-	12	1	
	Botswana	6	-	-	-	-	4	1	-	1		
	Egypt	35	19	2	-	-	-	2	-	1	11	
	Ethiopia	16	1	1	-	-	-	7	-	4	3	
	Hong Kong	8	7	-	-	-	-	-	-	-	1	
	Iran	54	23	20	-	4	-	-	-	3	4	
	Israel	10	10	-	-	-	-	-	-	-	-	
	Kuwait	4	3	-	-	-	-	-	-	1	-	
	Laos	3	-	-	-	-	-	-	-	3	-	
	Malawi	1	-	-	-	-	-	-	-	1	-	
	Malaysia	26	12	1	-	-	-	-	-	13	-	
	Mauritius	24	23	-	-	-	-	-	-	1	-	
	Mozambique	2	-	-	-	-	-	1	-	-	1	
	Myanmar	4	-	-	-	-	-	-	-	2	2	
	Namibia	4	-	-	-	-	-	1	-	2	1	
	Nepal	50	31	-	-	-	-	-	-	12	7	
	Nigeria	25	17	-	-	-	3	-	-	1	4	
	Pakistan	35	10	9	-	9	-	-	-	6	1	
	Palestine	6	6	-	-	-	-	-	-	-	-	

Laboratory	Samples from	Total	O	A	C	Asia 1	Sat 1	Sat 2	Sat 3	Untyped	NVD	Comments
	South Korea	15	2	-	-	-	-	-	-	11	2	
	Saudi Arabia	36	10	11	-	-	-	-	-	2	13	
	Sudan	37	6	5	-	-	-	6	-	6	14	
	Thailand	59	28	23	-	-	-	-	-	8	-	
	UAE	6	6	-	-	-	-	-	-	-	-	
	Vietnam	35	21	8	-	-	-	-	-	5	1	
	Zambia	3	-	1	-	-	-	1	1	-	-	
	Zimbabwe	4	-	-	-	-	-	2	-	1	1	
USA	USA	4401	-	-	-	-	-	-	-	-	4401	Samples tested for differential diagnosis
Totals		8219	1063	643	-	37	61	58	6	193	5832	

Appendix 2 - Vaccine matching studies undertaken by network partners during 2016

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:

M	Matched with the vaccine
B	Borderline
N	Not matched with the vaccine

For VNT:

$r_1 \geq 0.3$ – 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

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

For LB-ELISA:

$r_1 \geq 0.4$ – 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

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

Argentina

214 determinations in collaboration with QIA, Korea.

Botswana

Name of Field Isolate	Name of Vaccine strain	Vaccine strain	
		2D-VNT r1 value	Name of Vaccine strain 2D-VNT r1 value
SAT 1/MAL1/2016	SAT105	0.40	SAT109 0.50
O/MUS02/2016	O-Manisa	0.38	
SAT 3/ZAM05/2015	SAT306	0.35	
SAT 3/ZAM06/2015	SAT306	0.39	
SAT 2/MOZ01/2015	SAT2035	0.60	
SAT 2/BOT03/2016	SAT251	0.53	
SAT 2/ZIM01/2016	SAT251	0.72	SAT2035 0.40

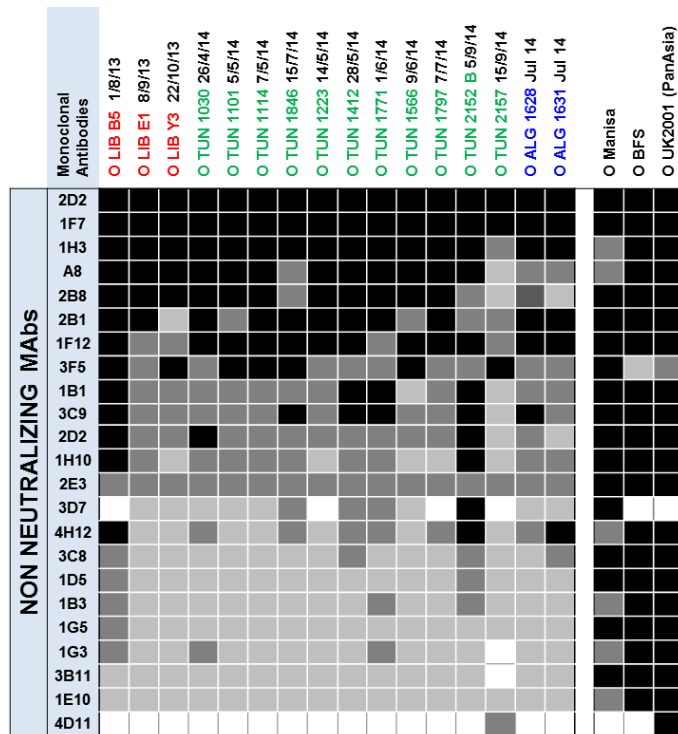
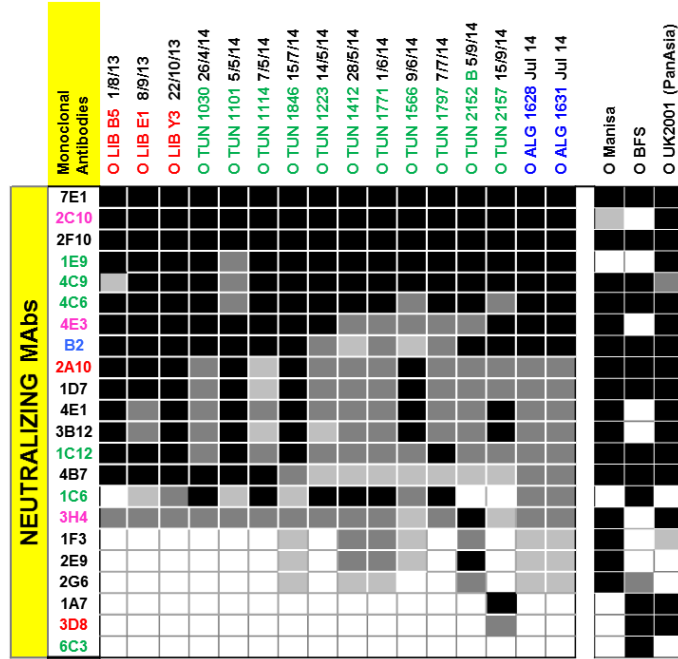
India

Serotype	Number	Vaccine strain
O	57	O IND R2/1975
A	6	A IND 40/2000
Asia-1	2	Asia-1 IND 63/1972

Italy

The antigenic profile of isolates from the Maghreb 2014-2015 epidemic wave was analysed by using serotype-specific (FMDV type O) monoclonal antibodies.

Legend for MAbs: blu character, target site 1; green: target site 2; pink: target site 3; red: mixed target sites



NB: Strength of binding for each of the monoclonal antibodies is indicated by the relative darkness of the squares shown in the tables.

Kenya

VNT/LPBE	
Name of Field isolate (No.)	Vaccine strain
(15)	SAT1 T155/71
(25)	SAT2 K52/84
(20)	A K5/80
(25)	O K77/78

Note: all vaccine matching in progress

Thailand

	N	O/189/87 Thai vaccine strain r-value range		
		0 - 0.19	2.0 - 0.39	0.40 - 1.0
Thailand	23	0	0	23
Lao PDR	47*	Not Done		
Myanmar	22*	Not Done		

** Virus isolation could not be done, due to the small amount of virus obtained and bacterial contamination in samples*

Country	N	A/Lopburi/2012			A/Sakolnakorn/97		
		0-0.19	2.0-0.39	0.40-1.0	0-0.19	2.0-0.39	0.40-1.0
Thailand	15	4	7	4	-	-	15
Lao PDR	47	Not Done					
Myanmar	22	Not Done					

Russia

Name of Field isolate	Vaccine strain (Serotype A)						
	A22 N550	A22 Iraq/64	A Iran/97	A TUR/06	A Sea-97 /2013	A Iran/05/2013	A ARRIAH/2016
A/Armenia/16	N	N	N	N	N	N	M
A/Mongolia/16	N	nd	N	M	M	N	N

Turkey

Field Isolates	Vaccine strain		
	Asia1 Shamir	Asia1 TUR11	Asia1 TUR 14
As1 Sindh 08 (2015 isolate)	N	N	M

Field Isolates	Vaccine strain		
	O1 Manisa	O TUR07	O TUR14
O QOM-(2015 isolate)	M	M	N
O QOM-(2015 isolate)	M	M	N

Field Isolates	Vaccine strain
	GVII
A05 (2006 isolate)	N
A05 (SIS10 / 2011 isolate)	N
A05 (SIS10 / 2015 isolate)	N

United Kingdom

Sample	Serotype	Topotype	Strain	O 3039	O Manisa	O/TUR/5/2009	O/SKR/7/10	O/Russia/2000*
HKN/8/2015	O	CATHAY	-	N	N	N	N	M*
HKN/9/2015	O	CATHAY	-	N	N	N	N	M*
EGY/18/2016	O	EA-3	-	N	N	N		
EGY/7/2016	O	EA-3	-	N	M	N		
ETH/1/2016	O	EA-4	-	M	N	M		
PAK/49/2015	O	ME-SA	ANT-10	M	M	M		
PAK/30/2015	O	ME-SA	BAL-09	M	M	M		
MUR/06/2016	O	ME-SA	Ind-2001d	M	M	M		
MUR/07/2016	O	ME-SA	Ind-2001d	M	M	M		
SAU/1/2016	O	ME-SA	IND-2001d	M	M	M		
SAU/7/2016	O	ME-SA	IND-2001d	M	M	M		
PAK/22/2015	O	ME-SA	Pak-98	M	M	M		
TAI/16/2015	O	ME-SA	PanAsia	M	M	M		
IRN/25/2016	O	ME-SA	PanAsia-2	M	N	M		
AFG/04/2016	O	ME-SA	PanAsia-2 ^{ANT-10}	M	M	M		
AFG/12/2016	O	ME-SA	PanAsia-2 ^{ANT-10}	M	M	M		
AFG/15/2016	O	ME-SA	PanAsia-2 ^{ANT-10}	M	M	M		
AFG/16/2016	O	ME-SA	PanAsia-2 ^{ANT-10}	M	M	M		
SAU/18/2016	O	ME-SA	PanAsia-2 ^{ANT-10}	M	M	M		
MAY/1/2015	O	SEA	Mya-98	M	M	M		
MAY/10/2016	O	SEA	Mya-98	M	M	M		
MAY/17/2014	O	SEA	Mya-98	M	M	M		
MAY/5/2016	O	SEA	Mya-98	M	M	M		
TAI/26/2015	O	SEA	Mya-98	M	B	M		
TAI/26/2016	O	SEA	Mya-98	M	N	B		
TAI/37/2016	O	SEA	Mya-98	M	N	M		
TAI/9/2015	O	SEA	Mya-98	M	B	M		
NIG/01/2016	O	WA	-	N	N	B		
NIG/04/2016	O	EA-3	-	N	N	B		
NIG/12/2016	O	EA-3	-	M	M	M		
NIG/19/2016	O	EA-3	-	M	M	M		

* homologous neutralisation titre is below the acceptable limit and caution should be taken when interpreting these results.

Sample	Serotype	Topotype	Strain	A22 IRQ	A IRN 05	A/TUR/20/2006	A/Eritrea	A/IND/40/2000*	A/TUR/11	A/TUR/14	A/MAY/97	A/SAU/95
ZAM/1/2016	A	AFRICA	G-I	N	N	N	N					
EGY/3/2016	A	AFRICA	G-IV	N	N	N	M					
ETH/19/2015	A	AFRICA	G-IV	N	N	N						
IRN/12/2015 [†]	A	ASIA	G-VII					N	N	N		
IRN/8/2015 [†]	A	ASIA	G-VII					N	N	N		
IRN/8/2016	A	ASIA	G-VII	N	N	N						
SAU/1/2015 [†]	A	ASIA	G-VII					N	N	N		
SAU/19/2016	A	ASIA	G-VII	N	N	N						M
PAK/53/2015	A	ASIA	Iran-05 ^{FAR-09}	N	M	N						
AFG/5/2016	A	ASIA	Iran-05 ^{FAR-11}	N	N	N						M
PAK/31/2015	A	ASIA	Iran-05 ^{FAR-11}	N	N	M						
MAY/15/2014	A	ASIA	Sea-97	M	N	N					M	
TAI/20/2016	A	ASIA	Sea-97	N	N	N						
TAI/23/2016	A	ASIA	Sea-97	M	M	N						
IRN/6/2016	A	ASIA	SIS-10	M	M	N						

[†] Additional vaccine matching data can be found in 2015

Sample	Serotype	Topotype	Strain	Asia 1 Shamir	Asia 1 IND 8/79
TUR/37/2014	Asia 1	ASIA	Sindh-08	N	N
TUR/12/2015	Asia 1	ASIA	Sindh-08	N	N
PAK/28/2015	Asia 1	ASIA	Sindh-08	N	
PAK/38/2015	Asia 1	ASIA	Sindh-08	N	
IRN/26/2016	Asia 1	ASIA	Sindh-08	N	
AFG/6/2016	Asia 1	ASIA	Sindh-08	M	
AFG/10/2016	Asia 1	ASIA	Sindh-08	M	

Sample	Serotype	Topotype	Strain	SAT 1/RHO/12/78
ZIM/10/2015	SAT 1	II(SEZ)		B
ZIM/14/2015	SAT 1	II(SEZ)		N
BOT/5/2015	SAT 1	III		M
NIG/1/2015	SAT 1	X	-	N
NIG/2/2015	SAT 1	X	-	N

Sample	Serotype	Topotype	Strain	SAT 2 Eritrea	SAT 2 ZIM/7/83
MOZ/3/2015	SAT 2	I		M	M
ZIM/13/2015	SAT 2	II		M	M
ZIM/20/2015	SAT 2	II		N	B
ZIM/25/2015	SAT 2	II		M	M
ZIM/5/2015	SAT 2	II		B	N
BOT/3/2015	SAT 2	III		M	M
EGY/5/2015	SAT 2	VII	Alx-12	M	M
ETH/16/2015	SAT 2	VII	Alx-12	M	N
EGY/44/2012	SAT 2	VII	Ghb-12	M	B
SUD/9/2013	SAT 2	VII	Ghb-12	M	M

Sample	Serotype	Topotype	Strain	SAT3 Zim
ZAM/3/2015	SAT 3	II		N

Appendix 3 - Nucleotide sequence analysis

FMDV nucleotide sequence data for phylogenetic analysis (1041 sequences which include some complete viral capsids sequences* and complete genomes†)

Laboratory	Samples from	Region	O	A	C	Asia 1	Sat 1	Sat 2	Sat 3
Belgium	Nigeria	Capsid				Ongoing			
	Malawi					1			
Botswana	Mauritius		5						
	Zimbabwe						3		
China	China	VP1	22	16					
Ethiopia	Ethiopia	VP1	1	1				7	
France	Mauritius	VP1	9						
	India	VP1	70	6		2			
	India	Capsid	57	6		2			
	India	Complete Genome	17						
	Algeria	VP1	5						
	Algeria	Complete Genome	5						
Italy	Tunisia	VP1	12						
	Tunisia	Complete Genome	12						
Kenya	Kenya	VP1	25	38			32	25	
Nigeria	Nigeria	VP1	17				3		
	Armenia	VP1		4					
	Mongolia	VP1		3					
Russia	Russia	VP1				4			
	Russia	Complete Genome				3			
South Africa	Mauritius	VP1	1						
	Mozambique	VP1						1	
South Korea	South Korea	VP1	20						
	South Korea	Complete Genome	2						
	Lao PDR	VP1	2						
Thailand	Myanmar	VP1	7						
	Thailand	VP1	54	18					
Turkey	Turkey	VP1	72	58					
	Turkey	Capsid	2	1					
	Afghanistan	VP1	10	1	3				
	Bhutan	VP1	6						
	Botswana	VP1				4	1		
	Egypt	VP1	19	2			2		
	Ethiopia	VP1	1	1			7		
	Hong Kong	VP1	7						
	Iran	VP1	23	22	4				
	Israel	VP1	10						
UK	Kuwait	VP1	3						
	Laos	VP1	1						
	Malawi	VP1							
	Malaysia	VP1	12	1					
	Mauritius	VP1	23						
	Mauritius	Complete Genome	1						
	Mozambique	VP1					1		
	Myanmar	VP1	1						

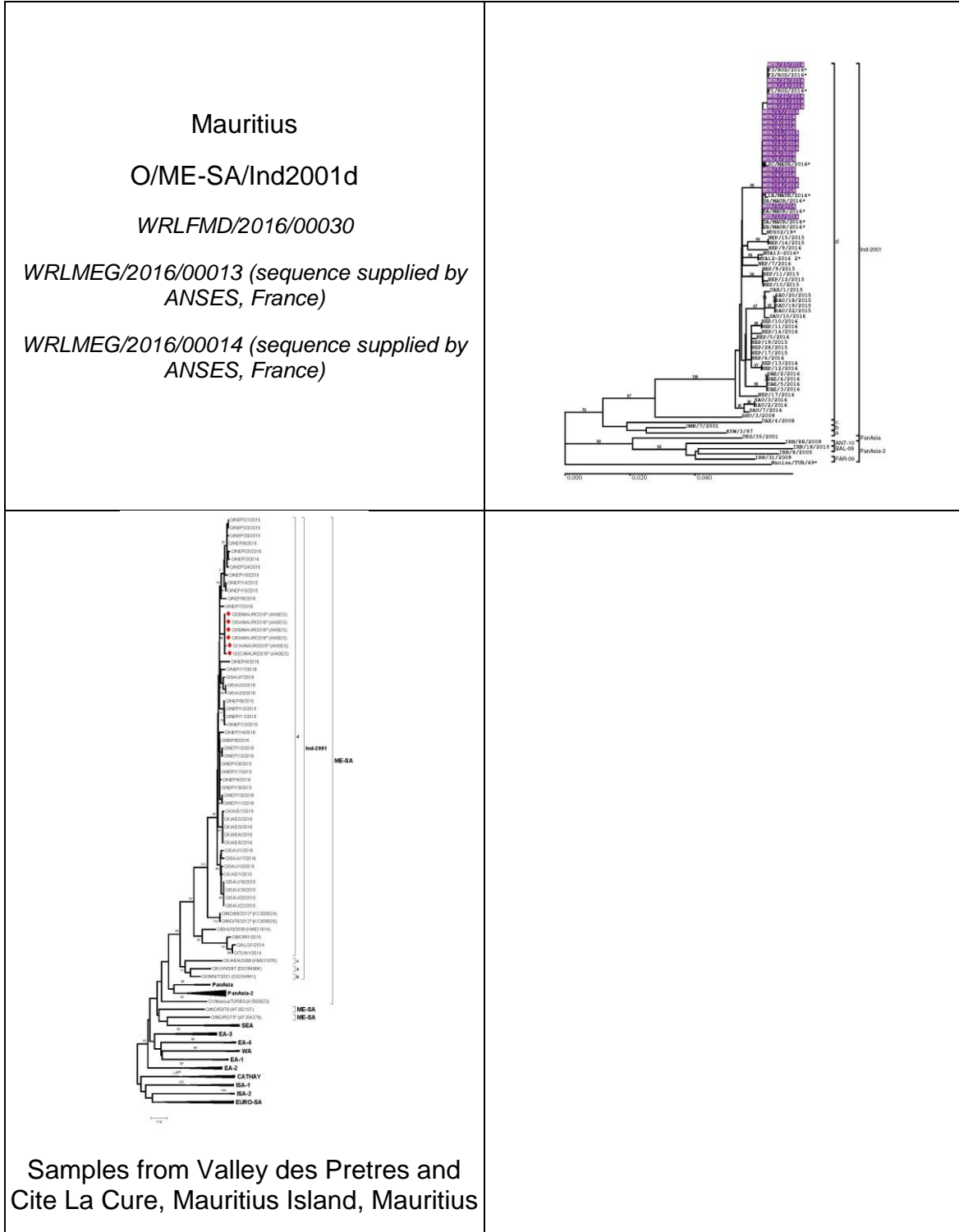
Laboratory	Samples from	Region	O	A	C	Asia 1	Sat 1	Sat 2	Sat 3
	Namibia	VP1					1		
	Nepal	VP1	31						
	Nigeria	VP1	17			3			
	Pakistan	VP1	10	9	9				
	Palestinian Autonomous Territories	VP1	6						
	Saudi Arabia	VP1	11	11					
	South Korea	VP1	7						
	Sudan	VP1	6	5			6		
	Thailand	VP1	28	23					
	UAE	VP1	6						
	Vietnam	VP1	21	8					
	Zambia	VP1		1			1	1	
	Zimbabwe	VP1					2		
USA	USA	Complete Genome	2		2	1			1

Appendix 4 - Selected Phylogenetic trees

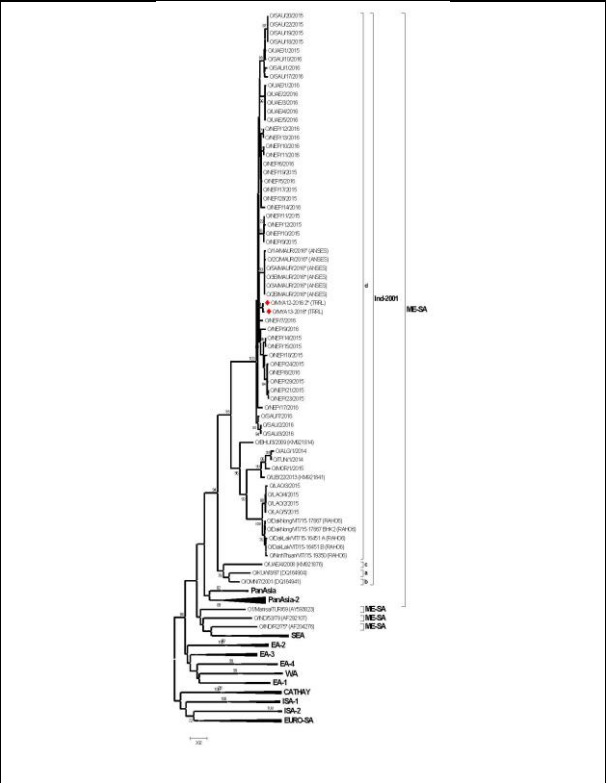
Lists by County

Detailed sequencing reports can be found at :

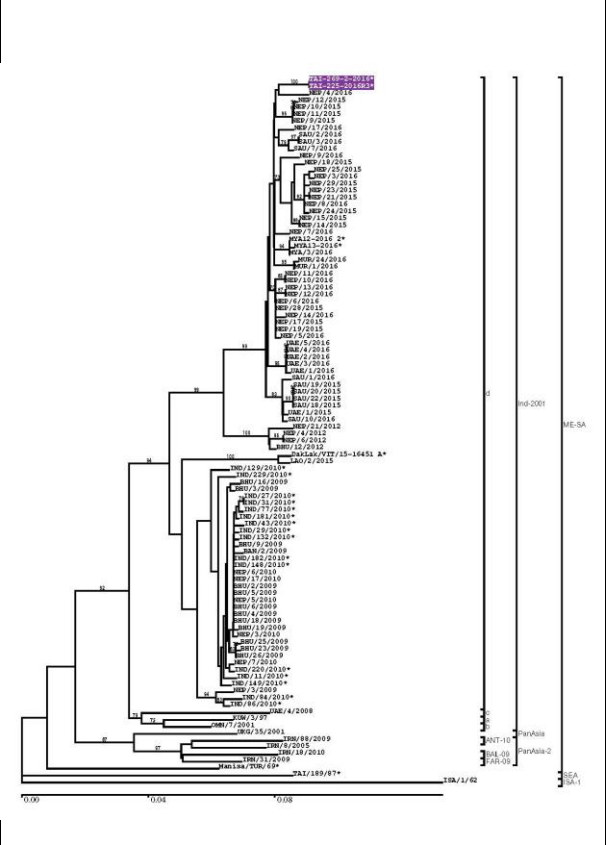
http://www.wrlfmd.org/fmd_genotyping/index.html



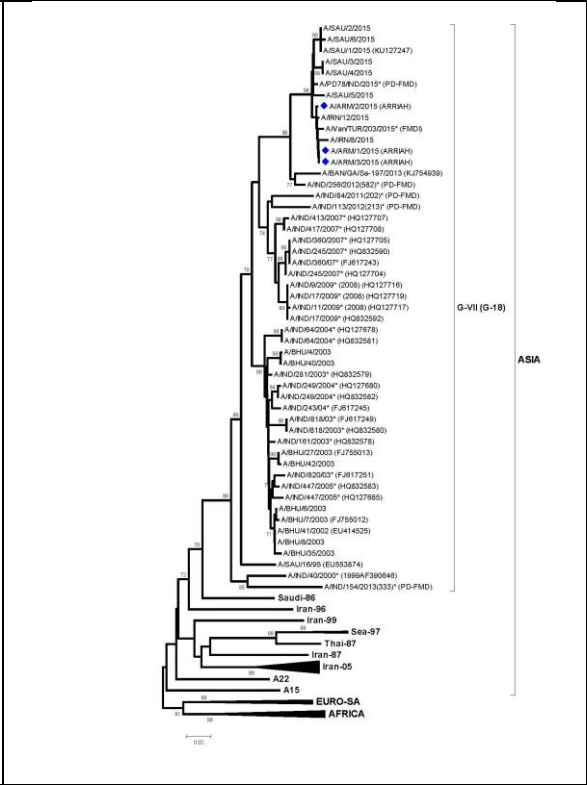
Myanmar
O/ME-SA/Ind2001d
WRLMEG/2016/00015 or 16 (sequence
supplied by RRLSEA, Thailand)



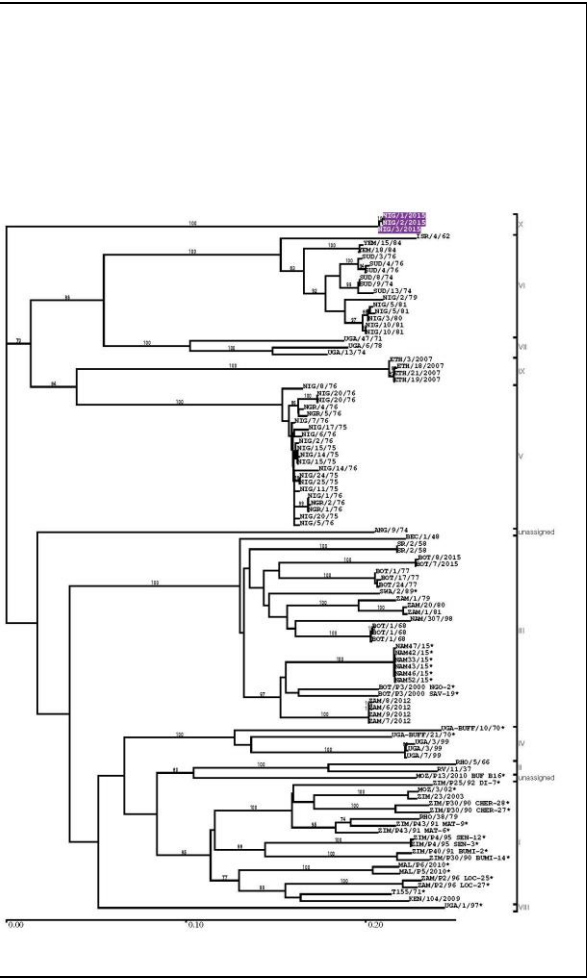
Thailand
O/ME-SA/Ind2001d
WRLMEG/2016/00023 (sequence supplied by
RRLSEA, Thailand)



Armenia
A/ASIA/G-VII
*WRLMEG/2015/00021 (sequence supplied by
FGBI-ARRIAH, Russia)*



Nigeria
SAT 1/X
WRLFMD/2016/00034



Appendix 5 - Report from the 11th OIE/FAO FMD Laboratory Network Meeting. ANSES, Maisons-Alfort, Paris, France: 30th of November - 2nd of December 2016



Regional Reports [1st December 2016]

Global Overview, Dr Don King (WRLFMD, Pirbright)

This presentation highlighted the results for samples tested recently at WRLFMD, Pirbright (www.wrlfmd.org) and reviewed the current global FMD status. Continuing on from the theme from last year's meeting, the main message of the talk was that there appears to be an upsurge in long-distance trans-pool movements of FMD virus from Pools 1 and 2 (recent high-profile examples O/ME-SA/Ind-2001d and A/ASIA/G-VII). In Europe, the greatest concerns relate to the emergence of the A/ASIA/G-VII lineage that has spread to the margins of Anatolian Turkey (close to the FMD-free [with vaccination] zone in Thrace) since *in vitro* and *in vivo* data indicates that vaccines (containing A-SAU-95 or A-Iran-05-like viruses) supplied by Merial and MSD are unlikely to provide protection. Further cattle studies to evaluate A22 and A-May-97 are planned for December 2016 at CVI-Lelystad.

Pool 1: South East Asia, RRLSEA (Packchong), Dr Wilai Linchongsubongkoch

Samples (n=255) collected in Thailand and Myanmar were tested; additional samples (n=47) from Lao PDR were all negative. The genome results were as following:

- Thailand (n=72) O/SEA/Mya-98, O/ME-SA/Ind2001d and A/Asia/Sea-97

- Lao (n=2) O/ME-SA/Ind-2001d (samples from 2015)
- Myanmar (n=7) O/SEA/Mya-98, O/ME-SA/Ind2001d

Vaccine matching were carried out using the locally produced vaccines: O/189/87 appears to match the new emerging O/ME-SA/Ind2001d [although data is still urgently required to support the use of this vaccine against this emerging lineage in the field], A/Sakolnakorn/97 continues to show a good a match while A/Lopburi/2012 has a decreased match against serotype A viruses in the region. An inter-laboratory proficiency testing scheme (PTS) was organised (17 regional participants).

Pool 1: East Asia and China, LVRI, Dr Yanmin Li

In 2016 samples were received from China (n=23) of which fourteen were serotype O (remainder negative). In order to support active surveillance in northeast and southeast China, approx. 4000 oropharyngeal and tissue sample were collected and tested by real-time RT-PCR. These samples collected from apparently healthy animals (without clinical signs) yielded serotype O (O/CATHAY, O/SEA/Mya-98) and serotype A (A/ASIA/Sea-97) sequences. These are the first confirmed reports of O/CATHAY in mainland China. Approximately, 6000 sera were also tested by LPBE and 3ABC ELISA in these parts of the country.

The locally vaccines produced are:

- Serotype A Recombinant vaccine Re-A/WH/09
- Serotype O O/China99 and O/Mya98/BY/2010
- Serotype Asia 1 Asia 1/JSL/06

A PTS assessing real-time RT-PCR was distributed to 31 regional laboratories and all laboratories provided satisfactory results. National and international training was carried out including Myanmar. The lab provided both antibody kits (LPBE O, A and Asia 1) and antigen kits (multi-RT-PCR and real-time PCR).

Pool 1: Korea and East Asia, Animal and Plant Quarantine Agency (QIA) , Dr Jong-hyeon Park

During 2016, outbreaks in South Korea have occurred (due to the O/SEA/Mya-98 lineage). Up to March 2016, 21 farms in the west of the country were affected by FMD and sequence data indicates that the causative virus strain is a unique sub-clade of O/SEA/Mya-98. Additional farms (147 pig holdings and 11 cattle farms) were NSP positive in the same area of the country indicating that FMD virus may be circulating more widely. International vaccine available are O1 Manisa+O 3039. Since November 2016, additional vaccines (O Campos, O Primosky) have been deployed for emergency purposes because of limited supply of other vaccines. Post-vaccination monitoring in cattle and fattening pigs indicates good results with structural protein O ELISAs showing a 95% and 65% protection level. The laboratory currently organises national PTS twice a year (n=6). There is a collaborative network with RRLSEA and other regional partners.

Pools 1 and 3: Russia, ARRIAH, Dr Dmitry Lozovoy

Over the last twelve months, samples have been tested from Armenia (A/ASIA/G-VII, n=4), Russia (n=108), Kazakhstan (n=16) and Mongolia (A/Sea-97, n=5). New vaccine strains (A/Armenia/16 and A/Mongolia/16) have been

prepared to meet the challenges of these FMD virus lineages that are circulating in the region. The recent Asia 1 FMD cases that have occurred in Russia (October 2016) is due to a FMD virus that is phylogenetically closely related to Asia 1/Shamir/89 (with 12 nt substitutions); and an official investigation is ongoing to understand the source of these outbreaks. Other recent outbreaks in the east of Russia (close to the Chinese border) have been characterized as belonging to the O/ME-SA/Ind2001d lineage; which is yet another example of the long distance spread of this lineage. A PTS was organised for Armenia, Azerbaijan, Belarus, Moldavia, Tajikistan and Kyrgyzstan.

Pool 2: India, PD-FMDV, Dr Jitendra Biswal

This presentation reviewed the latest situation for FMD in India. Samples (n=672) have been collected and tested in 2015/16 from different regions in the country. These are dominated by the O/ME-SA/Ind2001d lineage – comprising 244/252 positive samples. Serotype A/G-VII (18) has split into two genetic sub-lineages and only the VP3-59 deletion group is now seen in the country. Serotype Asia 1 grouped into lineage C is restricted to the Northern region of India. The vaccine strains used in the region are: O/IND/R2/1975, A/IND/40/2000 and Asia 1/IND/63/1972. In order to address, antigenic variability within serotype A, three new candidate vaccine strains (strain-1, strain-2 and strain-3) are being evaluated; it is proposed that the most promising of these (strain 1) will move into vaccine production shortly.

Pool 3: Turkey and Pool 3, ŞAP Institute, Dr Fuat Ozyoruk

Over one thousand samples (1128) collected within Turkey have been tested during 2016. Real-time RT-PCR and typing RT-PCR assays have been used to detect serotypes O (n=399) and A (n=444 [emerging A/ASIA/G-VII lineage]), while an additional 74 samples were only positive on pan-serotypic FMDV assays. The current circulating strains are: A/ASIA/G-VII^{BAN-12} and O/ME-SA/PanAsia-2^{QOM-15}; no A/ASIA/IRN-05 samples or serotypes Asia 1 has been detected in 2016. This presentation also provided an overview of the FMD virus lineages that are circulating more widely in Pool 3; where notably no FMD cases due to the O/ME-SA/Ind-2001d lineage have been detected in countries to the north of the Arabian Gulf. In response to the A/ASIA/G-VII outbreaks, a new vaccine was manufactured and is now being used in Turkey, where in Thrace vaccine coverage >90% in is achieved in large ruminants [2x year] and small ruminants [1x year] – this vaccine is also now being used in private farms in Saudi Arabia.

North Africa, IZSLER, Dr Santina Grazioli

No clinical samples or sera were sent to Brescia in 2016. Therefore, the work presented described the results of full-genome sequencing studies for samples collected from the O/ME-SA/Ind-2001 outbreaks in North Africa in 2014 and 2015. These data support a logical spread of FMD virus from Libya (in 2013) to Morocco (in 2015), and highlight two independent introductions of the virus from Tunisia into Algeria. A PTS was organised for ten Balkan countries for RT-PCR and ELISA. IZSLER has sold 1116 ELISA kits to 38 countries, which is a 35% increase since 2015. A new antigen ELISA kit comprises a single kit format that includes serotypes O, A, Asia 1, C, SAT 1 and SAT 2. The validation work carried

out by the WRLFMD shows an increased sensitivity and specificity as compared to the polyclonal ELISA.

West Africa and Mauritius, ANSES, Dr Labib Bakkali Kassimi

Dr Bakkali Kassimi provided an overview of the situation in West Africa; highlighting data presented at the recent 1st Regional Roadmap meeting Lomé, Togo. For Pool 5 (West Africa), there has been a modest increase in the number of samples received since 2013; however there are still gaps in our understanding of FMD epidemiology in the region. Serological data presented on behalf of the FMD Laboratory in Senegal, provides evidence for the circulation of serotypes O and A in central and western parts of the country and Serotype SAT 2 in the south. Twenty seven percent of the samples were positive for NSP. The remainder of the talk covered the recent FMD outbreaks that have occurred in Mauritius (July 2016). Diagnostic results from ANSES (VI, Ag-ELISA, pan-serotypic RT-PCR and type-specific RT-PCRs) showed that the causative FMD virus was serotype O – subsequently confirmed by sequence analyses at ANSES and WRLFMD showing that this was yet another example of an unexpected movement of the O/ME-SA/Ind-2001d lineage. The epidemiological links to other countries where the O/ME-SA/Ind-2001d is circulating is being investigated.

Pool 4: East Africa, Embakasi, Kenya, Dr Abraham Sangula

Diagnostics results for samples (n=79) collected in Kenya were presented; highlighting the circulation of serotypes O (n=5), A (n=20), SAT 1 (n=25), SAT 2 (n=1). These data indicate that serotypes A and SAT 1 are increasing in the country. VP1 sequencing and vaccine matching studies are still underway and the toptype/lineage are not known at this time. The current local vaccine strains are SAT 1 T155/71 (NWZ), SAT 2 K52/84 (IV), A K5/80 (G1) and O K77/78 (EA1).

Pool 4 East Africa, NAHDIC, Ethiopia, Dr Daniel Gizaw

Results for 165 samples collected in Ethiopia were presented. This work is supported by WRLFMD (via an on-going OIE Twinning Project). Antigen ELISA detected serotypes O (n=69), A (n=24), SAT 1 (n=8) and SAT 2 (n=33). Sequencing carried out at WRL detected the following lineages: O/EA-4, SAT 2/VII^{Alx-12} and A/Africa/G-IV. Surveillance in small ruminants (11,939 sera) suggests that 7.4% are positive for FMDV. In addition to internationally supplied vaccines, locally produced vaccines for serotypes A, O and SAT 2 are available from the National Veterinary Institute.

Pool 5 West Africa, NVRI, Vom Nigeria, Dr Hussani Ularamu and, CODA-CERVA, Dr Kris De Clercq

Four FMD virus serotypes circulate in West Africa (O, A, SAT 1 and SAT 2). Work at NVRI, Vom is supported by an on-going OIE Twinning project with CODA-CERVA. During 2016, a genetically distinct SAT 1 FMD virus lineage was detected (and sequenced) in samples collected from Nigeria, for the first time this serotype has been detected (anywhere in West Africa) since 1981. Additional samples tested during 2016 comprised serotypes O (n=12) and A (n=2). Interestingly, these data suggest that mixed infections (samples where different FMDV serotypes) have been observed – also seen recently in Ethiopia.

NVRI is developing new vaccine strains (A Nig07/13, O Nig03/14, and SAT 2 Nig03/12) for use in the country. Additional data presented by CODA-CERVA reported a collaboration with BVI (Botswana) which resulted in three full genome sequences of a SAT 1, SAT 2 and O FMDV (published and available in GenBank).

Pool 4-6: Sub Saharan Africa, OVI, Dr Francois Maree

Results for samples tested in 2016 were presented: Mauritius (n=61), Mozambique (n=70), Namibia (n=1), Swaziland (n=142), UAE (n=1) and Zimbabwe (n=68). Sequence results for SAT 2/MOZ/1/2016 characterised the FMD virus as belonging to toptype 1, appearing to be a continuation of the 2014 outbreak. The FMD virus causing the SAT 3 outbreak in South Africa (control zone in Limpopo) was similar to SAT 3/KNP/1/08. Dr Maree also provided an overview of research activities at OVI, including work to understand FMDV persistence and transmission in buffalo in KNP.

Pool 4-6: Sub Saharan Africa, BVI-RRLSSA, Dr George Matlho

During 2016, BVI tested samples collected from Malawi (SAT 1 Topotype 1 virus pool 6), Mauritius (Serotype O/ME-SA/Ind-2001d) and Zimbabwe (SAT 2 Topotype 2 virus pool 6). Samples were also received from Botswana (n=6), Benin (n=22), DR Congo (n=3) and Zambia (n=10); however, no virus was detected. Vaccine matching work was undertaken at BVI providing evidence that SAT105 and SAT109 is matched to the field strains circulating in Malawi, SAT251 and SAT2035 is matched to the SAT 2 viruses in Zimbabwe, and O-Manisa is matched to the O/ME-SA/Ind-2001 virus recovered from Mauritius.

Pool 7: South America, PANAFTOSA, Dr Rosanna Allende

FMDV was detected during retrospective analysis of samples collected in 2013 from FMD outbreaks in Venezuela. These were characterised as serotype A, genetically most closely related to earlier FMD viruses recovered from Venezuela [these samples represent the most recent FMD outbreaks anywhere in South America]. Collaborative programs are in place with Venezuela and post vaccination monitoring is currently underway for the border region (~4000 samples have been collected for LPBE testing – serotypes O and A). PANAFTOSA organised a PTS (FMDV and vesicular stomatitis virus) for antigen ELISA and 13 laboratories participated. All South American countries and Panama also have collaborative program with the FMDV regional antigen bank and are in the process of updating the minimum standards for bio-risk management in laboratories handling FMDV.

Pool 7: South America, SENASA, Dr Andrea Pedemonte

No clinical samples from FMD suspect cases have been received at SENASA for testing. Argentina has five FMD-free (without vaccination) zones recognised. Serological surveillance has been undertaken to (i) define vaccine-induced population immunity, and (ii) demonstrate the absence of FMD virus circulation. During 2016, 40,326 serum samples have been tested for these purposes.

Update from NCFAD, Winnipeg, Dr Charles Nfon

Five hundred suspect vesicular disease samples (from 33 different submissions) from pigs have been submitted for testing. Of these, 144 (29%), were found to be positive for Seneca Valley virus (SVV). Serological data (cELISA) for 299

samples also provided evidence for SVV circulation in 30% of samples. Validated diagnostic tests for SVV available at NCFAD include: real-time RT-PCR (2C), cELISA and VNT. This talk also summarised *in vivo* vaccine evaluation studies performed recently in Canada (as part of collaborative projects with CSIRO, Australia). Results suggest that O₁ Manisa can protect sheep from challenge with O/SKR/2010 (O/SEA/Mya-98 lineage). Similarly, A22 IRQ appears to be effective against A/VIT/15/2012 (A/ASIA/Sea-97 lineage) challenge in sheep: high potency vaccine protected 83% (5 of 6 sheep) at 4dpv. Lastly, Asia 1 Shamir vaccine appears to be protective against Asia 1 PAK/19/2014: 4 of 5 sheep challenge at 4dpv were protective. Studies were also carried out in pigs comparing both monovalent and bivalent vaccines in serotype A vaccines (A/May-97 and A22 IRQ). The bivalent appears to be more protective although statistically it may not be significant due to the small sample size.

Update from USA, NVSL-STAT-VS-APHIS-USDA, Dr Consuelo Carrillo

As part of on-going surveillance, FMD suspect cases (n=451) were investigated. None were positive for FMDV; however, an increasing number have been found to be positive for SVV. Primers used for SVV diagnosis have recently been updated to accommodate recent field samples. In addition to SVV, the meeting discussed whether these vesicular disease cases could be caused by another agent.

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Meeting participants:

Name	Organisation	Email
Abraham Sangula	Embakasi, Kenya	aksangula@gmail.com
Aldo Dekker	CVI, Lelystad, The Netherlands	aldo.dekker@wur.nl
Andrea Pedemonte	SENASA, Argentina	apedemon@senasa.gob.ar
Anna Ludi	The Pirbright Institute, UK	anna.ludi@pirbright.ac.uk
Anna Tarasova	FGBI ARRIAH, Russia	tarasova@arriah.ru
Artem Metlin	FGBI ARRIAH, Russia	metlin@arriah.ru
Charles Nfon	NCFAD, Canada	Charles.nfon@inspection.gc.ca
Consuelo Carrillo	NVSL, USDA-APHIS-VS, USA	consuelo.carrillo@aphis.usda.gov
Daniel Gizaw Demississie	NAHDIC, Ethiopia	nebiyudan@gmail.com
David Lefebvre	CODA-CERVA, Belgium	David.Lefebvre@coda-cerva.be
Dmitry Lozovoy	FGBI ARRIAH, Russia	mail@arriah.ru
Donald King	The Pirbright Institute, UK	donald.king@pirbright.ac.uk
Emiliana Brocchi	IZSLER, Italy	emiliana.brocchi@izsler.it
Francois Maree	ARC-OVI, South Africa	mareef@arc.agric.za
Fuat Özyörük	Şap Institute, Turkey	fuato@sap.gov.tr; fuat2004@gmail.com
George Matlho	BVI, Botswana	gmatlho@bvi.co.bw
Husseini Gulak Ularamu	NVRI, Nigeria	ularamuhussaini@yahoo.co.uk
Jijun He	LVRI, China	hejjun@caas.cn
Jitendra K Biswal	PD-FMD, India	jkubiswal@gmail.com
Jong-Hyeon Park	QIA, Republic of Korea	parkjhvet@korea.kr
Kees VanMaanen	EuFMD/FAO, Rome, Italy	Cornelius.VanMaanen@fao.org
Kingkarn Boonsuya Seeyo	NIAH, Thailand	kingkarn.BS3244@hotmail.co.th
Kris De Clercq	CODA-CERVA, Belgium	kris.declercq@coda-cerva.be
Maria Teresa	EuFMD/FAO, Rome, Italy	Maria.Scicluna@fao.org
Michael Eschbaumer	FLI, Germany	michael.eschbaumer@fli.de
Min Kyung Park	OIE, Paris, France	m.park@oie.int
Rossana Allende	PANAFTOSA, Brazil	rallende@paho.org
Samia Metwally	FAO, Rome, Italy	Samia.Metwally@fao.org
Santina Grazioli	IZSLER, Italy	santina.grazioli@izsler.it
Wilai Linchongsubongkoch	NIAH, Thailand	wilaifmd@loxinfo.co.th
Yanmin Li	LVRI, China	liyanmin@caas.cn
Labib Bakkali Kassimi	Anses, Maison Alfort, France	labib.bakkali-kassimi@anses.fr
Stéphan Zientara	Anses, Maison Alfort, France	szientara@vet-alfort.fr
Sandra Blaise-Boisseau	Anses, Maison Alfort, France	Sandra.blaise-boisseau@anses.fr
Benoit Durand	Anses, Maison Alfort, France	Benoit.durand@anses.fr
Gina Zanela	Anses, Maison Alfort, France	Gina.zanela@anses.fr
Aurore Romey	Anses, Maison Alfort, France	Aurore.romey@anses.fr
Maud Marsot	Anses, Maison Alfort, France	Maud.marsot@anses.fr
Anthony Relmy	Anses, Maison Alfort, France	Anthony.relmy@anses.fr
Kamila Gorna	Anses, Maison Alfort, France	Kamila.gorna@anses.fr