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

Annual Report 2017

Editors:

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1 OIE/FAO FMD Reference Laboratory 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 2017 - 31st December 2017

1.3 Collated input from

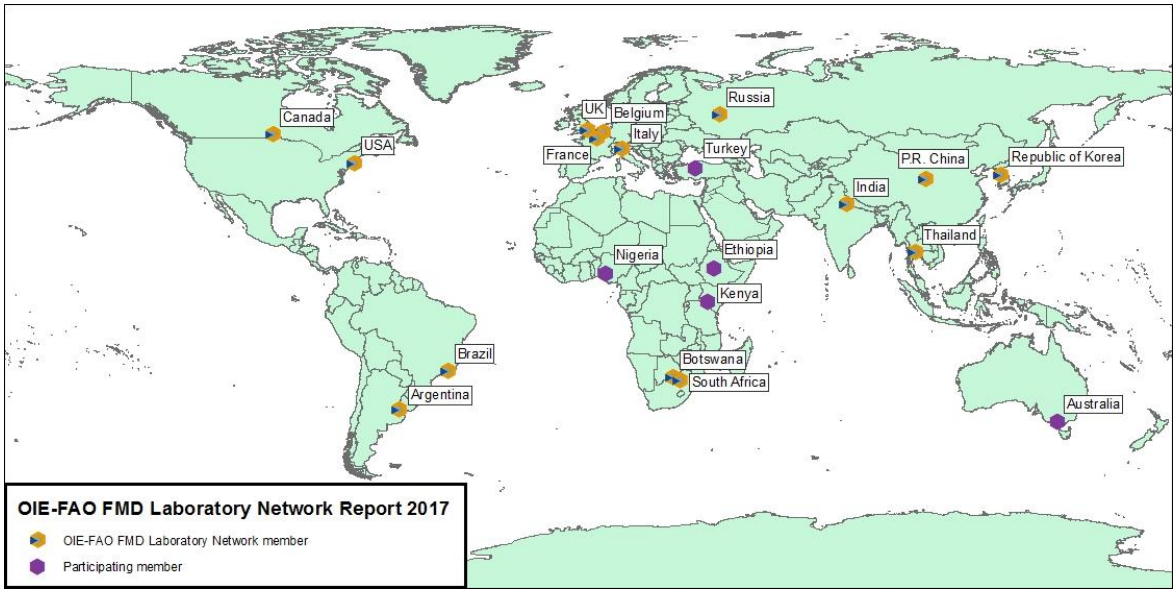


Figure 1-1: Participating laboratories

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:

Australian Animal Health Laboratory (AAHL)

Geelong, Australia

Foot and Mouth Disease Laboratory

Embakasi, Kenya

ŞAP INSTITUTE (and WELNET FMD)

Ankara, Turkey

NATIONAL Animal Health Diagnostic & Investigation Center (NAHDIC)

Sebeta, Ethiopia

National Veterinary Research Institute

Vom, Plateau State, Nigeria

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 2017) 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

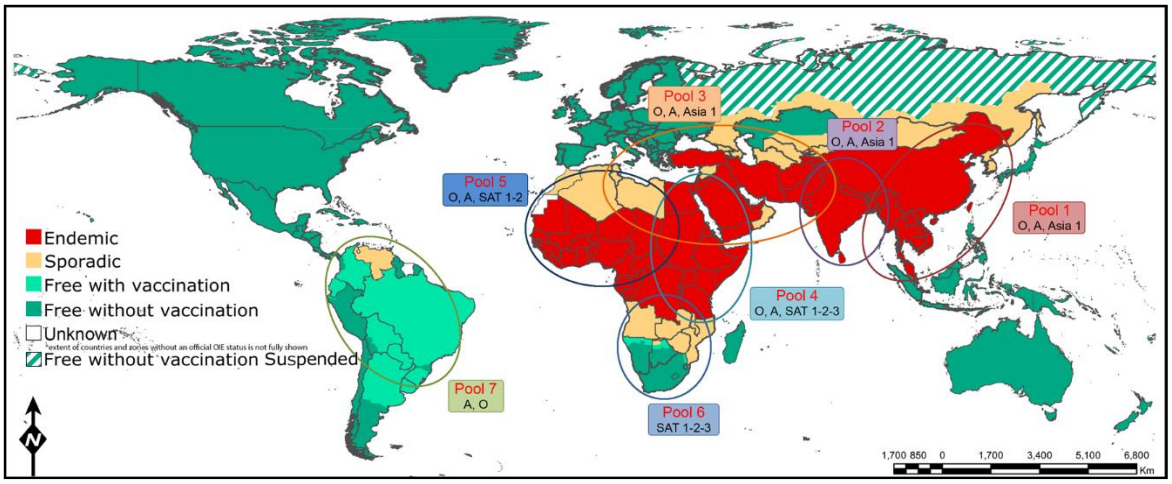


Figure 2-1: Distribution of the seven endemic pools of FMD showing conjectured status of FMD in countries during 2017. Virus circulation and evolution within these regional virus pools results in changing priorities for appropriately adapted vaccines. Periodically, viruses spread between pools and to 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 2017

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 2017, 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 2017 (data collated in*

Table 2-1*).*

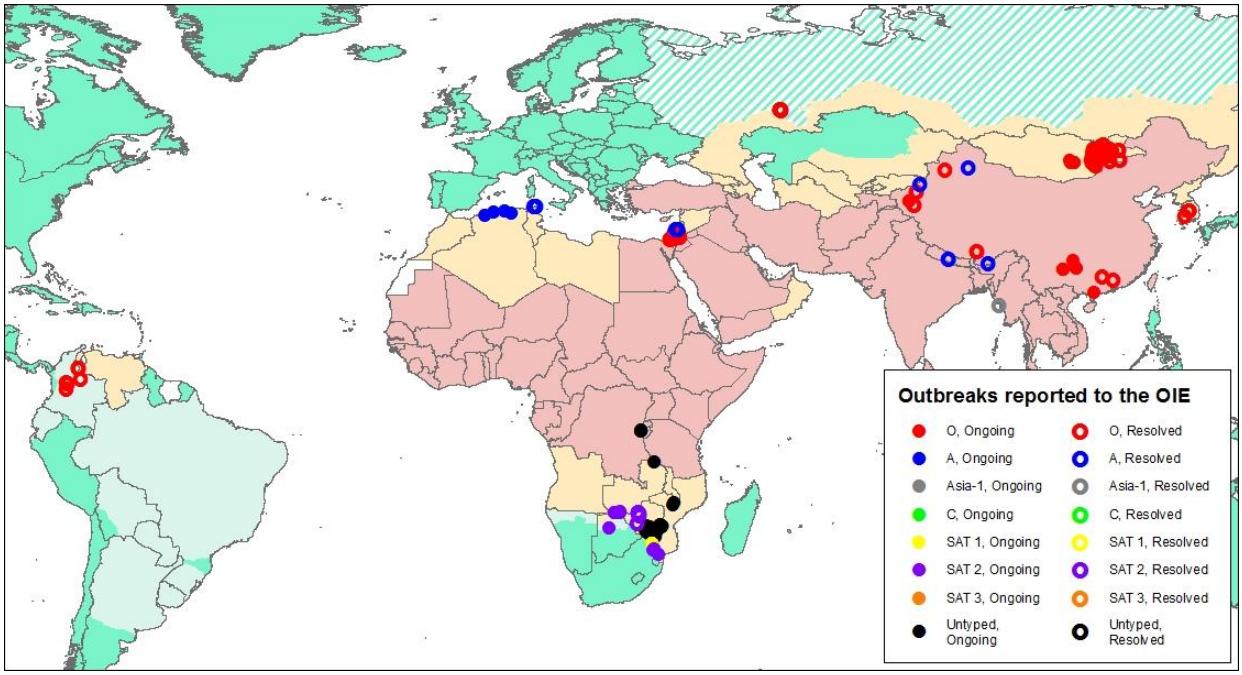


Figure 2-2: Map indicating the location of significant epidemiological events and disease outbreaks reported to OIE in immediate notifications or follow-up reports in 2017 (data available from: http://www.oie.int/wahis_2/public/wahid.php/Diseaseinformation/Immsummary.

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

Table 2-1: New FMD outbreaks reported to OIE during 2017 (data retrieved from WAHIS on www.oie.int on 15th March 2018). 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	8	12	15	15	19	9			…				78
Bhutan			6						3				9
Burkina Faso	5	2	4		1		1	8	9	3	11	5	49
Cambodia	14	10	11	3	8	3			…				49
Colombia						2			…				2
Egypt	46	29	23	11	3								112
Eritrea		1	1			1	1	1	3			1	9
Ethiopia			56						...				56
Iran			471						…				471
Israel		1			3				…				4
Jordan		1	3						…				4
Kenya	12	5	1			3	2	4	14	18	10	6	75
Malaysia	2	3	10	2					…				17
Mali			0					1					1
Mozambique	0	0	0	0	0	0	0	0	0	0	0	1	1
Myanmar	4	1	2	1	1				…				9
Namibia			0				4	1	1	0	0	0	6
Nepal	7	7	12	9	8	2			…				45
Nigeria	3						2	6	73	1			85
Oman	17	11	30	116	21	5			…				200
Palestinian A. T.		2			3	1			…				6
Saudi Arabia	2	1							…				3
South Africa			3		2				…				5
Sudan	2		1						…				3
Tanzania		1	3	2	3	1	2	2		1		3	18
Thailand	16	6	5		1	2	1	4	5	24	44	18	126
Tunisia				2					…				2
Turkey	51	34	48	11	5	22	23	7	21	23	16	54	315
Uganda			1		7	1			…				9
United Arab Emirates			1	1					…				2
Vietnam			0				2	2		6			10
Zambia	0	0	1	0	0	2	1	2	0	0	0	0	6
Zimbabwe	2	2	2	0	1	0			…				7

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

2.2 Official status of countries and zones during 2017

The official status of OIE member countries is shown in Figure 2-3

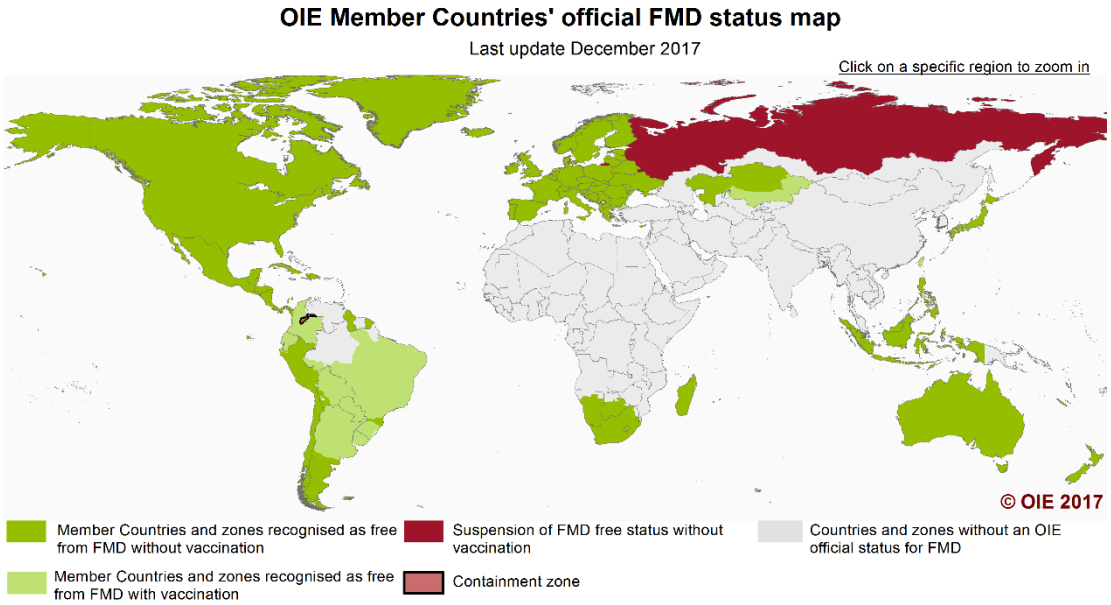


Figure 2-3: Official FMD status for OIE member countries. Data provided from the OIE: http://www.oie.int/en/animal-health-in-the-world/official-disease-status/fmd/en-fmd-carte/

2.3 Overview of the activities of the OIE/FAO FMD Laboratory Network during 2017

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 1500 clinical samples from suspect cases of FMD were tested by laboratories in the Network (and associated laboratories) during 2017. These samples were collected from 40 countries from all seven FMD endemic pools 1 to 6 (Figure 2-4). **However, sampling within these pools is not equivalent:** surveillance within West and Central Africa (Pool 5) is particularly sparse and efforts are currently underway with the network to improve sample collection and testing in this region.

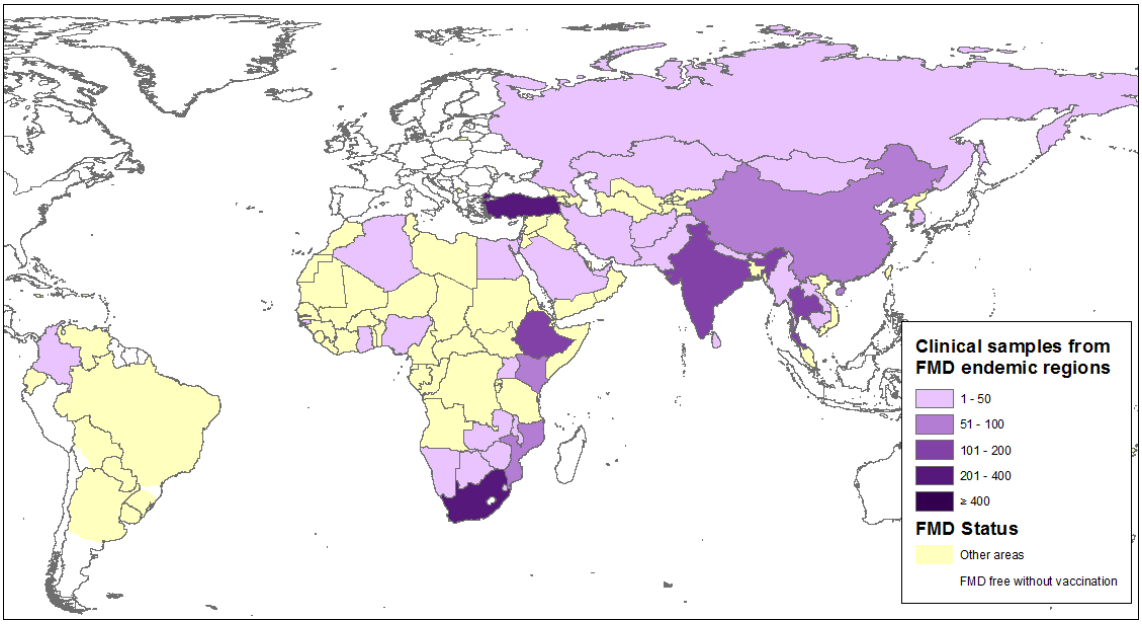


Figure 2-4: Distribution of samples collected from suspect cases of FMD (highlighted in purple) and tested by the OIE/FAO FMD Laboratory network during 2017. Areas recognised as FMD free without vaccination are shaded white, all other areas (including FMD free with vaccination) are shaded pale yellow.

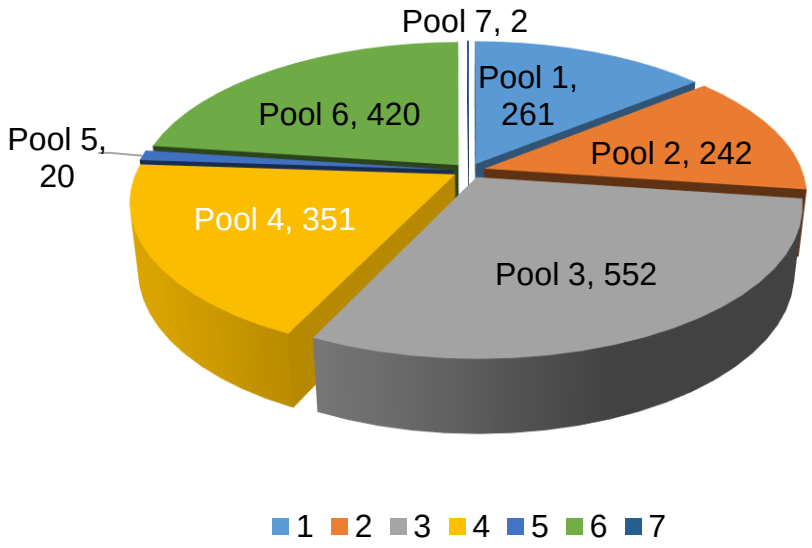


Figure 2-5: Clinical samples (n=1848) tested for FMD investigation (virology) by the OIE/FAO FMD Laboratory Network from FMD endemic countries during 2017 and their distribution across the seven FMD endemic pools (see Figure 2-1)

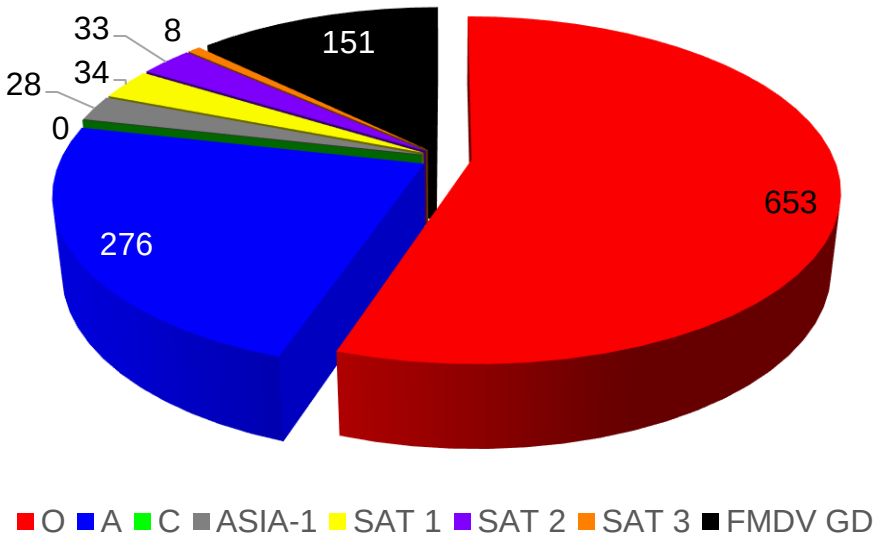


Figure 2-6: Summary of results for characterised isolates (n=1183) from FMD endemic countries were reported by the Network during 2017. FMDV GD denotes samples that were only positive using molecular (RT-PCR methods), while a further 674 samples were tested but found to be negative for FMDV using all diagnostic methods.

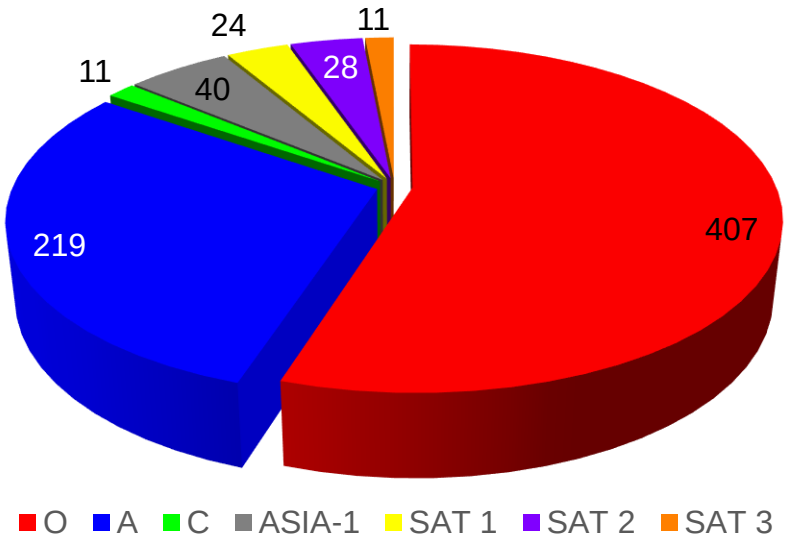


Figure 2-7: Summary of 740 samples (viruses and field isolates) that were sequenced (VP1/capsid/complete genome) during 2017 (see Appendix 3).

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 PANAFTOSA can also be found respectively at: http://www.wrlfmd.org/ and at: http://new.paho.org/panaftosa.

Serotype C has not been detected since 2004 when the last cases due to the serotype were recognised in Kenya and Brazil. Our 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 were submitted to the OIE for consideration and have been included in a resolution adopted by 85th General Session of the OIE (Resolution 30).

Resolution No. 30 (Foot-and-Mouth Disease serotype C)

Adopted by the World Assembly of Delegates of the OIE on 23 May 2017 in view of an entry into force on 26 May 2017)

1. OIE Member Countries, other organisations or laboratories suspecting or identifying the presence of FMDV serotype C should as soon as possible share FMD viral material and information about the FMD viruses with OIE/FAO Reference Laboratories for confirmation and report its presence through the WAHIS.
2. The OIE/FAO Reference Laboratory network provides services to OIE Member Countries and to the OIE to assist with confirmatory testing of suspected FMD serotype C samples and reporting to the OIE of any positive results.
3. OIE Member Countries should assess the risks and the relevance of practices related to the use of FMDV serotype C for vaccination to progressively stop unjustified practices and consider the benefit of replacing routine vaccination against FMDV serotype C by its inclusion in vaccine antigen banks.
4. OIE Member Countries should urge vaccine manufacturers to stop the use of FMDV serotype C in vaccine challenge experiments and to consider halting the production of FMDV serotype C vaccines and inclusion in multivalent FMD vaccines except for holding in vaccine banks.
5. Countries and laboratories with the support of the network of OIE/FAO Reference Laboratories for FMD are encouraged to participate in and coordinate diagnostic and research activities related to surveillance for FMD serotype C at the international level partaking in the Global FMD Control Strategy.

2.4 Regional distribution of different FMD viral lineages

In regions where FMD is endemic, continuous evolution of the virus generates geographically discrete lineages that are genetically distinct from FMD viruses found elsewhere. The conjectured global status for FMD (see Figure 2-1) masks the underlying complexity of FMDV virus distribution in the different pools (at serotype, topotype and lineage levels). This report showcases a new format to display how different FMD lineages ciruculate in different regions of the world. Using a new tool (called PRAGMATIST) that has been developed in partnership between WRLFMD and EuFMD, these

analyses accommodate the latest epidemiological data collected by the Network and presented in this report regarding FMDV lineages detected in samples to assess the relative importance of the viral strains circulating within each *source regions* (see Table below). Based on these data, a *prevalence score* is defined by estimating the proportion of each of the local viral strains that would be represented if 100 animals infected with FMDV were randomly selected from each source area.

Table 2-2: Conjectured distribution of important FMDV lineages in different endemic regions. For each of the regions, data represent the relative importance of the different lineages [*prevalence score* estimated as a proportion (%) of total FMD cases that occur in domesticated host animals].

FMDV lineage	West Eurasia	East Asia	North Africa	Southern Asia	East Africa	West and Central Africa	Southern Africa	South America
O/ME-SA/PanAsia-2	35	-	-	-	-	-	-	-
O/ME-SA/PanAsia	-	10	-	-	-	-	-	-
O/SEA/Mya-98	-	33	-	-	-	-	-	-
O/ME-SA/Ind2001	6	20	35	80	-	-	-	-
O/EA or O/WA	3	-	20	-	45	37	-	-
O/EURO-SA	-	-	-	-	-	-	-	74
O/CATHAY	-	10.5	-	-	-	-	-	-
A/ASIA/Sea-97	-	25	-	-	-	-	-	-
A/ASIA/Iran-05	25.5	-	-	-	-	-	-	-
A/ASIA/G-VII	17.5	-	-	16	-	-	-	-
A/AFRICA	-	-	35	-	24	25	-	-
A/EURO-SA	-	-	-	-	-	-	-	26
Asia-1	12.5	1.5	-	4	-	-	-	-
SAT 1	-	-	-	-	10	10	27	-
SAT 2	0.5	-	10	-	20	28	57	-
SAT 3	-	-	-	-	1	-	16	-
C	-	-	-	-	-	-	-	-

In order to help visualise the changing patterns in FMDV distribution and recognise risks for the emergence of new lineages, the Network has reviewed available intelligence for epidemiologically important FMDV lineages (Table 2-2), focussing on those that have already demonstrated a potential for long-distance trans-pool spread: O/ME-SA/Ind-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.

The current known and conjectured distribution of these different FMD viral lineages are represented in the maps below: The extent of current distribution for each of the viral lineages is represented within the black lines, while the location of individual outbreaks (dots) and affected countries (shaded colours, according to dates) are shown. NB: Arrows are drawn to highlight the regions that are now threatened by these lineages and text boxes highlight some of the headline events and changes that have occurred during 2017

FMDV O

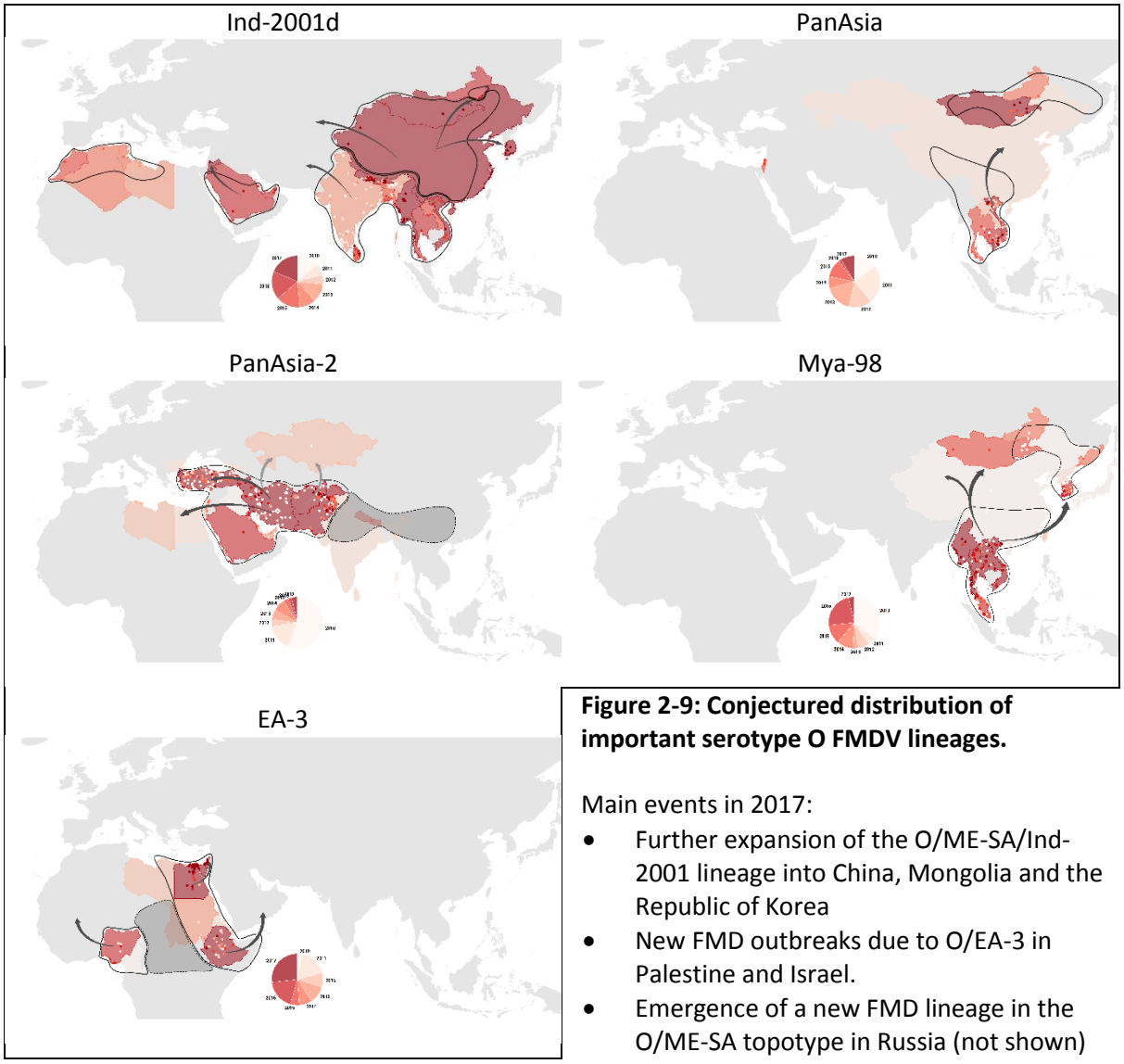


Figure 2-9: Conjectured distribution of important serotype O FMDV lineages.

Main events in 2017:

- Further expansion of the O/ME-SA/Ind-2001 lineage into China, Mongolia and the Republic of Korea
- New FMD outbreaks due to O/EA-3 in Palestine and Israel.
- Emergence of a new FMD lineage in the O/ME-SA topotype in Russia (not shown)

FMDV A

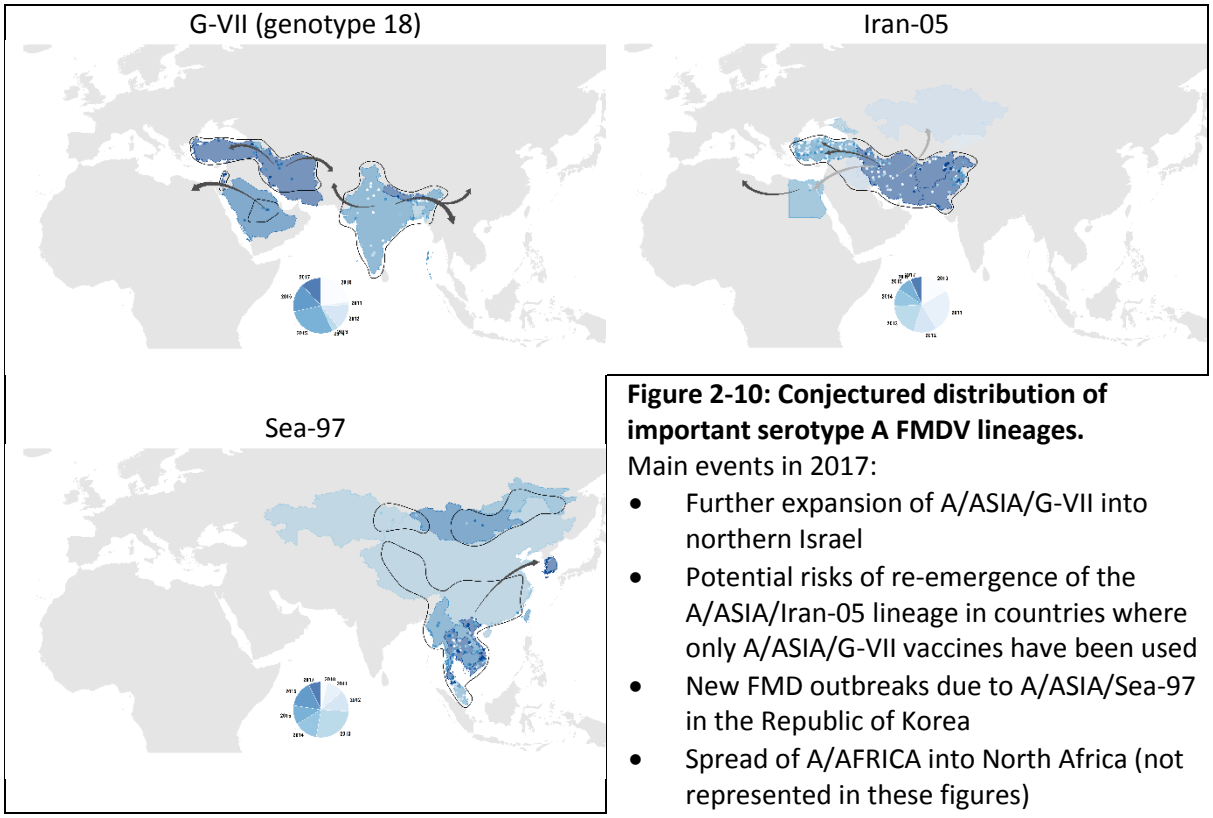


Figure 2-10: Conjectured distribution of important serotype A FMDV lineages.
Main events in 2017:

- Further expansion of A/ASIA/G-VII into northern Israel
- Potential risks of re-emergence of the A/ASIA/Iran-05 lineage in countries where only A/ASIA/G-VII vaccines have been used
- New FMD outbreaks due to A/ASIA/Sea-97 in the Republic of Korea
- Spread of A/AFRICA into North Africa (not represented in these figures)

FMDV Asia 1

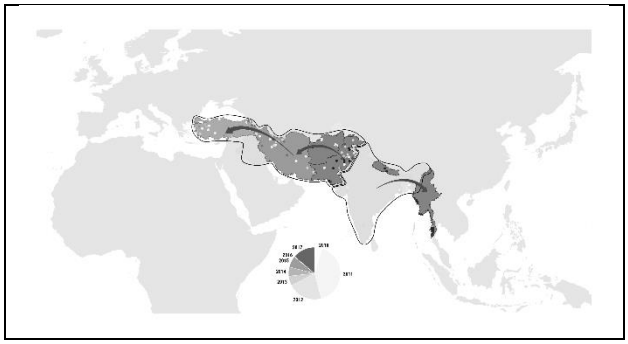


Figure 2-11: Conjectured distribution of serotype Asia 1.
Main events in 2017:

- Asia 1 detected in Myanmar during 2017 – representing the first cases due to this serotype in Southeast Asia for >10years
- Indications of an upsurge in cases due to ASIA/Sindh-08 across West Eurasia

FMDV SAT 2

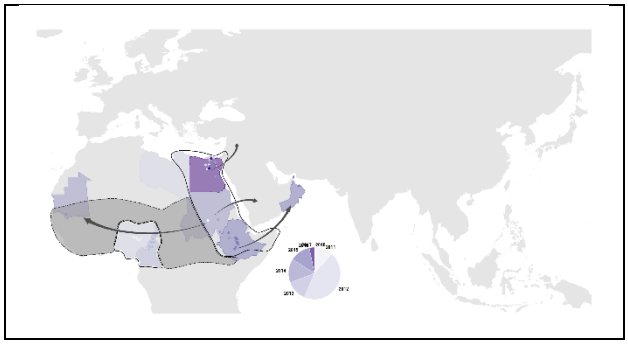


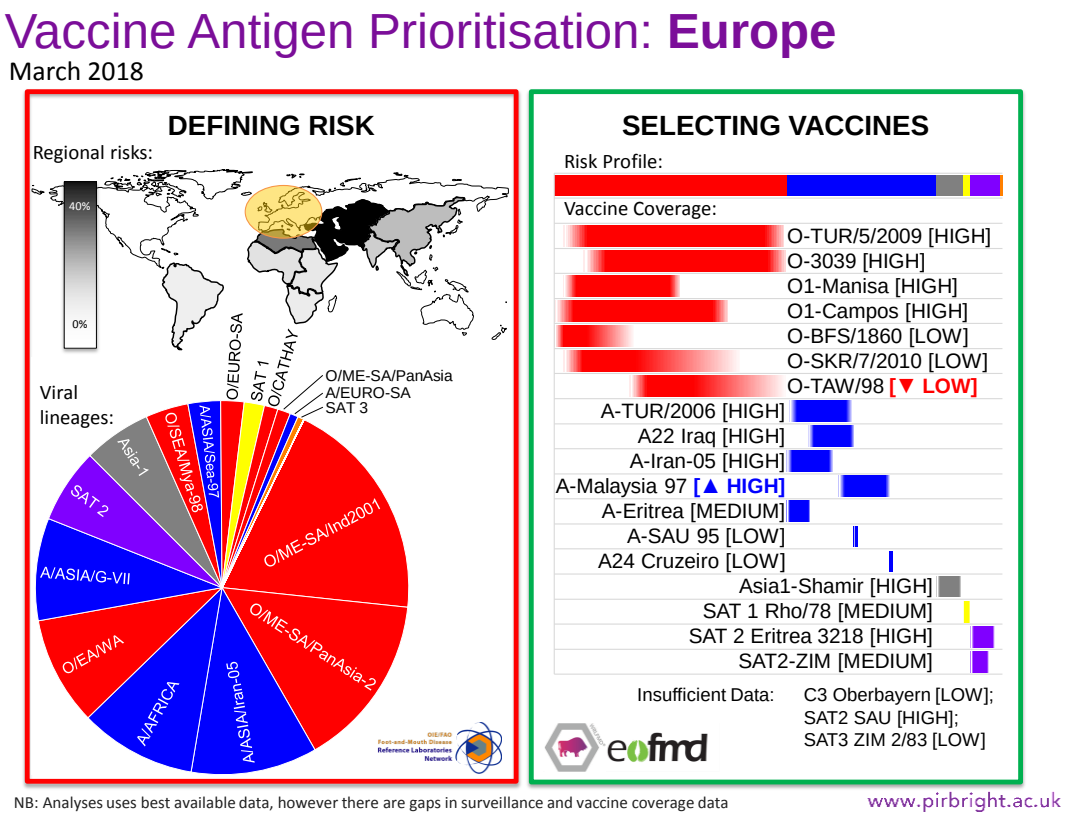
Figure 2-12: Conjectured distribution of serotype the SAT 2 (topotype VII) FMDV lineage.
Situation:
Spread of this FMD virus lineage into North Africa (Egypt) and Palestine raises risks of on-ward spread into other countries in the neighbourhood.

2.5 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 2-3 below. Details of vaccine matching work undertaken by the OIE/FAO FMD Laboratory Network are summarised in Appendix 2 - .

Outputs from WRLFMD are generated with a new tool (called PRAGMATIST) that has been developed in partnership between WRLFMD® and EuFMD. These analyses accommodate the latest epidemiological data collected by the Network regarding FMDV lineages that are present in different source regions (see Table 2-2 above), as well as available *in vitro*, *in vivo* and field data to score the ability of vaccines to protect against these FMDV lineages.

Table 2-3: Recommendations from WRLFMD on FMD virus strains to be included in FMDV vaccine antigen bank for Europe



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

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

3.1 Pool 1 Regional synopsis

3.1.1 Conjectured circulating FMD viral lineages in Pool 1 during 2017

- Serotype O:
  - SEA/Mya-98
  - ME-SA/PanAsia
  - ME-SA/Ind2001d
  - CATHAY
- Serotype A:
  - ASIA/Sea-97
- Serotype Asia-1:

Table 3-1: Overview of samples collected and tested from Pool 1 in 2017 (countries highlighted in purple; graph represents clinical submissions since 2005)

Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
LVRI, Lanzhou, China	China	58	5649
QIA, Republic of Korea	Republic of Korea	9	796285
FGBI ARRIAH,Russia	Mongolia	19	5400
RRL SEA Pakchong, Thailand	Lao PDR, Myanmar, Thailand	112	16832
WRLFMD, UK	Cambodia, Hong kong, SAR of PRC, Republic of Korea (South), Laos, Mongolia, Myanmar, Thailand	63	0

Pool 1 headlines: Changes to FMD status in 2017:

- Since 2015, the O/ME-SA/Ind-2001 lineage has **rapidly** spread from South Asian countries into mainland Southeast Asia. In 2017, this lineage has become more established in the region (outbreaks in Thailand and Myanmar), and has spread further with new outbreaks being reported in China, Mongolia and the Republic of Korea. Retrospective analyses of samples collected from Mongolia indicate that this lineage has been present in the country since 2015 (see Appendix 4), findings which pre-date the emergence of O/ME-SA/Ind-2001 in other countries in the neighborhood. These reports now raise questions about the timeline by which this lineage was introduced into East Asian countries.
- New FMD outbreaks due to serotype Asia 1 were reported in Myanmar (Rakhine State) in February 2017. These were the first reported cases due to this serotype anywhere in East and Southeast Asia since 2006 (in Vietnam and China). Sequence data from RRL-SEA indicates that these outbreaks were caused by a FMD virus that is most closely related to samples collected from Bangladesh (from 2013) and therefore represent a new introduction of this serotype into Southeast Asia (see Appendix 4).
- Endemic strains normally found in southeast Asia continue to be detected in the region:
    - Continued FMD cases in PDR Lao, Myanmar, Thailand and Vietnam (2016) due to the O/SEA/Mya-98 lineage. In China, sequence data provides evidence for two genetic groups within O/SEA/Mya-98 lineage affecting either cattle (2016-17) or pigs (2012-17).
    - Field cases in Mongolia due to the O/ME-SA/PanAsia viral lineage.
    - O/CATHAY detected in Vietnam (for a sample collected in 2016) and in China as part of a surveillance program
    - Outbreaks in Thailand, Vietnam, Republic of Korea and China due to the A/ASIA/Sea-97 viral lineage. During February 2017, simultaneous FMD outbreaks due to serotypes O (O/ME-SA/Ind-2001d) and A (A/ASIA/Sea-97) occurred in South Korea (see Appendix 4). These cases represent at least two new incursions of FMDV into the country, although the precise source in East or Southeast Asia has not been identified.

3.1.2 Vaccine recommendations for Pool 1

- Internationally produced vaccines:
    - O: Campos, Manisa, Nakornpathom, Primosky, 3039
    - A: Malaysia/97, Iraq/64 & A22-IRQ.
    - Asia 1: Shamir
- Locally produced vaccines (at RRL SEA):
    - O: 189/87 (Udornthani/87)
    - A: Sakolnakorn/97
    - Asia1: Petchaburi/85
- Locally produced vaccines (at FGBI ARRIAH):
    - A/Zabaikalsky/RUS/2013
    - O PanAsia-2

- Asia1/Sindh-08
- Locally used vaccine strains (by Chinese manufactures):
  - O/Mya-98 (O/Mya98/BY/2010), O/HK99
  - Re-A/Sea-97 (Re-A/WH/09), AF72
  - Asia1/GV (Asia1/JSL/06).

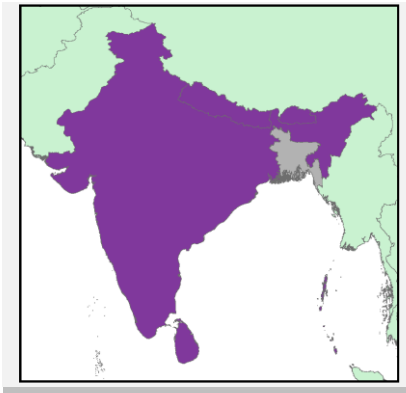
These are produced as: Type O and Type A (monovalent vaccines), Type O-A and Type O-Asia1 (bivalent vaccine), Type O-A-Asia1 (multi-valent vaccine) and a synthetic peptide vaccine (Type O for use in pigs only). In China vaccination occurs 2 times a year (in spring and autumn), where more than 1 billion doses are produced and administered per year

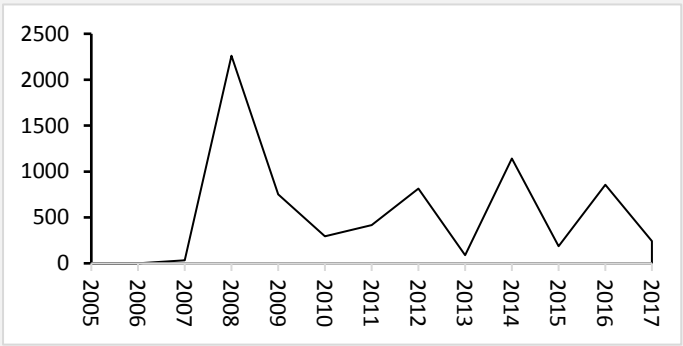
3.2 Pool 2 Regional synopsis

3.2.1 Conjectured circulating FMD viral lineages in Pool 2 during 2017

- 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:

Table 3-2: Overview of samples collected and tested from Pool 2 in 2017 (countries highlighted in purple; graph represents clinical submissions since 2005)





Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
ARC-OVI, South Africa	Mauritius	0	9
PDFMD, India	India	150	0
WRLFMD, UK	Bhutan, Nepal, Sri Lanka	92	0

Pool 2 headlines: Changes to FMD status in 2017:

- Two viral lineages (O/ME-SA/Ind-2001 and A/ASIA/G-VII) that are endemic in Pool 2 have spread beyond this pool to cause FMD outbreaks in other regions. The precise routes by which these viruses are being spread between endemic pools needs to be defined.
- FMDV serotype O (O/ME-SA/Ind-2001) continues to be dominant in the region accounting all of the submissions into the Indian FMD Reference Laboratory (PD-FMD, Mukteswar).
- Genetic analyses provide evidence for two sub-lineages of O/ME-SA/Ind-2001- O/ME-SA/Ind-2001e now dominates viruses characterised in India, while outbreaks due to the earlier O/ME-SA/Ind-2001d have declined, although this virus is still present in Bhutan and Nepal, as well as countries outside of Pool 2.
- Elsewhere in the region, A/ASIA/G-VII has been detected in Bhutan and Nepal

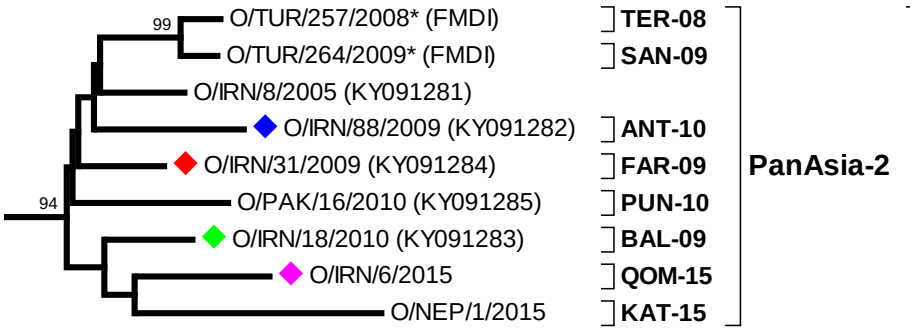
3.2.2 Vaccine recommendations for Pool 2

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

3.3 Pool 3 Regional synopsis

3.3.1 Conjectured circulating FMD viral lineages in Pool 3 during 2017

- Serotype O:
  - ME-SA/PanAsia-2 [comprising at least two viral sublineages (ANT-10 and QOM-15) present in different countries – see figure 3-1 below].
  - ME-SA/Ind-2001d (via introductions from South Asia)
  - EA-3 (in Israel & Palestinian Autonomous Territories)
- Serotype A:
  - ASIA/Iran-05 [comprising 4 predominant viral sublineages (SIS10, SIS-12, SIS-13 and FAR-11) – see figure 3-2 below]
  - ASIA/G-VII
- Serotype Asia-1:
  - ASIA/Sindh-08



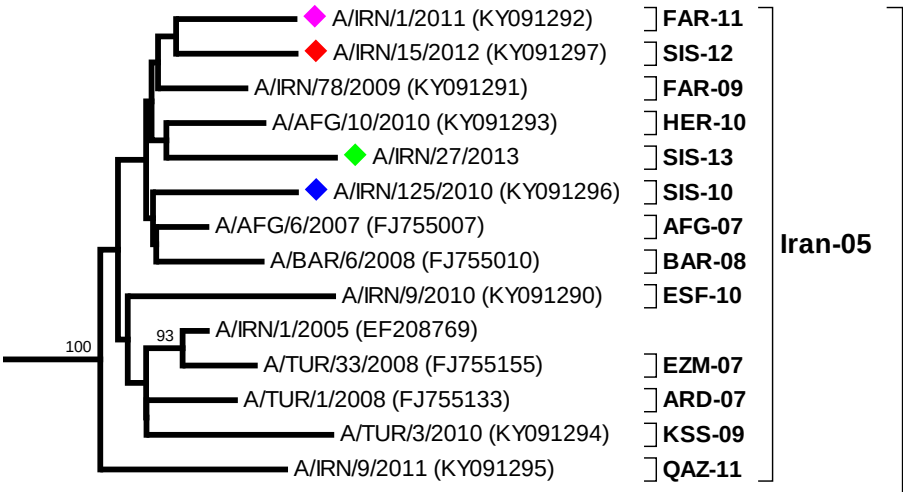
ANT-10	Country	2013	2014	2015	2016	2017
◆	Afghanistan	■	■		■	■
	Armenia					
	Azerbaijan					
	Georgia					
	Iran	■		■	■	■
	Iraq					
	Kazakhstan					
	Krygystan					
	Pakistan	■	■	■	■	■
	Russia					
	Syria					
	Tajikistan					
	Turkey	■				
	Turkmenistan					
	Uzbekistan					

FAR-09	Country	2013	2014	2015	2016	2017
◆	Afghanistan					
	Armenia					
	Azerbaijan					
	Georgia					
	Iran	■		■		
	Iraq					
	Kazakhstan					
	Krygystan					
	Pakistan					
	Russia					
	Syria					
	Tajikistan					
	Turkey	■	■	■		
	Turkmenistan					
	Uzbekistan					

BAL-09	Country	2013	2014	2015	2016	2017
◆	Afghanistan					
	Armenia					
	Azerbaijan					
	Georgia					
	Iran			■		
	Iraq					
	Kazakhstan					
	Krygystan					
	Pakistan			■		
	Russia					
	Syria					
	Tajikistan					
	Turkey					
	Turkmenistan					
	Uzbekistan					

QOM-15	Country	2013	2014	2015	2016	2017
◆	Afghanistan					
	Armenia					
	Azerbaijan					
	Georgia					
	Iran				■	■
	Iraq					
	Kazakhstan					
	Krygystan					
	Pakistan					
	Russia					
	Syria					
	Tajikistan					
	Turkey					■
	Turkmenistan					
	Uzbekistan					

Figure 3-1: Recent distribution of O/ME-SA/PanAsia-2 sublineages (ANT-10, FAR-09, BAL-09 and QOM-15) in countries within Pool 3



SIS-10	Country	2013	2014	2015	2016	2017
◆	Afghanistan					
	Armenia					
	Azerbaijan					
	Georgia					
	Iran	■	■	■	■	
	Iraq	■				
	Kazakhstan					
	Krygystan					
	Pakistan					
	Russia	■				
	Syria					
	Tajikistan					
	Turkey	■	■	■		
	Turkmenistan					
	Uzbekistan					

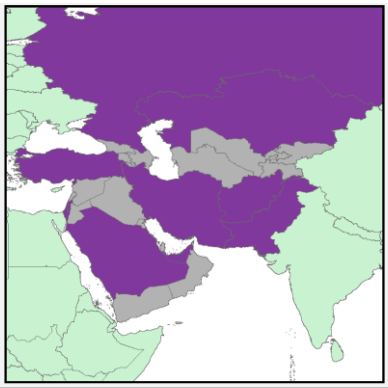
SIS-12	Country	2013	2014	2015	2016	2017
◆	Afghanistan					
	Armenia					
	Azerbaijan					
	Georgia					
	Iran					
	Iraq					
	Kazakhstan					
	Krygystan					
	Pakistan	■				
	Russia					
	Syria					
	Tajikistan					
	Turkey					
	Turkmenistan					
	Uzbekistan					

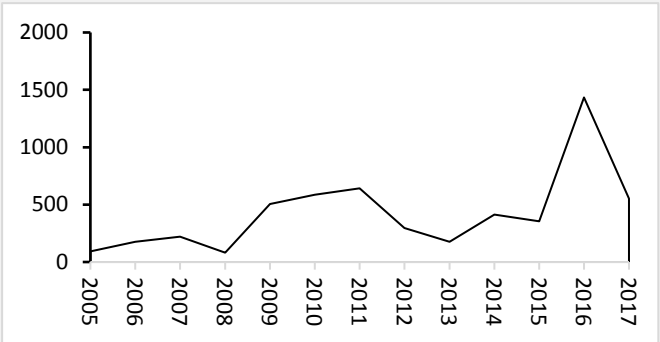
SIS-13	Country	2013	2014	2015	2016	2017
◆	Afghanistan					■
	Armenia					
	Azerbaijan					
	Georgia					
	Iran	■		■	■	■
	Iraq					
	Kazakhstan					
	Krygystan					
	Pakistan		■	■	■	■
	Russia					
	Syria					
	Tajikistan					
	Turkey					
	Turkmenistan					
	Uzbekistan					

FAR-11	Country	2013	2014	2015	2016	2017
◆	Afghanistan	■			■	■
	Armenia					
	Azerbaijan					
	Georgia					
	Iran	■	■			■
	Iraq					
	Kazakhstan					
	Krygystan					
	Pakistan	■	■	■	■	■
	Russia					
	Syria					
	Tajikistan					
	Turkey					
	Turkmenistan					
	Uzbekistan					

Figure 3-2: Recent distribution of A/ASIA/Iran-05 sublineages (SIS-10, SIS-12, SIS-13 and FAR-11) in countries within Pool 3. Recent samples from Turkey also indicate that FAR-05 and FAR-09 sublineages may still be circulating in the region)

Table 3-3: Overview of samples collected and tested from Pool 3 in 2017 (countries highlighted in purple; graph represents clinical submissions since 2005)





Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
FGBI ARRIAH, Russia	Russia	8	303650
ŞAP Institute, Turkey	Iran, Turkey	359	22906
ARC OVI, South Africa	UAE	30	42
WRLFMD, UK	Afghanistan, Iran, Israel, Kazakhstan, Pakistan, Palestinian Autonomous Territories, Saudi Arabia	155	0

Pool 3 headlines: Changes to FMD status in 2017:

- Russia's status as FMD-free (without vaccination) was suspended following the outbreak of FMD in Bashkortostan. Serotype O was detected and sequence analyses demonstrated that these outbreaks were caused by an O/ME-SA virus that does not belong to any of the recognized lineages that have been previously described (i. e., PanAsia, PanAsia-2 or Ind-2001). The most closely related sequences at WRLFMD were from Pakistan (2014) and Iran (2013), although data (generated by ARRIAH – see Appendix 4) for unreported FMD outbreaks in Central Asia share closer genetic identity.
- New FMD outbreaks in Palestine and Israel have been caused by FMD viruses from the O/EA-3 topotype (see Appendix 4) that are most closely related to samples collected from Egypt (also in 2017).
- Since 2013, two new FMD lineage have been introduced into the region from South Asia (Pool 2):
  - The A/ASIA/G-VII (aka G-18) FMD viral lineage from the Indian sub-continent has spread further in 2017 to cause new outbreaks in northern Israel (see Appendix 4), in addition to those previously recognised in Saudi Arabia, Iran, Turkey and Armenia.
  - During 2017, the O/ME-SA/Ind-2001 lineage has spread further to cause new FMD outbreaks in Jordan

3.3.2 Vaccine recommendations for Pool 3

Internationally produced vaccines

- MSD and Boehringer-Ingelheim (Merial)*:
    - O/ME-SA/PanAsia-2 (or suitable alternative)
    - O/Manisa
    - A Iran-05 (or A TUR 06)
    - A22/Iraq
    - Asia-1 Shamir
- Locally produced vaccines (at ARRIAH):
    - O/PanAsia-2
    - A/ASIA/G-VII
    - Asia-1/Sindh-08
    - A/ASIA/Iran-05 (from the Russian isolate /Krasnodarsky/RUS/2013)
- Locally produced vaccines (other suppliers in the region):
    - SAP FMD Institute, Ankara, Turkey (including A/ASIA/G-VII lineage)
    - Vetal
    - MEVAC

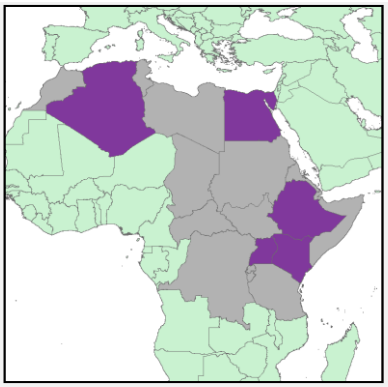
* Merial (BI) are expected to release a new vaccine tailored to the A/ASIA/G-VII lineage in 2017/18

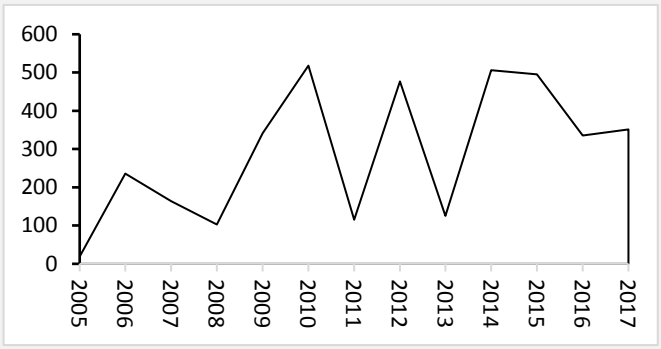
3.4 Pool 4 Regional synopsis

3.4.1 Conjectured circulating FMD viral lineages in Pool 4 during 2017

- 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 (Algeria, 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 in 2017 (countries highlighted in purple; graph represents clinical submissions since 2005)





Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
RRLSS, BVI, Botswana	Uganda	21	119
NAHDIC, Ethiopia	Ethiopia	112	17700
IZSLER, Italy	Algeria, Kenya	6	1535
FMD Laboratory, Kenya	Kenya	84	190
ARC OVI, South Africa	Kenya	0	2
WRLFMD, UK	Algeria, Egypt, Ethiopia, Kenya, Uganda	128	0

Pool 4 headlines: Changes to FMD status in 2017:

- During March 2017, IZSLER (Brescia, Italy) received samples from Algeria and Tunisia which were characterised as belonging to the serotype A/AFRICA/G-IV lineage. This is the first time that this FMDV serotype has been reported in Algeria since 1977, and sequence data indicates that these outbreaks are due to FMD viruses that have originated from West Africa (most closely related to isolates from Nigeria, 2015 - ~98% nucleotide identity).
- O/ME-SA/Ind-2001 viral lineage has not spread further in North Africa during 2017
    - 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 (see Appendix 4)

3.4.2 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

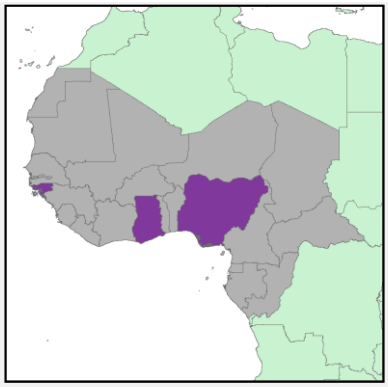
- Locally produced vaccines from NVI (Ethiopia):
  - Topotype O, EA 3
  - Topotype A , Africa 3
  - Topotype SAT 2, XIII
- Locally produced vaccines from BVI (Botswana) and ME-VAC (Egypt)

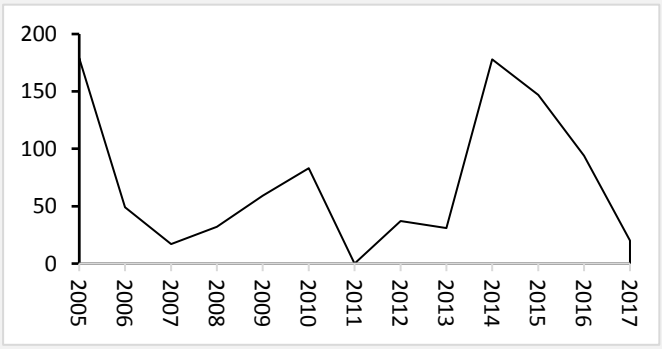
3.5 Pool 5 Regional synopsis

3.5.1 Conjectured circulating FMD viral lineages in Pool 5 during 2017

- 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 in 2017 (countries highlighted in purple; graph represents clinical submissions since 2005)





Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
NVRI, Nigeria	Nigeria	17	486
ANSES, France	Chad, Guinea-Bissau, Nigeria	1	53
CODA-CERVA, Belgium	Nigeria	0	338
WRLFMD, UK	Ghana	2	0

Pool 5 headlines: Changes to FMD status in 2017:

- Amount of samples tested from this region remains low, hampering efficient monitoring of the regional FMD situation
  - Serotypes O, A, and SAT2 have been identified in 2017 by Network laboratories (ANSES reported detection of O/WA and SAT 2 in samples collected from Guinea-Bissau (2016) and Chad, respectively, and BVI/WRLFMD detect serotype O in Ghana [see appendix 4]).
  - Research projects are currently underway to evaluate simple sampling methods for the region employing lateral-flow devices, which can be used locally for case

3.5.2 Vaccine recommendations for Pool 5

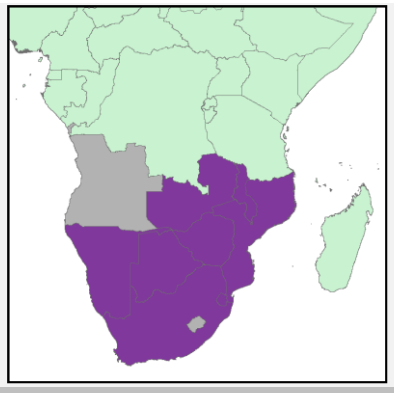
- Internationally produced vaccines:
  - O/Manisa
  - O/Maghreb
  - O/PanAsia-2 (or equivalent)
  - O: 3039
  - A: Eritrea
  - SA**T** 2: Eritrea & Zimbabwe
- Locally produced vaccines
  - O: WA and EA-3 topotypes
  - A: West Africa (G-IV) topotype (lineage)
  - SAT 1: Topotype X
  - SAT 2: Topotype VII

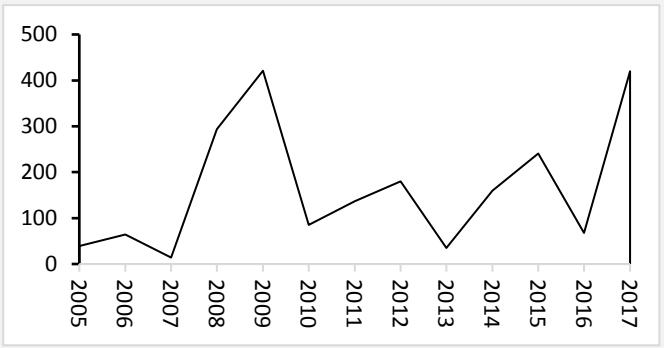
3.6 Pool 6 Regional synopsis

3.6.1 Conjectured circulating FMD viral lineages in pool 6 during 2017

- 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 3-4: Overview of samples collected and tested from Pool 6 in 2017 (countries highlighted in purple; graph represents clinical submissions since 2005)





Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
RRLSS, BVI, Botswana	Botswana, Lesotho, Malawi, Namibia, Zambia, Zimbabwe	57	353
ARC-OVI, South Africa	Mozambique, Namibia, South Africa, Swaziland	357	17167
WRLFMD, UK	Botswana, Malawi, Namibia, Zambia, Zimbabwe	6	0

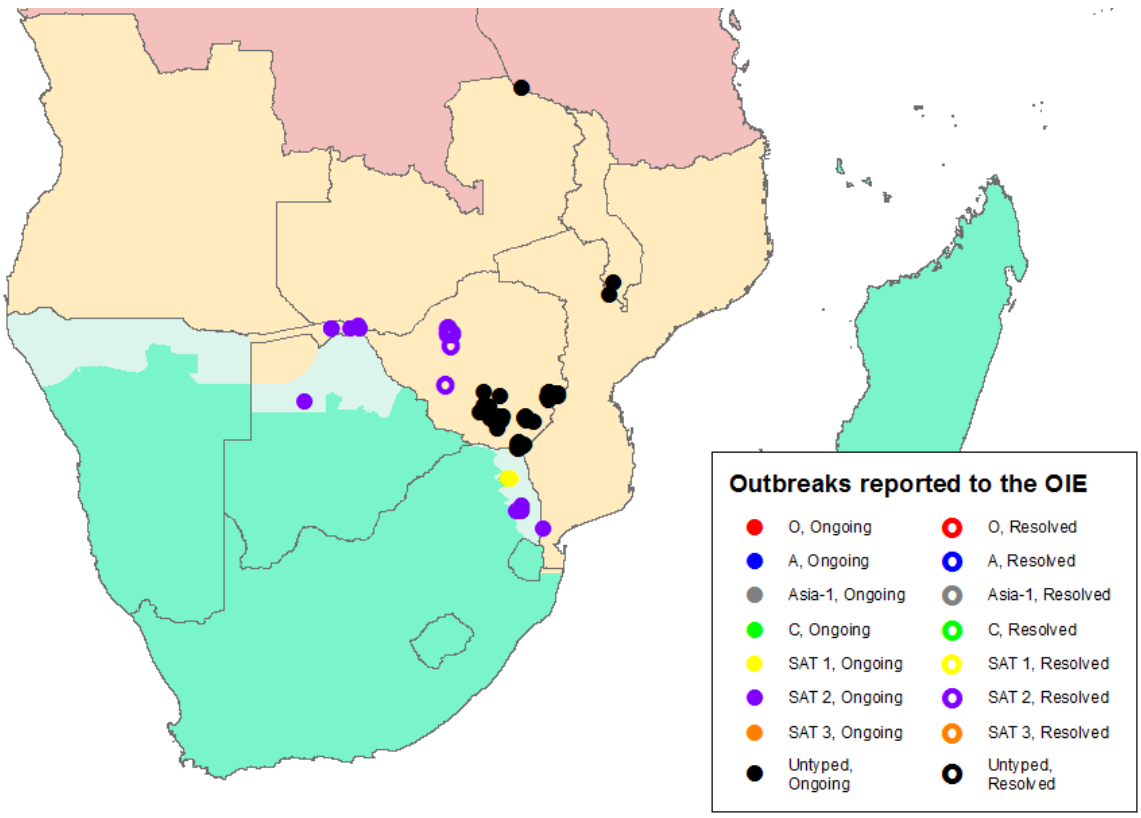


Figure 3-3: An overview of FMD outbreaks from southern African countries for events reported to the OIE during 2017.

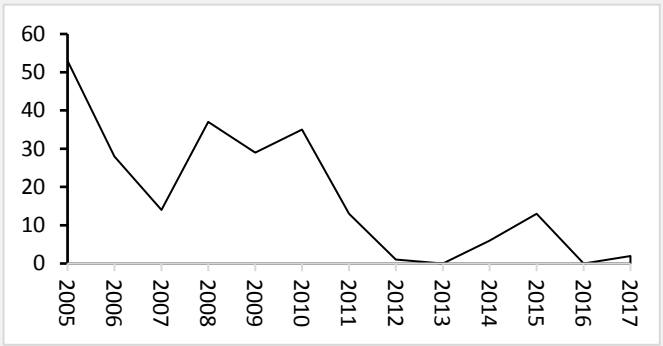
Pool 6 headlines: Changes to FMD status in 2017:

- Outbreaks due to three serotypes (SAT 1, SAT 2 and SAT 3 [see appendix 4])
- In 2017 network laboratories have identified:
    - SAT 1 from Mozambique, South Africa, Zambia and Zimbabwe
    - SAT 2 from Botswana, Mozambique, Namibia, South Africa, Zambia and Zimbabwe
    - SAT 3 from Mozambique and Zambia
- There is no overall change in epidemiological pattern since the samples from South Africa were in the FMD Protective Zone adjacent to the KNP so the outbreak did not impact the OIE status.

3.6.2 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

3.7 Pool 7 Regional synopsis



Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
PANAFTOSA, BRAZIL	COLOMBIA	2	0

Pool 7 headlines: Changes to FMD status in 2017:

- Between 1st June and 20th July 2017 there were outbreaks of serotype O in the Cundinamarca, Arauca and Norte de Santander regions of Colombia. On detection of FMD the Colombian Agricultural and Livestock Institute (ICA) initiated health protocols and immediately applied the quarantine to the locations. These outbreaks led to the suspension of Colombia's FMD-free (with vaccination status). This status was reinstated in December, with the exception of the territory within a FMD containment zone.
- Phylogenetic analysis by PANAFTOSA indicates that the strain is very similar to a strain of Venezuelan origin (see Appendix 4)

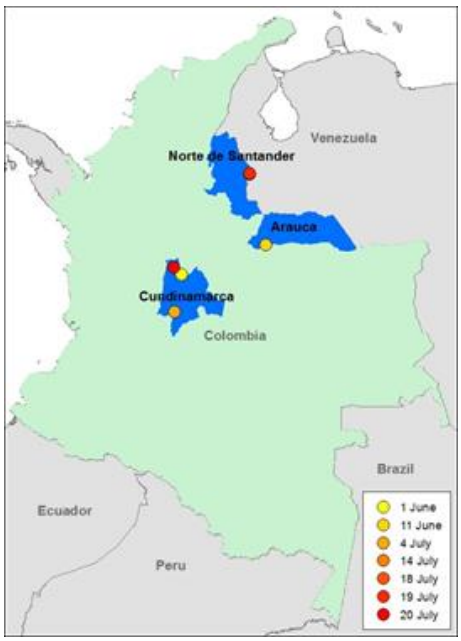


Figure 3-41: FMD outbreaks reported in Colombia during 2017

3.7.1 Vaccine recommendations for Pool 7

- Internationally produced vaccines:
  - All vaccines used in the region are produced in South America (Argentina, Brazil, Colombia, Paraguay & Venezuela have vaccine manufacturers)
- Locally produced vaccines
  - O: O_1 Campos
  - A: A_{24} Cruzeiro, A/Arg/2001
  - C: C_3 Indaial

4 Improving the quality of laboratory tests from FMD reference laboratories

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

Australia

Proficiency testing for FMD molecular (PCR) and serology (ELISA) was provided to the Australian State laboratories and New Zealand under the Laboratories for Emergency Animal Disease, Diagnosis and Response (LEADDR) network. Two rounds of FMD PCR and one round of FMD ELISA was provided to the LEADDR network in 2017.

Brazil

- Proficiency test organized – 2016
  - FMDV/VSV typing by ELISA
  - 13 lab participants
- Ongoing 2017 Proficiency test
  - FMD/VSV typing by PCR

China

- National PT for major animal disease organized by CADC and RL in April 2017
  - funded by MoA
  - FMD blind samples prepared and provided by FMDRL
  - 32 provincial labs were invited and 29/32 labs correct.

Kenya

- Nakuru Training Courses
  - FMD diagnosis and outbreak investigation for EU and Kenyan Vets

Republic of Korea

The national proficiency tests in South Korea (2017)

- Regional Diagnostic Centers (7) for FMD antigen and antibody test (twice a year)

Thailand

Round 5 (2017) inter-laboratory comparison

- 17 participating laboratories
    - 9 FMD laboratories in Thailand [all results received]
    - 8 FMD laboratories in South Eastern Asia (Vietnam (2), Myanmar, Lao PDR, Malaysia, Brunei, Singapore & Cambodia) [4 results received, 4 in progress]

United Kingdom

	Phase XXVIIII (2016)		Phase XXX (2017)	
Total invited laboratories[1]	94		81	
Total number of shipments[1]	70		70	
EURL funded participants				
Participants from European Union (funded by EURL for FMD)	28 (EU member states)		27 (EU member states)	
% of labs meeting target performance[4]	Cat-1	0 %	Cat-1	0 %
	Cat-2	0 %	Cat-2	0 %
	Cat-3	60.71 %	Cat-3	44.44 %
	Cat-4	39.29 %	Cat-4	55.56 %
EUFMD funded participants				
Participants from Global Network Labs[2]	BVI Botswana, Brazil, Canada[3], China, Ethiopia, Kenya, Nepal, Nigeria, Russia, South Africa, Thailand, USA[3].		Argentina, Botswana, Brazil, Canada[3], Ethiopia, Kenya, Nigeria Russia, South Africa, Thailand, USA[3].	
% of labs meeting target performance[4]	Cat-1	0 %	Cat-1	0 %
	Cat-2	0 %	Cat-2	0 %
	Cat-3	60 %	Cat-3	72.73 %
	Cat-4	40 %	Cat-4	27.27 %
Participants from EuFMD Member states (non-EU)	Albania, Georgia, Macedonia, Norway, Serbia, Switzerland, Turkey		Albania, Israel, FYR Macedonia, Norway, Georgia, Serbia, Switzerland, Turkey	
% of labs meeting target performance[4]	Cat-1	0 %	Cat-1	0 %
	Cat-2	0 %	Cat-2	0 %
	Cat-3	66.6̇ %	Cat-3	75 %
	Cat-4	33.3̇ %	Cat-4	25 %
Participants from neighbourhood countries	Algeria, Armenia, Azerbaijan, Iran, Lebanon, Moldova, Montenegro, Morocco, Tunisia		Algeria, Armenia, Azerbaijan, Egypt, Jordan, Kosovo, Lebanon, Moldova, Morocco, Tunisia.	
% of labs meeting target performance[4]	Cat-1	0 %	Cat-1	0 %
	Cat-2	0 %	Cat-2	0 %
	Cat-3	77.7̇ %	Cat-3	70 %
	Cat-4	22.2̇ %	Cat-4	30 %
Summary of EUFMD funded participants				
Invited				
Panels shipped	Panel 1	23	Panel 1	22
	Panel 2	23	Panel 2	23
	Panel 3	26	Panel 3	25
	Panel 4	14	Panel 4	15

Total number of participants funded by EUFMD	26	25	
Self-funded participants			
Participants		Australia, Kazakhstan, Namibia, Pakistan, Senegal, Singapore, Swaziland, UAE, & Zambia	
% of labs meeting target performance[4]		Cat-1 Cat-2 Cat-3 Cat-4	0 % 0 % 44.44 % 55.56 %

*[1] Additional laboratories (non-NRL) participate in the PTS at their own expense; [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.*

USA

- FMD rRT- PCR Proficiency Testing Scheme with 45 US NLAHN.
- FMD rRT- PCR Proficiency Testing Scheme with COPEG-LADIVES, Panama.

4.2 Supply of reagents

Argentina

Type of Reagent	Quantity	Recipient of the reagent
Hyper-immune guinea pig sera A24 Cruzeiro-A ARG 2001-O1 Campos-C3 Indial	100 vials x 1 ml	Argentina and Paraguay
FMD challenge viral suspension for PPG test A24 Cruzeiro -Arg 2001-O1 Campos	1500 vials x1 ml	Argentina
Viral Inactivated Antigen	224ml	Argentina
Typing ELISA	16 x 5 plates	Argentina, Uruguay and Paraguay
3 ABC ELISA	5 x 100 plates	Argentina
Reference Sera NSP	3 vials x 1 ml	South Korea

Australia

- External quality assured controls were supplied to LEADDR laboratories for PCR and ELISA.
- The role out to the Australian LEADDR network of the PrioCHECK® FMDV NS ELISA to standardise capability was undertaken in 2017.

Botswana

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	50ml of SAT 306 rabbit sera	BNVL/ Botswana
FMDV antigen kits	50ml Each SAT1-3 ELISA reagents and controls	CVL/Zimbabwe

Canada

Type of reagent	Quantity	Recipient of the reagent (Laboratories / Countries)
FMDV antigen kits (Rabbit and Guinea pig antibody pairs for SAT1,2,3 double antibody sandwich ELISA)	6 ml	Botswana Vaccine Institute(BVI) / BITRI
SAT 2 strip test reagents (Biotin-F76 -10 SAT 2, Gold conjugated F21-42)	400 µl and 500 µl	Botswana Vaccine Institute(BVI) / BITRI
Purified mAb F21140SO6 (against FMDV/O) and F10140SA6 (against FMDV/A)	500 µl each	Cambivac Ltd. UK

China

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
LPBE-O	6962	Veterinary laboratories; large scale breeding companies; China
LPBE-Asia1	3244	
LPBE-A	3329	
NSP-3ABC-ELISA	2004	
SPCE(type A, O; pilot)	145	
Antigen ELISA	0	FMDRL only
Conventional Mult-RT PCR	286	Provincial veterinary laboratory in China
Real-time RT-PCR	683	
Typing real-time RT-PCR	214	

France

- Master-Mix duplex rtRT-PCR

- Cell line
- Inactivated antigen
- FMDV RNA
- RNA extraction kit
- LFD and extraction kit

India

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	94,380 (NSP-DIVA Kit)	Regional and collaborating centres of AICRP on FMD, India
FMDV antigen kits	6,000 (S-ELISA)	Regional and collaborating centres of AICRP on FMD, India & Sri Lanka

Italy

Country or organization		FMDV antigen detection ELISA type O, A, C, Asia1, SAT1-2	NSP Ab ELISA KIT	SP Antibody ELISA Kit				
			3ABC	FMDV O	FMDV A	FMDV Asia1	FMDV SAT2	FMDV SAT1
Training FAO		6	4	3	1	1		
Asia	South Korea	8						
	Singapore	1		1	1	1		
	Vietnam	2						
	Taiwan	1		3	2			
	Mongolia	10		14	13	5		
	China	5	2	590	290	60		
Central Asia & WestEurasia	Pakistan	75	10	18	17	17		
	Kazakhstan			730	3	3		
	Turkey	6		3	4	3		
	Georgia			2	2	2		
Middle East	UAE			26	26			
	Israel	5		1	1	1		
	Saudi Arabia	6						
Africa	Egypt		10	7	7		7	
	Mauritius	1						
	Algeria	6	20	5	5			
	Morocco	1			3			
	Senegal	1						
	Sudan	3		3	3	3	3	
	Nigeria	2	1	1	1			
	Kenya	9	4	4	4		4	4
Countries FMDV-free	New Zealand	1			1	1	1	
	Slovenia	1	1					1
	Lithuania	1						
	Japan			1	1	1		
	Brazil	1						
	Romania	1	1	1	1	1		
	Sweden	1						
	Ireland	2		1	1	1	1	
	Belgium	1					2	
	Albania	1	1	1	1	1		
	Austria	1						
	Croatia	1		1	1	1	1	
	Poland	1		1	1	1	1	
Total number of kits		**155**	**50**	**1414**	**389**	**102**	**20**	**5**

Republic of Korea

Type of Reagent	Product name	Details	Quantity	Recipient of the reagent (Lab/Countries)
Antigen Test	Biosign FMDV Ag test	Ag rapid kit for Pan serotypes	50	Mongolia
	APQA FMDV O Ag rapid kit	Ag rapid kit for O serotype (trial version)	50	
	APQA FMDV A Ag rapid kit	Ag rapid kit for A serotype (trial version)	50	
Antigen Test	Biosign FMDV Ag test	Ag rapid kit for all serotypes	35	Sri Lanka
	APQA FMDV O Ag rapid kit	Ag rapid kit for O serotype (trial version)	50	
	APQA FMDV A Ag rapid kit	Ag rapid kit for A serotype (trial version)	50	
	APQA FMDV Asia1 Ag rapid kit	Ag rapid kit for Asia1 serotype(trial version)	50	
Antibody Test	VDpro FMDV NSP Ab ELISA	NSP Ab ELISA	192	
	VDpro FMDV Type O ELISA	SP Ab ELISA for type O	192	
Antigen Test	Biosign FMDV Ag test	Ag rapid kit for all serotypes	35	Vietnam
	APQA FMDV O Ag rapid kit	Ag rapid kit for O serotype (trial version)	50	
	APQA FMDV A Ag rapid kit	Ag rapid kit for A serotype (trial version)	50	
	APQA FMDV Asia1 Ag rapid kit	Ag rapid kit for Asia1 serotype(trial version)	50	
Antigen Test	Biosign FMDV Ag test	Ag rapid kit for Pan serotypes	35	Myanmar
	APQA FMDV O Ag rapid kit	Ag rapid kit for O serotype (trial version)	50	
	APQA FMDV A Ag rapid kit	Ag rapid kit for A serotype (trial version)	50	
	APQA FMDV Asia1 Ag rapid kit	Ag rapid kit for Asia1 serotype(trial version)	50	
Antibody Test	Bionote FMDV NSP Ab ELISA	NSP Ab ELISA	480	

Type of Reagent	Product name	Details	Quantity	Recipient of the reagent (Lab/Countries)
Antigen Test	Biosign FMDV Ag test	Ag rapid kit for Pan serotypes	35	LAO PDR
	APQA FMDV O Ag rapid kit	Ag rapid kit for O serotype (trial version)	50	
	APQA FMDV A Ag rapid kit	Ag rapid kit for A serotype (trial version)	50	
	APQA FMDV Asia1 Ag rapid kit	Ag rapid kit for Asia1 serotype(trial version)	50	
Antigen Test	Biosign FMDV Ag test	Ag rapid kit for Pan serotypes	35	Cambodia
	APQA FMDV O Ag rapid kit	Ag rapid kit for O serotype (trial version)	50	
	APQA FMDV A Ag rapid kit	Ag rapid kit for A serotype (trial version)	50	
	APQA FMDV Asia1 Ag rapid kit	Ag rapid kit for Asia1 serotype(trial version)	50	
Antibody Test	VDpro FMDV NSP Ab ELISA	NSP Ab ELISA	192	
	VDpro FMDV Type O ELISA	SP Ab ELISA for type O	192	
Antigen Test	Biosign FMDV Ag test	Ag rapid kit for all serotypes	35	UK(Pirbright)
	APQA FMDV O Ag rapid kit	Ag rapid kit for O serotype (trial version)	100	
	APQA FMDV A Ag rapid kit	Ag rapid kit for A serotype(trial version)	100	
	APQA FMDV Asia1 Ag rapid kit	Ag rapid kit for Asia1 serotype(trial version)	100	
Antigen Test	APQA FMDV Ag rapid kit	Ag rapid kit for 3diff/PAN (trial version)	120	FAO(For Nepal, Kenya)

Russia

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	96	Kazakhstan, South Korea, Vietnam
FMDV antigen kits	12	Kazakhstan, Kyrgyzstan

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 = 26 sets Type A = 25 sets Type Asia1 = 13 sets	Type O = 2 sets Type A = 3 sets Type Asia1 = 1 set (Lao PDR)	Specific programme; - Providing of complete set of ELISA reagent for inter-laboratory comparison testing round 5/2017 Total 18 sets FMD labs in Thailand = 9 sets, SEA Labs = 8 sets
Guinea pig detecting antibody for type O, A and Asia1	Type O = 28 sets Type A = 29 sets Type Asia1 = 16 sets	Type O = 2 sets Type A = 3 sets Type Asia1 = 1 set	
inactivated & concentrated antigen (50X) for type O, A and Asia1	Type O = 120 ml Type A = 59 ml Type Asia1 = 29 ml	Type O = 5 ml Type A = 7 ml Type Asia1 = 2 ml	
Control serum for C++, C+ and C-	C++ = 175 ml C+ = 175 ml C- = 160 ml	C++ = 30 ml C+ = 30 ml C- = 30 ml	

United Kingdom

Country	Number of vials	Serotype	Reagent type
Belgium	1	A	Antisera
Switzerland	77	NSP	NSP
South Korea	111	O, A, C, Asia 1	Antigen, antisera, controls
Vietnam	701	O, A, C, Asia 1	Antigen, antisera, controls
Poland	109	O, A, C, SAT 1, SAT 3, Asia 1	Antigen, antisera, controls
Russia	8	O, A, SAT 1, Asia 1	Controls
New Zealand	5	O, SAT 1, SAT 2, SAT 3	Antigen
UK	12	O, A, NSP	Antigen, antisera, NSP
Romania	3	C, SAT 3	Antigen, antisera
Lithuania	4	O, A	Controls
Total	1031		

FMD viruses provided to other FMD labs and commercial companies:

Country	volume	Serotype	Reagent type
Argentina	9 ml	O, A, Asia-1	Viral isolate
Belgium	12.6 ml	O, A	Viral isolate
Japan	4.8 ml	O, A	Viral isolate
The Netherlands	1.8 ml	O, A	Viral isolate
Russia	7.2 ml	SAT 2	Viral isolate
United Kingdom (BI)	43.2ml	O, A	Viral isolate
Total	78.6 ml		

In addition to FMDV, SVV isolates were sent to Belgium (3.6 ml) and Ireland (3.6 ml)

USA

Reagents provided to COPEG-LADIVES (Panama) for FMD and VSV Antigen ELISA (Kits)

4.3 Training courses organised by Network partners

Argentina

- Vesicular Disease Diagnosis – Senacsa, Paraguay
- FMD Vaccine Quality Control - QIA, South Korea
- FMD Vaccine Quality Control - Nigeria

Australia

- Recent Advances in emergency Animal Diseases Annual Symposium, 18th – 19th October 2017.
    - This course is designed for veterinarians, animal health managers, diagnosticians and livestock industry representatives as part of their continued education.
    - Talks were presented on various diseases including FMD.

Brazil

- International workshop for FMD differential diagnosis
    - 30 participants from all COSALFA countries

Belgium

In November 2017, CODA-CERVA organised a two-weeks training course for 3 scientists from Nigeria (NVRI) and 1 scientist from Ethiopia (NVI).

Botswana

- Outbreak investigations and molecular characterization of foot and mouth disease viruses circulating in south-west Niger
    - PhD student
    - BVI as a technical centre
    - Collaborating with University of Liege, Belgium
- Genetic and antigenic characterization of foot and mouth disease virus strains isolated in 2011 and 2015 in Ngamiland, Botswana
    - MSc student, Molecular Biology – One Health

- Collaboration with Sokoine University of Agriculture, Tanzania
- Outbreak investigations and molecular characterization of foot-and-mouth disease viruses circulating in southern Ghana.
  - MSc Student, Microbiology
  - Collaborating with University of Botswana

Canada

- Foreign Animal Disease Recognition course (for Canadian veterinarians mainly but also international).
- 22 FMDV 3ABC ELISA and 45 FMDV RRT-PCR panels provided to the Canadian Animal Health Surveillance Network (CAHSN) laboratories.
- Training of CAHSN lab analyst on FMDV RRT-PCR.
- Training of Botswana Institute for Technology Research and Innovation (BITRI) scientists/technicians on FMDV antigen detection by ELISA and lateral flow strip test.

China

- National Training
  - Reports or seminars at workshops organized by provincial labs
    - FMD epidemiology; Surveillance/PVM; Vaccination; Prevention and control
  - 10 series of Training Courses jointly organized by FMDRL and Diagnosis Center, LVRI
    - Focuses on lab operating; ~600 persons joined (Lab staff from provincial laboratories and vets from big farms)
  - Biosafety training
  - Field training (sampling during active surveillance)
- International Training
  - International training workshop on TADs (FMD, PPR, Pox…) diagnosis technologies , 10^{th}-24^{th} September 2017
    - A project directed by Dr Yanmin Li; Funded by MoST, China; Lectures and experimental operations; 15 Trainees from 8 countries (Thailand, Pakistan, Kazakhstan, Mongolia, Egypt, Sudan, South Sudan and Burundi)

France

One week training at the Animal Health Laboratory, Reduit, Mauritius

Republic of Korea

- Laboratory diagnostic training of regional veterinarians from Regional Diagnostic Centres
  - 3 times
  - 40 Vets
- Scientific and Technical Training for Asian Countries (5th Workshop)
  - FMD diagnosis and surveillance, FMD vaccine evaluation
  - 10 participants from 5 Asian countries (Vietnam, Cambodia, Lao PDR, Sri Lanka & Myanmar)
  - 5th to 13th September 2017

South Africa

- "Molecular detection of FMDV"
  - For staff of Makerere University and UVRI, Uganda
  - Run by Drs Scott and Maree
- Optimisation of ELISA and quality.
  - Training run at BVI, Botswana
  - Run by Nazeem Cassim and Brenda Botha
- Danika van der Merwe – student; University of Pretoria

Russia

- Advanced training in up-to-date epidemiology, diagnosis, prevention and control of FMD, Sheep and Goat pox and Peste des petits ruminants.
  - 16 trainees from 4 Russian Federation regions.
- Three workshops on epidemiology, diagnosis and control of FMD for Veterinary Services.
  - 208 trainees from 25 Russian Federation regions

Thailand

- Training on Immunohistochemistry testing.
  - RRL staff at Kodaira Laboratory, Japan
  - 24th-28th April 2017
- Hands-on Laboratory Training on Foot and Mouth Disease diagnosis Officer from Department of Animal Health (DAH), Vietnam.
  - 4 staff of RAHO6, DAH Vietnam to be trained at RRL, Pakchong
  - 22nd May to 2nd June 2017
  - Subject training :
    - Antigen typing ELISA, LP ELISA, RT-PCR and Sequencing
- International training Workshop on Major Transboundary Animal Diseases (TAD), FMD, PPR and Sheep /Goat Pox Diagnosis Technology

- LVRI, China
- 10th-14th September 2017.

- Scientific visit of 10 officers from Animal and Plant Quarantine Agency (QIA), South Korea on FMD diagnosis.
  - 7th December 2017.
- Scientific visit of 4 visitors from Taiwan under the Cooperation on Building Veterinary Capacity for Veterinary Drugs, Biological Products and Medicated Feed and Products Registration between Thailand and Taiwan (R.O.C)
  - 10th November 2017.

United Kingdom

- Training in vaccine-matching provided to APQA, Republic of Korea.
- Ethiopia - (WRLFMD and NAHDIC are currently collaborating on an OIE twining project)
  - Two scientists from WRLFMD visited NAHDIC to provide training in real-time RT-PCR and serological methods (including virus neutralisation test)
  - One scientist visited Pirbright for one-month training in advanced molecular methods (lineage-specific real-time RT-PCR and sequencing)
  - One scientist visited Pirbright for training in serological diagnostics
- Two-week residential training course for FMD diagnostics provided to scientists from Israel, Lithuania, New Zealand and Singapore.
- Training provided to a scientist from Ireland in FMD serological methods
- WRLFMD hosted a visiting scientist from Kazakhstan to develop tailored diagnostic methods for Central Asia
- WRLFMD hosted a visiting scientist from Japan to evaluate novel diagnostic methods for FMD
- Oct-Nov 2017: E-Learning training in FMD diagnostic methods provided to 106 participants from 49 countries (62 completed the course and received certificates).

USA

- FAD (foreign animal diseases, including FMD, CSF, ASF and others) Schools with US field veterinarians only.

4.4 Collaborative projects

Argentina

Collaborators	Purpose of collaboration	Outcomes
SENACASA (Paraguay)	Bilateral agreement	Bilateral agreement between SENACSA Paraguay laboratories and SENASA Argentina in diagnosis and control of Zoonoses, and Biosecurity and Biosafety
Vietnam	RAHO 6	FMD viral characterization
QIA (Republic of Korea)	FMD Vaccine Quality Control	Development of FMD new generation vaccines based on non-infectious viral capsids – PID 2013-2022

Australia

Collaborators	Purpose of collaboration	Outcomes
RRLSEA (Thailand), Regional Animal Health Office 6 (Vietnam)	Vaccine matching studies	
National Animal Health Laboratory (Lao PDR), laboratory in Nay Pyi Taw, Myanmar	Laboratory visits	
The Pirbright Institute (UK), Wageningen Bioveterinary Research (Netherlands)	Vaccine matching studies	Study the efficacy of a serotype A vaccine available in the Australian Vaccine Bank (AVB).
National Centre for Foreign Animal Diseases (Canada), MSD Animal Health	Vaccine matching studies	
FLI (Germany)	Virus inactivation studies	

Brazil

Collaborators	Purpose of collaboration	Outcomes
Department of Animal Production and Health Veterinary Service / Suriname-PANAFTOSA	NSP Serosurvey in support to OIE dossier for recognition of FMD free status	I-ELISA 3ABC/EITB non-reactive farms
COSALFA countries (all of South America & Panama)	FMDV Regional Antigen Bank	Constitutive Agreement approved by PAHO and COSALFA countries

COSALFA countries (all of South America & Panama)	Updating document of Minimum Standards for biorisk management in laboratories handling FMDV and/or its derivatives	Documents approved by 44th COSALFA (April 2017)

Belgium

Collaborators	Collaborative project	Outcomes
NVRI (Nigeria)	OIE twining project	Building the capacity of NVRI
BVI (Botswana)	Bilateral collaboration	
LNV (Burundi)	Bilateral collaboration	

Botswana

Collaborators	Purpose of collaboration	Outcomes
University of Botswana (Botswana), Keck Graduate Institute (USA)	Next Generation Vaccine	Plant based produced FMD vaccine for SATs
BITRI (Botswana), Canadian Food Inspection Agency (Canada)	Develop and validate LFD for detection of FMD Antigen in the field	Serotype specific detection of outbreak strain

Canada

Collaborators	Purpose of collaboration	Outcomes
Iowa State University (USA)	Validation of assays for FMDV antigen and antibody detection in swine oral fluids	Molecular and serological assays for FMDV detection in swine oral fluids
Botswana Institute for Technology Research / Botswana Vaccine Institute (Botswana)	Development of strip tests for SAT1,2 3 antigen; and NSP antibody detection	Field deployable FMDV diagnostic tests
Australian Animal Health Laboratory (Australia)	Emergency and improved vaccines for FMD	Knowledge of suitable vaccines for emerging/circulating FMD viruses

China

Collaborators	Purpose of collaboration	Outcomes
Korea Atomic Energy Research Institute (Republic of Korea)	Research and development of an attenuated edible FMD vaccine using salmonella as the vector	Korea collaborators visited LVRI in August 2017
Kazakh National Agrarian University (Kazakhstan)	Cooperative creation and application studies of new products for prevention and control of major transboundary animal diseases	The opening meeting of the project is held in Lanzhou on 16th November 2017
The University of East Anglia (UEA) (UK)	Exchange of vaccine technology for the delivery of oral vaccines to mucosal	Dr. Zhidong Zhang, Dr Yanmin Li and Dr Xiaodong Qin has visited Laboratory, UEA in Aug 2017
National Microbiology Laboratory - Public Health Agency of Canada (Canada), University of Manitoba (Canada)	Genetic variation in foot-and-mouth Disease Virus A/HUBWH strain under selective pressures of antibody and its correlation with vaccine potency	Examined the genetic variations of the FMDV under the antibody selective pressure

Ethiopia

Collaborators	Collaborative project	Outcomes
WRLFMD (UK)	OIE twining project	Building the capacity of NAHDIC in different FMD Diagnosis and antigen detection Molecular test, Serotyping using rRT PCR Vaccine matching

France

Collaborators	Purpose of collaboration	Outcomes
SLU, CODA-CERVA (Belgium), FLI (Germany), INRA	Transcriptovac project (Anihwa)	Host response gene signatures associated with FMDV infection, vaccination and persistence
CIRAD (France), IRED (ex Farcha laboratory)	Characterisation of FMDV circulating in Chad	

India

Collaborators	Purpose of collaboration	Outcomes
PIADC, USA	This collaborative research project is aimed at improving the understanding of Foot-and-Mouth Disease (FMD) ecology in endemic regions to provide the basis for effective control strategies.	The details are discussed in the following manuscript • Hayer SS *et al.* (2017) Quantitative characteristics of the foot-and-mouth disease carrier state under natural conditions in India. *Transbound Emerg Dis*, doi: 101111/tbed12627 • Ranjan *et al.* (2016) Foot-and-Mouth Disease Virus-associated abortion and vertical transmission following acute infection in cattle under natural conditions. *PLoS One*, **11**(12):e0167163 • Hayer SS *et al.* (2017) Foot-and-mouth disease virus transmission dynamics and persistence in a herd of vaccinated dairy cattle in India. *Transbound Emerg Dis* (Accepted) • Other manuscripts under preparation

Italy

Collaborators	Collaborative project	Outcomes
The Pirbright Institute, UK	Continuous validation and improvement of new diagnostic kits (ELISA)	• Use of recombinant reagents (Integrin, VLPs) in ELISA kits • New mAbs investigations • Quantification of cross-reactivity of SP Ab-ELISAs
USDA ARS PADC Foreign Animal Disease research, Plum Island NY, US	Study of interaction between FMDV and host proteins during infection	Production of mAbs to 2B
University of Tripoli, NCAH - Libya	Study of FMD epidemiology	(design study agreed in 2017, activities planned in 2018) • Country serosurvey • Collection of samples (OP) in suspect and seropositive farms to characterize FMD circulating viruses • Training of two PhD students
International Livestock Research Institute (ILRI)-Kenya	Kinetic and Evaluation of the immune response to field vaccination with tetravalent vaccine. Investigation of virus serotype diversity by serology	• Results of endpoint titration for serotypes O,A,SAT1 and SAT2 (and for NSP Ab) of sequential PV sera. • Results of endpoint titration for NSP Ab and for serotypes O,A,SAT1 and SAT2 of field sera collected in endemic settings.

North Africa, OIE, EuFMD	Field vaccination trials for evaluation of vaccines currently used in Maghreb region	• Preliminary tests done in Morocco, Algeria, Tunisia (IZSLER kits) • VNT at IZSLER (shipment problems to be solved)

Kenya

Collaborators	Purpose of collaboration	Outcomes
Kenya Wildlife Service (Kenya), PIADC - US Department of Agriculture (USA), University of Minnesota (USA)	Evaluating cross-species transmission of FMD in rangelands shared by buffalo and cattle in Kenya	Improved understanding of FMD transmission dynamics in Kenya
DVS Kenya (KENYA), EUFMD	FMD Real-Time training	EU and Kenyan Vets capacity for FMD outbreak diagnosis & investigation improved

Republic of Korea

Collaborators	Collaborative project	Outcomes
National Center for Veterinary Diagnosis, Department of Animal Health (Vietnam)	To carry out comparative studies of Avian influenza virus and Foot and mouth disease virus between Korea and Vietnam	Data and materials (2016~2024)
National Animal Health and Production Research Institute (Cambodia) & National Animal Health Laboratory (PDR Lao)	To study on genetic characterization of foot and mouth disease viruses and avian influenza virus in FMD and AI endemic countries (Cambodia and LAO PDR)	On going (2018~2022)
Ministry of Livestock, Fisheries & Rural Development: Livestock Breeding and Veterinary Department & other relevant departments (Myanmar)	Professional development in diagnosis of FMD in Myanmar (KOICA project)	On going

Nigeria

Collaborators	Collaborative project	Outcomes
CODA-CERVA (Belgium)	OIE twining project	Personnel training Implementation of SOPs Sample characterization including phylogenetic analysis
ANSES (France)	Rapid on site diagnosis of FMD and safe and cost-effective shipment of samples using lateral flow devices for laboratory diagnostic	Personnel training on LFD and sample shipment

Russia

Collaborators	Purpose of collaboration	Outcomes
Ministry of Agriculture (Russian Federation)	Second stage of animal health status improvement in Mongolia	Supply of emulsion FMD vaccine. Serum testing
FGBI ARRIAH (Russia)	Maintaining FMD freedom in the CIS countries	Program of FMD control until 2020 has been developed and approved by the Heads of the CIS members. FMD prevention measures have been continuously implemented

South Africa

Collaborators	Purpose of collaboration	Outcomes
The Pirbright Institute (UK)	NSF-EID funded project investigating Persistence of FMD in African buffalo	
University of Glasgow (UK), The Pirbright Institute (UK)	Improving the quality of foot-and-mouth disease (FMD) vaccines	Tracking the antigenic evolution of foot-and-mouth disease virus
PIADC – USDA (USA)	USDA funded project to Selection of appropriate candidate vaccine strains in emerging FMD outbreaks	ScFv binders to serotype A, SAT1, SAT2 and SAT3 viruses
Oxford University (UK)	Antigenic structure of FMDV	Antigenic refocusing of a SAT2 foot-and-mouth disease virus through dampening of epitope regions
Oxford University (UK)	Antigenic structure of FMDV	Symmetrical arrangement of positively charged residues around the five-fold pore of SAT type foot-and-mouth disease virus enhances binding to heparan sulphate
The Pirbright Institute (UK)	Structurally design of improved master seed virus	Evaluation of immune responses of stabilised SAT2 antigens of foot-and-mouth disease in cattle SAT2 foot-and-mouth disease virus (FMDV) structurally modified for increased thermostability
Dr P. Opperman, M. Chitray and F.F. Maree	Production of SAT-specific monoclonal antibodies for the development of a diagnostic ELISA	Novel buffalo antibody library with more than 107 binders

Thailand

Signed MOU on Research collaboration between NIAH, Japan and NIAH Thailand on 6th June 2017.

Collaborators	Collaboration project	Outcomes
National Institute of Animal Health (NIAH), Kodaira lab (Japan)	1) Research topic: FMDV Complete Genome Sequencing (continue) 2) Organise the Scientific Meeting on FMD research between RRL, Pakchong and NIAH, Kodaira. Which will be held in Kodaira, Japan, 15-16 Feb. 2018.	Scientific information on molecular epidemiology of FMDV and genomic variation information Exchange FMDVs for research collaboration under the MOU and specific MTA
Department of National Park wildlife and Plants Conservation (Thailand)	Preliminary sero-surveillance study of FMD disease in Wildlife	Basic information of FMDV serology in wildlife animals, zoo and national parks
National Institute of Animal Health (NIAH), Bangkok (Thailand)	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

United Kingdom

Collaborators	Collaborative project	Outcomes
Malaysian Government	Development of vaccine matching tests for Southeast Asia	Improvement of serological tests for vaccine matching
LLNL (USA) & Embakasi (Kenya)	Validation of RT-PCR methods for milk	Validation of RT-PCR methods for milk
IZSLER (Italy), ANSES (France) & Lelystad (The Netherlands)	Validation of NSP tests	Inter-laboratory exercise for NSP assays
IZSLER (Italy)	Development of FMD ELISA tests	New ELISA tests for FMD diagnosis
SUA (Tanzania) &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

USA

Collaborators	Collaborative project	Outcomes
Department of Homeland Security (USA)	International FMD Vaccine Trial Working Group	
OIE/FAO Reference laboratories network	FMD Vaccine Matching Working Group	

- Participant of the Department of Homeland Security's International FMD Vaccine Trial Working Group
- Participant of the OIE/FAO Reference laboratories network FMD Vaccine Matching Working Group

Appendix 1 - Details of clinical samples from field cases from countries in FMDV endemic regions tested during 2017

Laboratory	Samples from	Total	O	A	C	Asia 1	Sat 1	Sat 2	Sat 3	Untyped	NVD	Comments
ANSES	Guinea-Bissau	1	1	-	-	-	-	-	-	-	-	
BVI	Zimbabwe	21	-	-	-	-	5	2	-	-	14	
	Zambia	11	-	-	-	-	4	-	5	-	2	
	Uganda	21	1	-	-	-	-	1	-	-	19	
	Namibia	19	-	-	-	-	-	9	-	-	10	
	Malawi	1	-	-	-	-	-	-	-	-	1	
	Botswana	5	-	-	-	-	-	5	-	-	-	
FGBI ARRIAH	Russia	8	5	-	-	-	-	-	-	-	3	
	Mongolia	19	17	-	-	-	-	-	-	-	2	
FMD lab. (Kenya)	Kenya	84	29	11	-	-	18	7	-	-	19	
ICAR	India	150	150	-	-	-	-	-	-	-	-	
IZSLER	Algeria	6	-	6	-	-	-	-	-	-	-	
LVRI	China	58	19	8	-	-	-	-	-	-	31	
NAHDIC	Ethiopia	112	70	10	-	-	4	-	-	-	28	
OVI	South Africa	287	-	-	-	-	1	1	-	2	285	
	UAE	30	-	-	-	-	-	-	-	-	30	
	Swaziland	12	-	-	-	-	-	-	-	-	12	
	Mozambique	58	-	-	-	-	1	-	2	3	55	
PANAFTOSA	Colombia	2	2	-	-	-	-	-	-	-	-	
QIA	Korea, Republic of	9	8	1	-	-	-	-	-	-	-	
NVRI	Nigeria	17	6	5	-	-	-	6	-	-	-	
RRLSEA	Thailand	76	32	14	-	-	-	-	-	63	30	
	PDR Lao	5	2	-	-	-	-	-	-	4	3	
	Myanmar	31	19	-	-	2	-	-	-	29	10	
ŞAP Institute	Turkey	354	99	156	-	-	-	-	-	33	66	
	Iran	5	-	5	-	2	-	-	-	-	-	
WRLFMD	Afghanistan	38	5	9	-	2	-	-	-	22	-	
	Algeria	3	-	3	-	-	-	-	-	-	-	
	Bhutan	22	15	1	-	-	-	-	-	5	1	
	Botswana	1	-	-	-	-	-	1	-	-	-	
	Cambodia	5	3	3	-	-	-	-	-	-	-	1 dual infection: O & A
	Egypt	35	21	1	-	-	-	-	-	10	3	
	Ethiopia	81	31	-	-	-	-	-	-	22	28	
	Ghana	2	1	-	-	-	-	-	-	-	1	
	Hong Kong	4	3	-	-	-	-	-	-	-	1	
	Iran	24	9	9	-	-	-	-	-	4	2	
	Israel	8	8	-	-	-	-	-	-	-	-	
	Kazakhstan	5	-	-	-	-	-	-	-	-	5	
	Kenya	7	3	-	-	-	-	-	-	2	2	
	Korea, Republic of	3	2	1	-	-	-	-	-	-	-	
	Laos	2	2	-	-	-	-	-	-	-	-	
	Malawi	1	-	-	-	-	1	-	-	-	-	
	Mongolia	16	8	2	-	-	-	-	-	-	6	
	Myanmar	5	3	-	-	-	-	-	-	2	-	

Laboratory	Samples from	Total	O	A	C	Asia 1	Sat 1	Sat 2	Sat 3	Untyped	NVD	Comments
	Namibia	2	-	-	-	-	-	-	-	-	2	
	Nepal	50	26	3	-	-	-	-	-	16	5	
	Pakistan	45	14	11	-	22	-	-	-	3	1	6 dual infections: A & Asia-1
	Palestinian Autonomous Territories	10	8	-	-	-	-	-	-	-	2	
	Saudi Arabia	25	1	7	-	-	-	-	-	2	15	
	Sri Lanka	20	11	-	-	-	-	-	-	2	7	
	Thailand	28	18	10	-	-	-	-	-	-	-	
	Uganda	2	1	-	-	-	-	-	-	1	-	
	Zambia	1	-	-	-	-	-	-	1	-	-	
	Zimbabwe	1	-	-	-	-	-	1	-	-	-	
Totals		**1848**	**653**	**276**	**0**	**28**	**34**	**33**	**8**	**151**	**674**	

Appendix 2 - Vaccine matching studies undertaken by Network partners during 2017

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.

Australia

Potency determination of A Malaysia 97 against A/IRN/22/2015 (A/Asia/G-VII lineage) - Collaboration between AAHL, TPI and WBVR

This trial aimed to study the efficacy of a serotype A vaccine available in the Australian Vaccine Bank (AVB), A Malaysia 97 (A/MAY/97, when cattle were challenged with a serotype A FMD virus isolate, A/IRN/22/2015 (A/Asia/G-VII lineage). This lineage is of importance as it has emerged from the Indian subcontinent and caused major incursions into the Middle East and Asia.

In vitro studies performed internationally at various FMD reference laboratories, including the World Reference Laboratory, have indicated that no vaccine strain in the international vaccine banks will provide good protection against this virus. However, previous results indicated it is possible to get *in vivo* protection in some cases even when the *in vitro* studies predicted no protection. Therefore, we performed a pilot study in December 2016 where we compared two of the vaccine strains in the AVB with a limited number of animals (7 animals/group) and a single dose of vaccine, challenged at 21 days post vaccination. The A/MAY/97 vaccine provided 70% protection while A22 IRQ provided only 30% protection.

This current study estimated the potency of A/MAY/97 vaccine (>6PD_{50}; high potency vaccine) in a full potency test (PD_{50} test) according to the OIE Manual and European Pharmacopeia. It was a collaboration set up between The Pirbright Institute, Wageningen Bioveterinary Research (WBVR; formerly Central Veterinary Institute), Lelystad, in the Netherlands and the Australian Animal Health Laboratory (AAHL), to share costs and results and to advise their respective vaccine banks.

The potency test concurred with the results of the pilot study and with this heterologous challenge with A/IRN22/2015, the PD_{50} was approximately 6.47. The results showed that a high payload A MAY 97 vaccine with homologous PD_{50} >6 would be a suitable vaccine candidate against G-VII lineage viruses.

Brazil

Virus Strain	EPP "O" VN	R1
O/Arauca/Col/17	76.02	0.21
O1 Campos Br/58	97.98	

Botswana

Name of Field isolate	Name of Vaccine strain	2dmVNT
BOT03/17	SAT251	0.3

China

Field strain	strain	Vaccine strain O/MYA98/BY/2010	Methods used
16012	O/CATHAY	M	VNT
16058	O/Mya-98	M	VNT
17004	O/Mya-98	M	VNT
17016	O/Mya-98	N	VNT
Mya-98(2015)	O/Mya-98	M	VNT
17056	O/Mya-98	M	VNT
17006	O/Ind-2001	M	VNT and animal test

Ethiopia

No vaccine matching completed at NAHDIC. 8 samples were tested by vaccine matching at WRLFMD

India

- 2d-MNT
  - Tested against serotype O vaccine strain IND R2/1975
  - 46 samples (42 (91%) show homology)

Kenya

Name of Field Isolate	Vaccine strain O K77/78
K27/17	0.01
K34/17	0.25
K40/17	0.13
K42/17	0.03

Republic of Korea

VNT	Type O Vaccine strains			
	O1 Manisa	O 3039	O Campos	O primorsky
O/SKR/2017	0.80	0.21	0.49	0.62
	>1.0	0.41	0.32	0.45
	>1.0	0.40	0.50	0.41

VNT	Type A Vaccine strains				
	A22 IRQ 24/64	A IRN/2005	A/MAY/97	A/TUR/20 /2006	A24/ Cruzeiro
A/SKR/3/2017	0.69	0.46	0.14	0.01	0.19/ 0.07* 0.05*

Russia

FMDV isolate	Vaccine strain (r_1)				
	A Iran/97	A/Krasnodar/RUS/2013 (A Iran/05 SIS 10)	A/Zabaikalsky/2013 (A/Asia/SEA-97)	A22 Iraq/64	A /ARRIAH/2016 (A GVII)
A/Armenia/2016 (A GVII)	N	N	N	N	M

FMDV isolate	Vaccine strain (r_1)			
	O Manissa	O/Primorsky/ RUS/2012 (ME-SA Pan Asia)	O/SA/08 (O ME-SA PanAsia 2)	O/Primorsky/ RUS/2014 (O SEA Mya-98)
O/Zabaikalsky/2016 (O ME-SA Ind 2001)	M	M	M	M

Thailand

Country	**n**	**O/189/87 Thai vaccine strain**		
		0 - 0.19	2.0 - 0.39	0.40 - 1.0
Thailand	6*	-	-	6
Myanmar	6*	-	-	6

* all Ind2001d strains (r-value > 0.4, close related to O189/87 Thai vaccine strain)

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	13	6	3	4	0	4	9

Turkey

	Vaccine strain		
	O1 Manisa	OTUR07	OTUR14
O QOM-(2015 isolate)	N	M	N
O QOM-(2016 isolate)	N	M	N
O QOM-(2017 isolate)	N	M	N

	Vaccine strain	
	GVII	ATUR16 /GVII
A05 (2006 isolate)	N	N
A05 (SIS10 / 2011 isolate)	N	N
A05 (SIS10 / 2015 isolate)	N	N
GVII (BAN-12 / 2016 isolate)	M	M
GVII (BAN-12 / 2017 isolate)	M	M
GVII (SAM16 / 2016-2017 isolate)	M (Partially)	M

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

United Kingdom

Note:

N	No Match ($r_1 \leq 0.28$)
B	Borderline (r_1 is between 0.28 and 0.32)
M	Match ($r_1 \geq 0.32$)

Sample	Serotype	Topotype	Strain	O 3039	O 5911	O1 Manisa	O/TUR/5/2009	O Campos	O Campos 03	O Campos 04	O SKR
HKN/1/2017	O	CATHAY	-	N		N	N				
HKN/3/2017	O	CATHAY	-	N		N	N				
EGY/10/2017	O	EA-3	-	M		M	M				
EGY/26/2017	O	EA-3	-	M		B	M				
ETH/2/2017	O	EA-3	-	N		N	M				
ISR/1/2017	O	EA-3	-	B		N	M				
PAT 05/2017	O	EA-3	-	N		M	M				
ETH/11/2016	O	EA-4	-	N		N	M				
ETH/30/2016	O	EA-4	-	M		M	M				
ETH/50/2016	O	EA-4	-	B		M	M				
MYA/01/2017	O	ME-SA	Ind-2001	N		N	N				
MYA/05/2017	O	ME-SA	Ind-2001	B		B	M				
NEP/03/2017	O	ME-SA	Ind-2001	M		M	M				
NEP/1/2017	O	ME-SA	Ind-2001	N		N	M				
NEP/24/2017	O	ME-SA	Ind-2001	M		M	M				
NEP/35/2016	O	ME-SA	Ind-2001	M		N	M				
SKR/01/2017	O	ME-SA	Ind-2001	M	M	M	M	M	N	N	M
SKR/02/2017	O	ME-SA	Ind-2001	M	M	M	M	M	N	N	M
SRL/3/2017	O	ME-SA	Ind-2001	M		M	M				
SRL/7/2016	O	ME-SA	Ind-2001	M		M	M				
CAM/01/2016	O	ME-SA	PanAsia	B		N	M				
CAM/03/2016	O	ME-SA	PanAsia	N		N	M				
MOG/10/2017	O	ME-SA	PanAsia	N		N	M				
AFG/23/2017	O	ME-SA	PanAsia-2	M		M	M				
AFG/34/2017	O	ME-SA	PanAsia-2	M		M	M				
IRN/08/2017	O	ME-SA	PanAsia-2	M		B	M				
IRN/12/2017	O	ME-SA	PanAsia-2	M		N	M				
PAK/10/2016	O	ME-SA	PanAsia-2	N		N	N				
PAK/14/2017	O	ME-SA	PanAsia-2	M		B	M				
PAK/4/2017	O	ME-SA	PanAsia-2	N		N	N				

Sample	Serotype	Topotype	Strain	O 3039	O 5911	O1 Manisa	O/TUR/5/2009	O Campos	O Campos 03	O Campos 04	O SKR
SAU/27/2016	O	ME-SA	PanAsia-2	M		M	M				
LAO/02/2017	O	SEA	Mya-98	N		N	M				
TAI/01/2017	O	SEA	Mya-98	N		B	M				
TAI/40/2016	O	SEA	Mya-98	B		N	M				
GHA/1/2016	O	WA	-	N		N	B				

Sample	Serotype	Topotype	Strain	A22/IRQ	A/IRN/05	A/TUR/20/06	A/ERI/3/98	A/MAY/97	A24/Cruzeiro	VNT A Tur11 bvs tube2n	VNT A Tur14 bvs tube29
ALG/2/2017	A	AFRICA	G-IV	B	N	N	M				
ALG/3/2017	A	AFRICA	G-IV	B	N	N	B		N		
EGY/19/2016	A	AFRICA	G-IV	N	N	N	N				
IRN/4/2017	A	ASIA	G-VII	N	N	N				N	N
NEP/13/2017	A	ASIA	G-VII	N	N	N		N			
AFG/11/2017	A	ASIA	Iran-05	N	N	N					
AFG/25/2017	A	ASIA	Iran-05	B	N	N					
AFG/34/2011	A	ASIA	Iran-05	N	N	M		n/a			
IRN/2/2017	A	ASIA	Iran-05	M	N	B				M	N
IRN/7/2017	A	ASIA	Iran-05	M	N	M				N	B
PAK/12/2017	A	ASIA	Iran-05	M	M	N					
CAM/04/2016	A	ASIA	Sea-97	M	N	N					
CAM/05/2016	A	ASIA	Sea-97	M	N	N					
MOG/1/2016	A	ASIA	Sea-97	M	M	N					
MOG/2/2016	A	ASIA	Sea-97	M	M	N					

Sample	Serotype	Topotype	Strain	Asia 1 Shamir
AFG 22/2017	Asia 1	ASIA	Sindh-08	M

PAK 6/2017	Asia 1	ASIA	Sindh-08	N
PAK 17/2017	Asia 1	ASIA	Sindh-08	M

Sample	Serotype	Topotype	Strain	SAT 1/RHO/12/78
MAL 1/2016	SAT 1	I	-	N

Sample	Serotype	Topotype	Strain	SAT 2 Eritrea	SAT 2 ZIM/7/83
ZIM 1/2017	SAT 2	II	-	M	M
BOT 1/2017	SAT 2	III	-	M	M

Sample	Serotype	Topotype	Strain	SAT3 Zim
ZAM 1/2017	SAT 3	II	-	N

USA

- Calibrating VNT SOP using sera from vaccinated bovines of Serotype A

Appendix 3 - Nucleotide sequence analysis

FMDV nucleotide sequence data for phylogenetic analysis (740 sequences)

* Sequencing done by WRLFMD

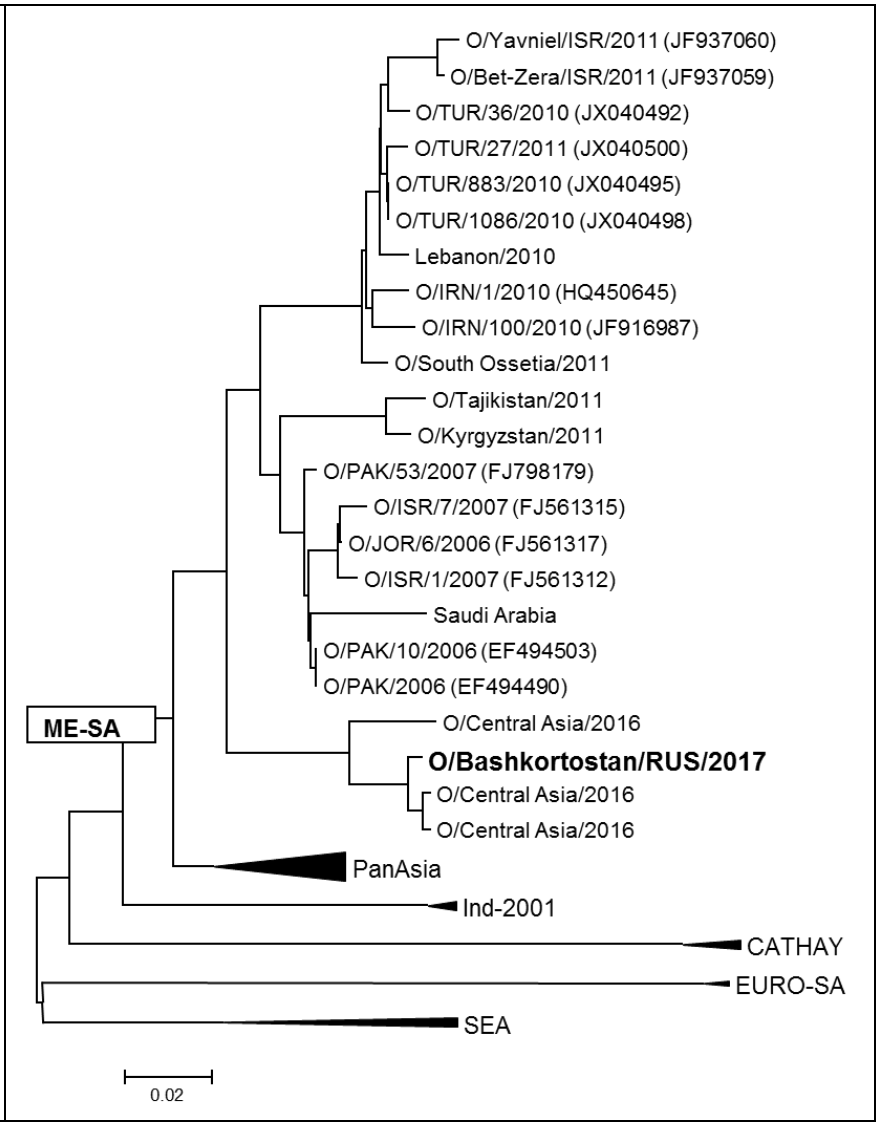
† US samples belong to the historical FADDL repository

Laboratory	Samples from	Region	Total	O	A	C	ASIA-1	SAT 1	SAT 2	SAT 3
ANSES	Guinea Bissau	VP1	1	1						
BVI	Zimbabwe	VP1	8					6	2	
	Zambia	VP1	9					4		5
	Namibia	VP1	9						9	
	Uganda	VP1	4	2					2	
	Botswana	VP1	5						5	
FADDL	USA†	Complete genome	57	8	15	11	13	5	3	3
	Uganda	Complete genome	8	5				2	1	
FGBI ARRIAH	Russia	VP1	5	5						
	Russia	Complete genome	1	1						
	Mongolia	VP1	12	12						
ICAR	India	capsid	44	44						
	India	Complete genome	15	15						
IZSLER	Algeria	VP1	6		6					
	Algeria	Complete genome	3		3					
LVRI	China	VP1	46	37	9					
	Republic of Korea	VP1	2	1	1					
NAHDIC	Ethiopia		27*	17*						
OVI	South Africa	VP1	2					1	1	
	South Africa	Complete genome	6					3	3	
	Mozambique	VP1	3					1		2
QIA	Republic of Korea	VP1	9	8	1					
		capsid	9	8	1					
		Complete genome	9	8	1					
RRLSEA	Thailand	VP1	30	17	13					
	PDR Lao	VP1	2	2						
	Myanmar	VP1	18	17			1			
ŞAP Institute	Turkey	VP1	129	23	106					
	Iran	VP1	7		5		2			
WRLFMD	Afghanistan	VP1	16	5	9		2			

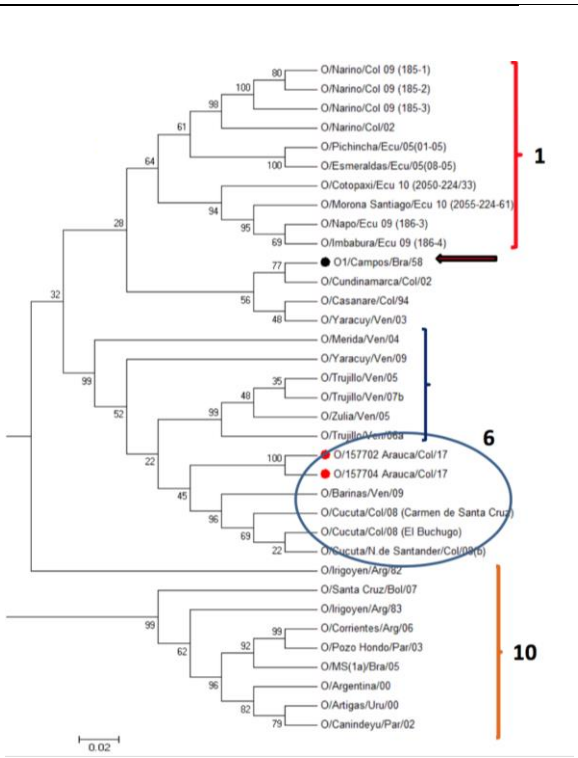
Laboratory	Samples from	Region	Total	O	A	C	ASIA-1	SAT 1	SAT 2	SAT 3
	Algeria	VP1	3		3					
	Bhutan	VP1	16	15	1					
	Botswana	VP1	1						1	
	Cambodia	VP1	6	3	3					
	Egypt	VP1	22	21	1					
	Ethiopia	VP1	31	31						
	Ghana	VP1	1	1						
	Hong Kong, SAR of PRC	VP1	3	3						
	Iran	VP1	18	9	9					
	Israel	VP1	8	8						
	Kenya	VP1	4	3				1		
	Republic of Korea	VP1	3	2	1					
	Laos	VP1	2	2						
	Malawi	VP1	1					1		
	Mongolia	VP1	10	8	2					
	Myanmar	VP1	4	3			1			
	Nepal	VP1	29	26	3					
	Pakistan	VP1	44	14	9		21			
	Palestinian Autonomous Territories	VP1	8	8						
	Saudi Arabia	VP1	8	1	7					
	Sri Lanka	VP1	11	11						
	Thailand	VP1	28	18	10					
	Uganda	VP1	1	1						
	Zambia	VP1	1							1
	Zimbabwe	VP1	1						1	

Appendix 4 - Selected Phylogenetic trees for 2017

Phylogenetic tree from FGBI ARRIAH, Vladimir, Russia:

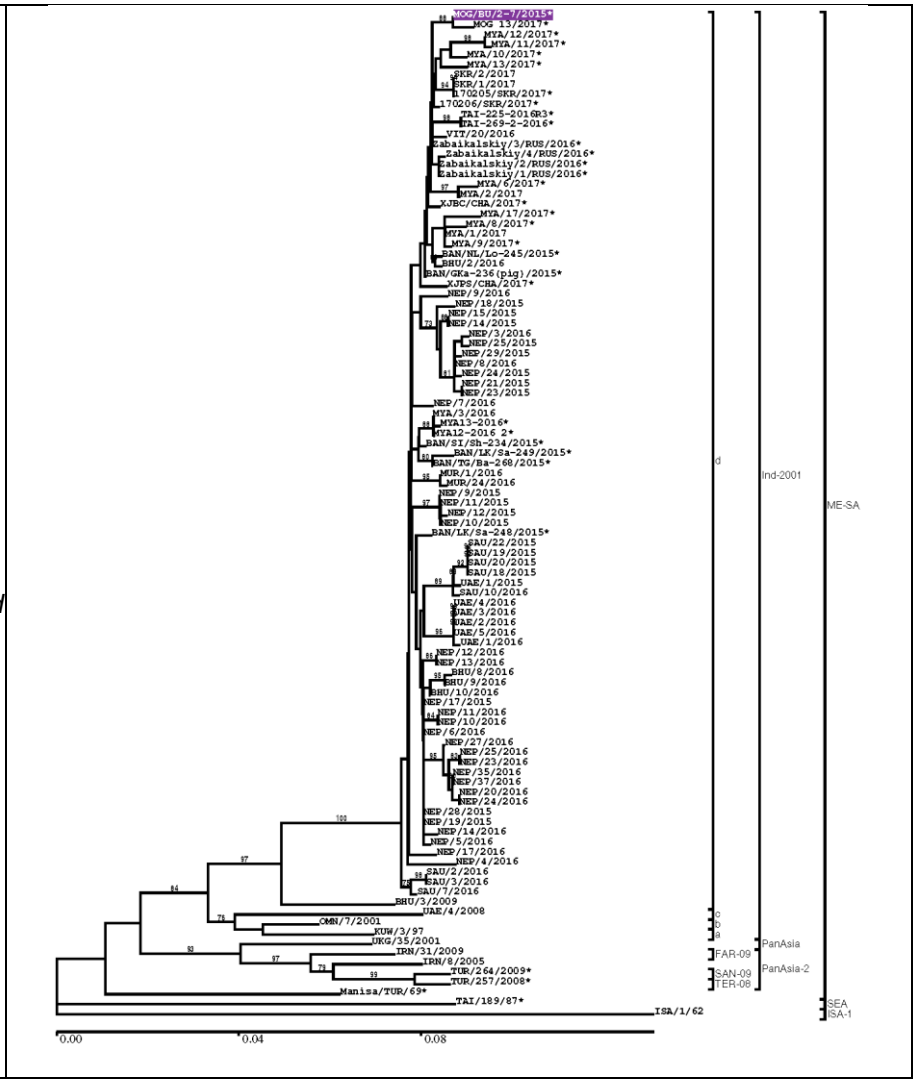
FMDV type O in Russia, 2017	

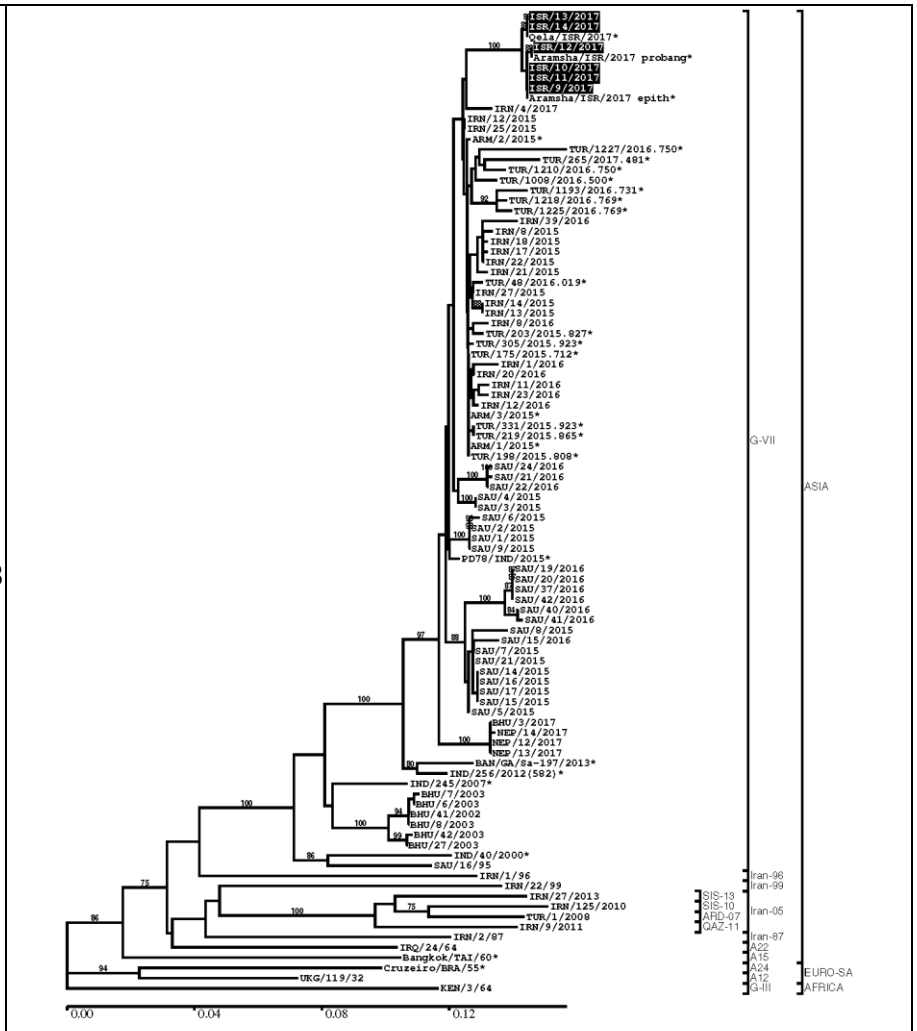
Phylogenetic tree from PANAFTOSA, Brazil:

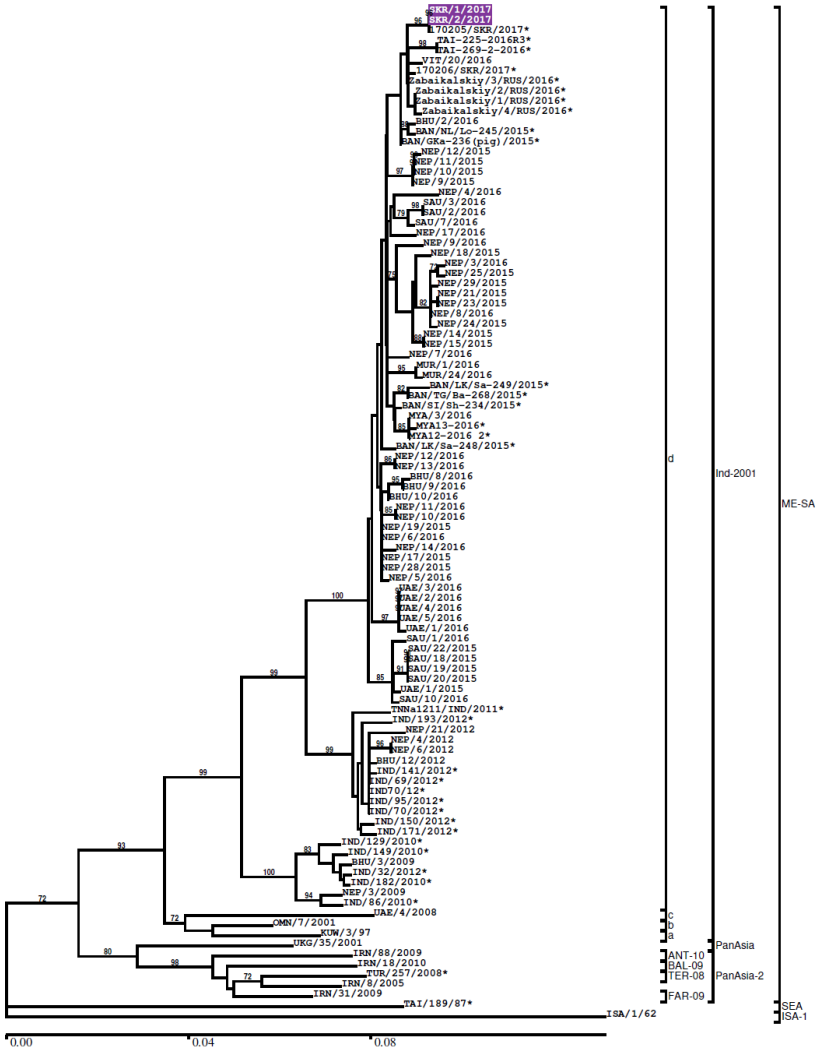
FMDV type O in Colombia, 2017	

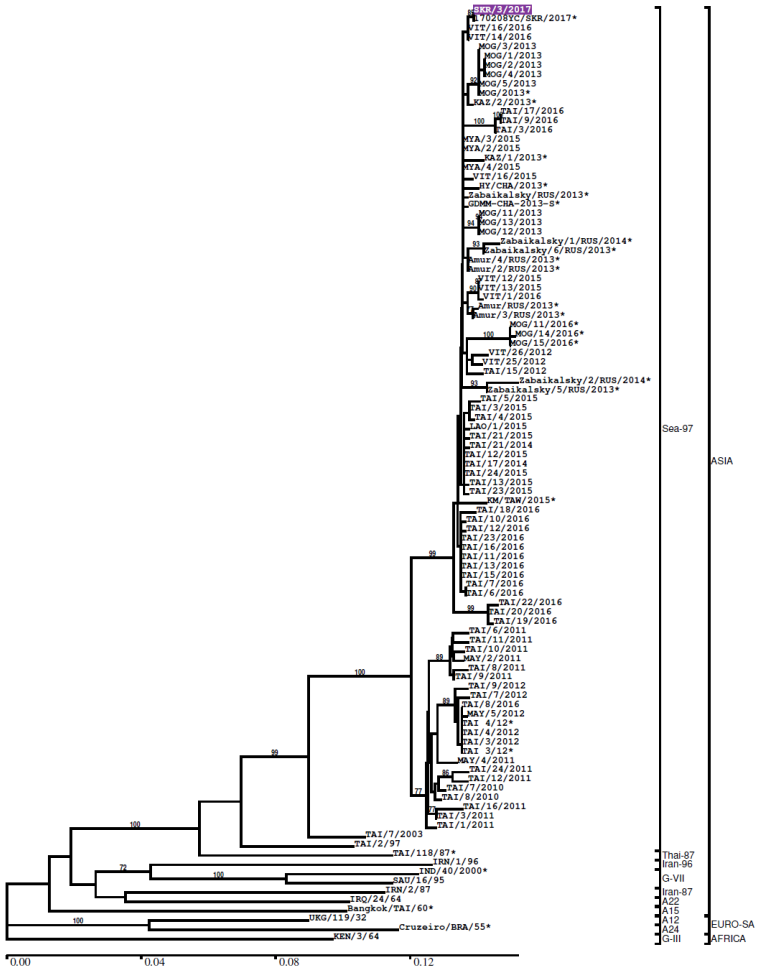
Phylogenetic trees from WRLFMD, The Pirbright Institute, UK:

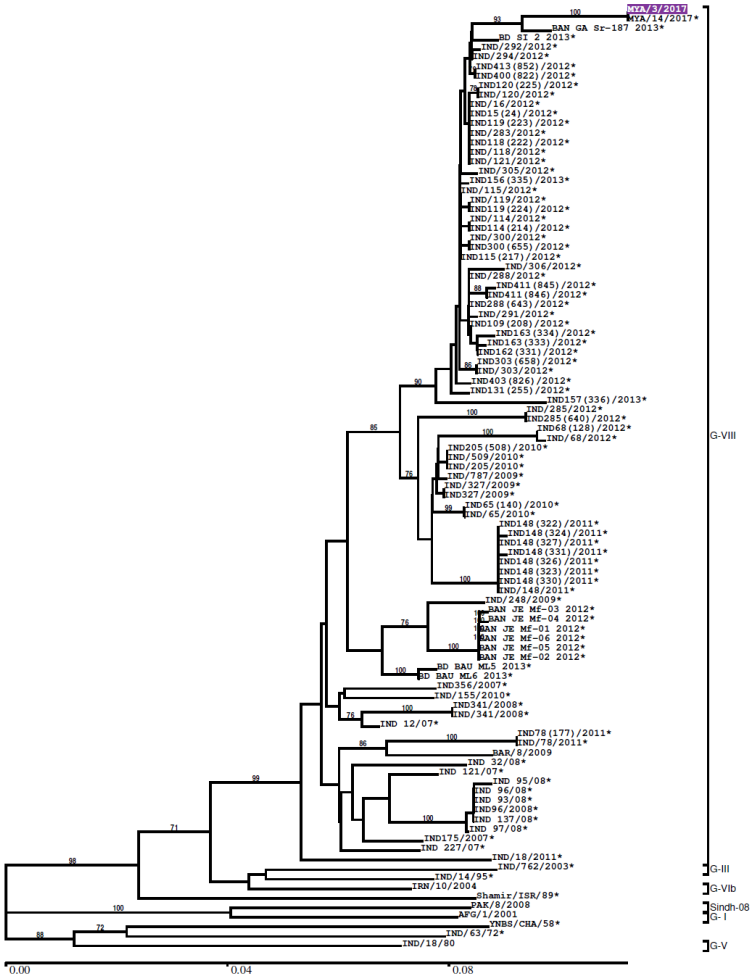
Detailed sequencing reports can be found at :
http://www.wrlfmd.org/fmd_genotyping/index.html

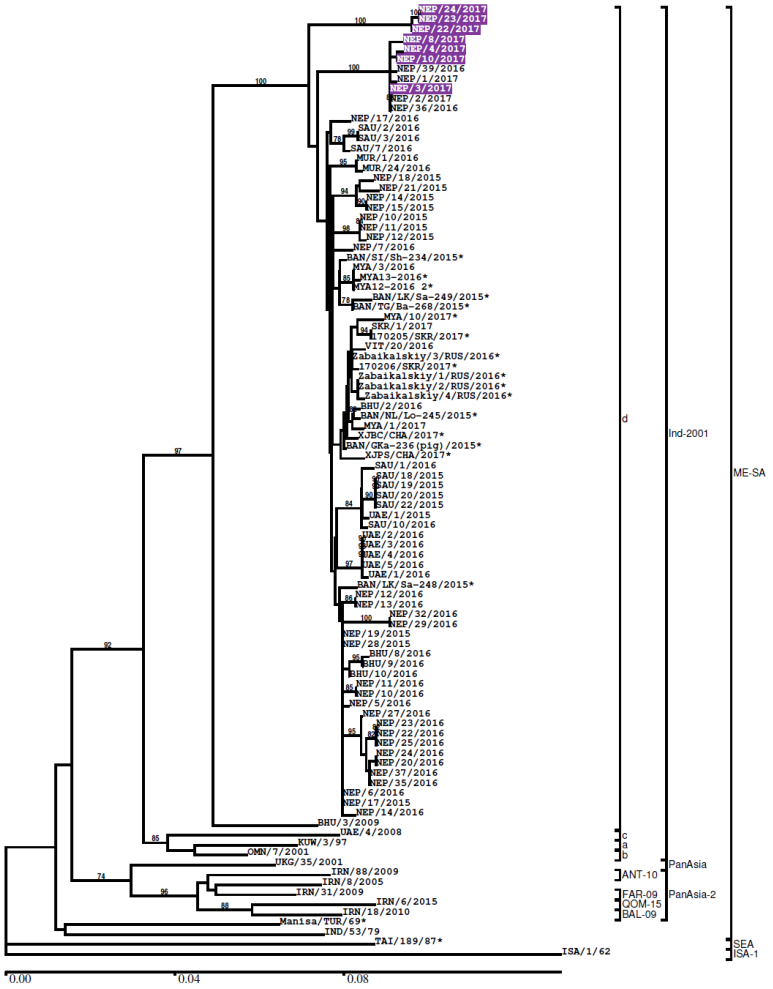
Mongolia O/ME-SA/Ind2001d *WRLMEG/2017/00052 (sequence retrieved from GenBank submitted by NIAH/NARO, Japan)*	

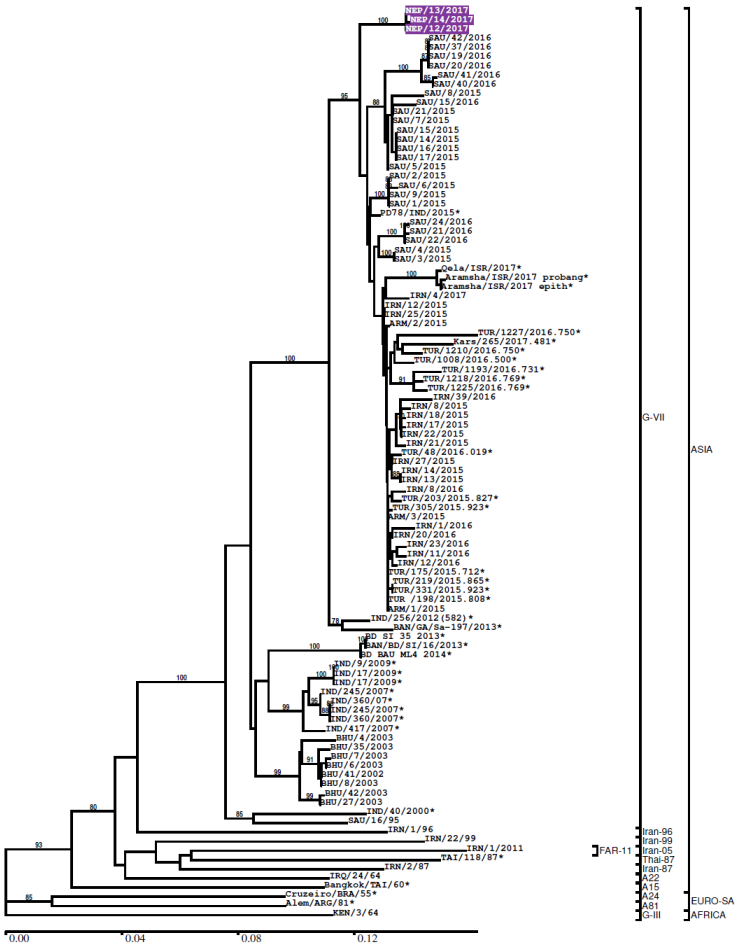
Israel A/G-VII WRLFMD/2018/00003	

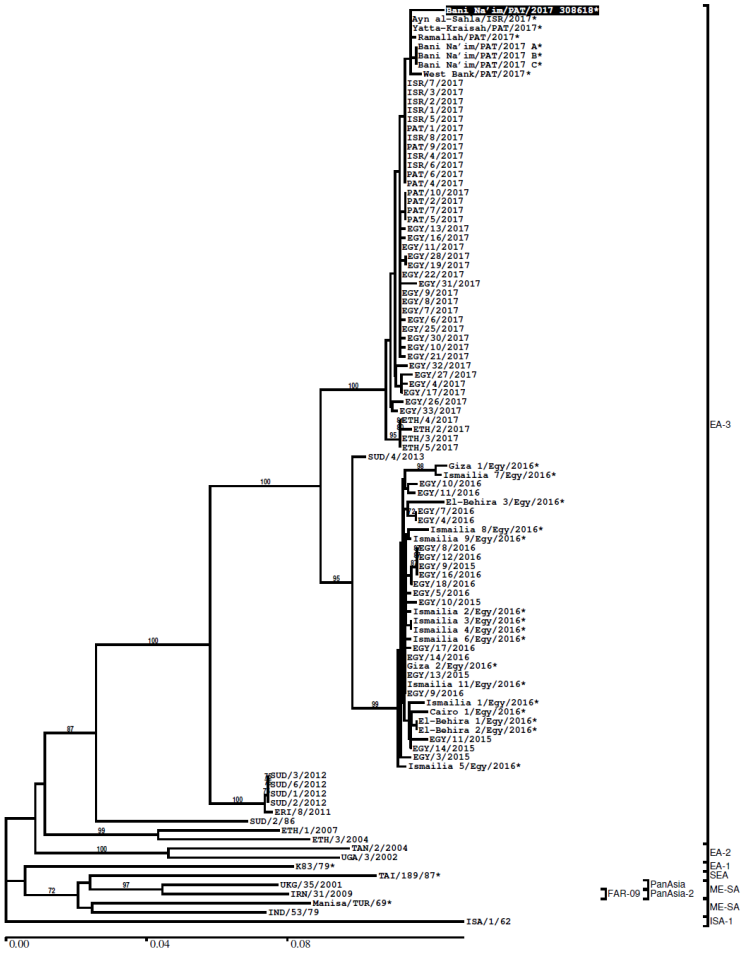
Republic of Korea O/ME-SA/Ind-2001d WRLFMD/2017/00001	**Report on FMDV O in South Korea, Republic of in 2017** **Batch: WRLFMD/2017/00001** 

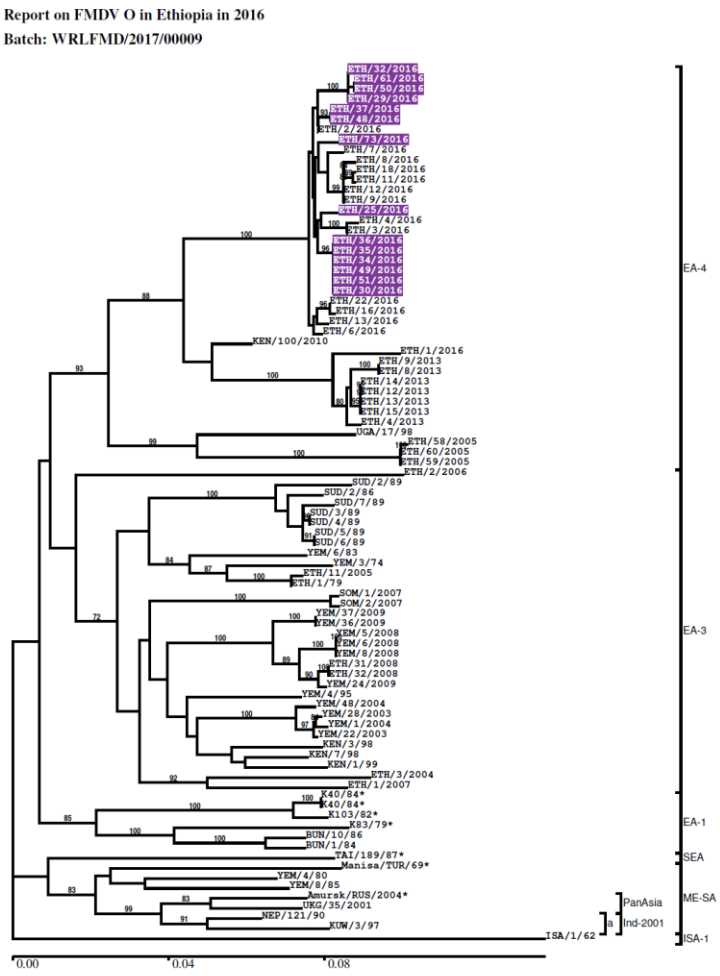
A/ ASIA/Sea-97	**Report on FMDV A in South Korea, Republic of in 2017** **Batch: WRLFMD/2017/00001** 

Myanmar Asia-1/ASIA *WRLMEG/2017/00056 (sequence supplied by RRL-SEA*	**Report on FMDV Asia1 in Myanmar in 2017** **Batch: WRLFMD/2017/00012** 

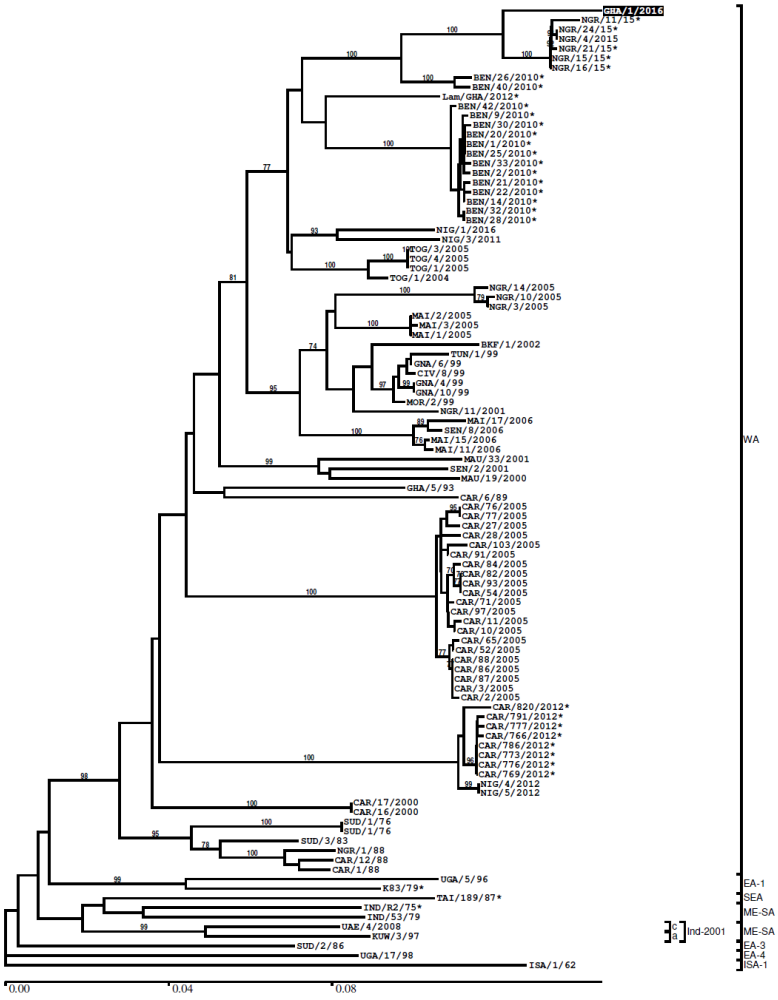
Nepal WRLFMD/2017/00016 O/ME-SA/Ind-2001d	**Report on FMDV O in Nepal in 2017** **Batch: WRLFMD/2017/00016** 

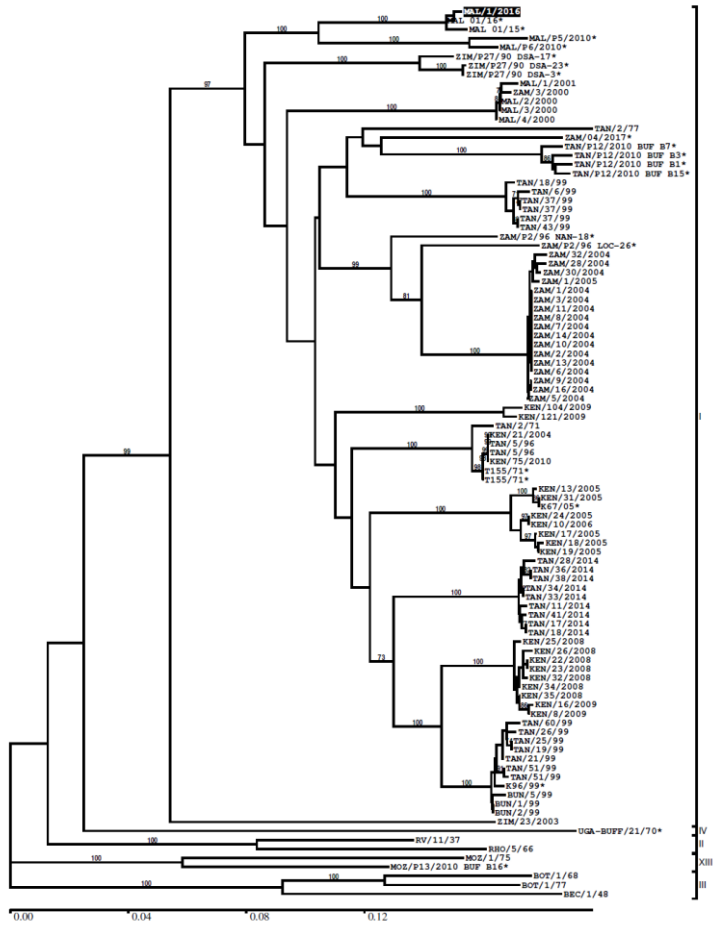
A/ASIA/G-VII	**Report on FMDV A in Nepal in 2017** **Batch: WRLFMD/2017/00016** 

Palestinian Autonomous Territories and Israel O/EA-3 WRLMEG/2017/00062 *also contains sequences from:* *WRLFMD/2017/00004 (Israel)* *WRLFMD/2017/00005 (Palestine)*	**Report on FMDV O in Palestinian AT in 2017** **Batch: WRLMEG/2017/00062** 

Ethiopia O/EA-4 WRLFMD/2017/00009	

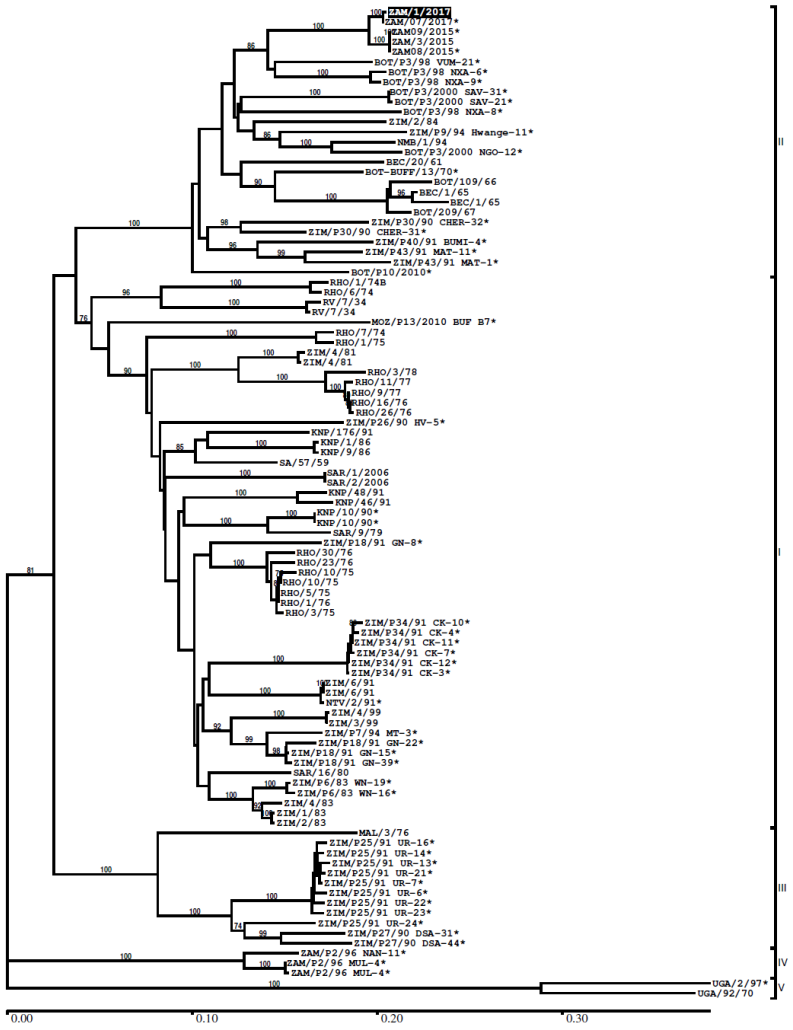
Algeria A/AFRICA/G-IV WRLFMD/2017/00006	**Report on FMDV A in Algeria in 2017** **Batch: WRLFMD/2017/00006** 

Ghana O/WA WRLFMD/2017/00024	**Report on FMDV O in Ghana in 2016** **Batch: WRLFMD/2017/00024** 

Malawi SAT 1 WRLFMD/2017/00025	**Report on FMDV SAT1 in Malawi in 2016** **Batch: WRLFMD/2017/00025** 

Botswana SAT 2/III WRLFMD/2017/00023	**Report on FMDV SAT2 in Botswana in 2017** **Batch: WRLFMD/2017/00023** 

Zimbabwe SAT 2/II WRLFMD/2017/00029	**Report on FMDV SAT2 in Zimbabwe in 2017** **Batch: WRLFMD/2017/00029** 

Zambia SAT 3/II WRLFMD/2017/00028	**Report on FMDV SAT3 in Zambia in 2017** **Batch: WRLFMD/2017/00028** 

Appendix 5 - The 12th Annual Meeting of the OIE/FAO FMD Reference Laboratories Network
Hosted by: ARC-Onderstepoort Veterinary Institute, Pretoria, South Africa
29th – 30thNovember 2017

Day 1

Global Overview: Dr Don King, WRLFMD

Presentation previewed the significant epidemiological events that have occurred during 2017covering points that were discussed in more detail in the individual presentations from the delegates:

- Spread of O/ME-SA/Ind-2001d – particularly in a number of East Asian countries
- The first field cases due to serotype Asia 1 in Southeast Asia (Myanmar) in ~ 10 years
- Emergence of a new genetic lineage of serotype O/ME-SA in Russia
- Evidence of FMD viruses of African origin (O/EA-3) and SAT 2 moving into the near East
- Further spread of the A/ASIA/G-VII lineage into northern Israel
- Outbreaks in North Africa (Algeria and Tunisia) due to A/AFRICA/G-IV most closely related to viruses from West Africa
- Clinical FMD cases in Colombia due to serotype O

Pool 1 Southeast Asia: Dr Wilai Linchonsubongkoch, RRLSEA

Samples (n=112) have been received recently from Thailand (representing O/SEA/Mya-98, O/ME-SA/Ind-2001d lineages), Lao PDR (O/SEA/Mya-98) and Myanmar (O/SEA/Mya-98, O/ME-SA/Ind-2001d, and Asia 1/G-VIII). Serum samples were also received from Thailand for NSP serology (n=16,832) and LP ELISA (n=3601). The most significant epidemiological event in 2017, was the Asia 1 outbreak in Myanmar, which was investigated by OIE SRR Bangkok. The outbreak started on 15thJanuary and was resolved by 6th of February - where 59 out of 1559 cattle demonstrated clinical signs in the affected villages. Laboratory analyses were hindered by the inability to recover live FMDV from clinical samples, but VP1 sequence data was obtained; characterising the virus as belonging to the G-VIII clade of serotype Asia 1 (most closely related to FMDVs of South Asia origin). Past outbreaks in Myanmar in 2005 were due to the Asia 1/G-IV lineage, so this is a new incursion into the SEA region.

Pool 1 East Asia and China: Dr Jijun He, LVRI

During 2017, clinical samples representing 19 serotype O and 8 serotype A samples were received to LVRI from 10 FMD outbreaks in China (8 serotype O and 2 serotype A). Sequence data for these cases,

indicates that the O/ME-SA/Ind-2001d lineage has now entered China and has been found in the extreme west of the country. During this period, the A/ASIA/Sea-97 lineage has also been detected (in cattle and pigs), while sequence evidence indicates that two genetic groups within O/SEA/Mya-98 lineage affecting either cattle (2016-17) or pigs (2012-17) are present. At the same time, the Chinese national surveillance program has continued to monitor Northeast and the border region of Southeast China; where probang and lymph node samples (n=2475) were collected. Of these samples, 18 have yielded positive results (14 and 4 from the O/SEA/Mya-98 and O/CATHAY lineages, respectively). Vaccine matching and immunogenicity studies for O/MYA98/BY/2010 have been performed showing good match against all representative local strains including those from the O/ME-SA/Ind-2001d lineage.

Pool 1 Korea and East Asia: Dr Jong-hyeon Park, APQA

During February 2017, simultaneous FMD outbreaks due to serotypes O (O/ME-SA/Ind-2001d) and A (A/ASIA/Sea-97) occurred in South Korea. These cases represent at least two new incursions of FMDV into the country, although the precise source in East or Southeast Asia has not been identified. In addition to clinical cases, pro-active surveillance (using NSP serology [n=257,857] with support from RT-PCR [n=1604]) has been undertaken which has not revealed any evidence for undisclosed circulation of FMDV on any farms. SP (serotype O) serology (n=328,914) has also been widely used to assess population immunity in vaccinated animals where levels of 97.0%, 92.1% and 76.3% have been detected in cattle, breeding pigs and fattening pigs, respectively. National vaccination campaign now recommends either O1 Manisa+O-3039 or O-Campos or O-Primorsky for pigs and O1 Manisa+O-3039+A22 for cattle.

Pools 1 and 3: Russia: Dr Alexey Mischenko, FGBI-ARRIAH

Serotype O has been detected in both Russia and Mongolia in 2017. The cases in Russia (O/Bashkortostan/RUS/2017), do not belong to the O/ME-SA/PanAsia-2 lineage and are most closely related to FMD viruses detected in a central Asian country in 2016. The serotype O viruses from Mongolia have been characterised as belonging to the O/ME-SA/Ind-2001d and O/ME-SA/PanAsia lineages (closely related to viruses isolated in China in 2011). O/ME-SA/Ind-2001 appears to be covered by the Russian vaccines; and for A/ASIA/G-VII a new vaccine virus has been produced (A/ARRIAH/2016). Only local produced vaccine is being used in Russia.

Discussion – What is preventing certain countries from reporting FMDV? It appears that a reluctance to report is associated with a fear that countries will lose lucrative commercial markets. In response to these problems, ARRIAH has tried to initiate a program in 2014 which aimed to provide vaccine, training and funding to the countries that reported FMD; however, the project didn't proceed.

Pool 2 India: Dr Don King on behalf of colleagues at ICAR, PD-FMD

Serotype O (from the O/ME-SA/Ind-2001 lineage) has been the only detected FMDV serotype in 2016-2017 from the 523 samples submitted for laboratory investigation. Sequence data indicates that there is now a second cluster of viruses within the O/ME-SA/Ind-2001 lineage circulating in India (tentatively named O/ME-SA/Ind-2001e with a nucleotide divergence of 7.4% from the Ind-2001d lineage). No dramatic spread of FMD was recorded during the past twelve months and most outbreaks are relatively mild in nature only involving a few animals. Vaccine-matching performed using the O/IND R2/1975 strain shows 91% antigenic homology (for 42 isolates).

Pool 3 Turkey and the West Eurasia Laboratory Network (WELNET FMD): Dr A. Naci Bulut, Şap Institute, Ankara, Turkey

Sequence data indicates that the FMDV lineages currently present in Turkey are O/ME-SA/PanAsia-2^{Qom-15}, A/ASIA/G-VII (including a sub-lineage called A/ASIA/G-VII^{SAM-16}), while serotype Asia 1 has not been recorded since 2015.Retrospective analyses (back to 2006) shows that successive waves of FMDV representing different serotypes affect the country in a cyclical manner. Samples (n=22,906) have also been tested for FMDV-specific antibodies to assess vaccine performance and disease-free status of certain regions in the country. Additional samples (n=5) from Iran (A/ASIA/Iran-05$^{FAR-05\ and\ FAR-09}$ and serotype Asia 1) have also been characterised. The presentation also reviewed challenges for FMD control in the region and sustainability of WELNET FMD.

Discussion: The new A/ASIA/G-VII vaccine does not appear to protect against the A/ASIA/Iran-05 lineage, which is currently circulating in Iran; therefore A/Iran-05 vaccine strain will be included in the 2018 vaccination strategy. ARRIAH and Merial/BI recommends that both A/Iran-05 vaccine and A/ASIA/G-VII vaccine be included.

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

During 2017, there have been reports of FMD outbreaks due to serotype O (EA-2), A (AFRICA/G-1), SAT 1 (NWZ) and SAT 2 (IV) in Kenya. Most samples were serotype SAT 1 (n=17) and serotype O (n=25). A collaboration with Plum Island (USA) is sequencing FMDVs recovered from cases in both buffalo and cattle, and is also undertaking NSP serology in these two species. The quadravalent vaccine from KEVEVAPI is recommended for use in the country.

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

During 2017, NAHDIC has received 112 samples for virological testing purposes. The serotypes detected were O (n = 70), A (n = 10) and SAT 1 (n = 4). This is a change from previous years where most outbreaks were caused by serotype SAT 2. The Western and Central parts of the country appear to have different circulating strains for serotype O (EA-3 and EA-4. NSP serology indicates 11.6% of small ruminants and 31.7% of cattle have FMDV-specific antibodies. Testing has also been performed for export certification purposes (687 sera from small ruminants and 2163 sera from cattle were positive).

Discussion: relating to NSP test results in Ethiopia, if an animal is positive for NSP they cannot be exported out of the region.

Pool 5: Nigeria and West Africa: Dr Hussaini Ularamu, NVRI

Serotypes O (O/EA-3 and O/WA), A (A/AFRICA/G-IV), SAT 1 (X) and SAT 2 (VII) are circulating in Nigeria. The current strategy is to target clinical samples (n=70 from 2017) rather than serological samples since the country is endemic. Recent data generated with the antigen ELISA (from IZSLER), shows that SAT 1 viruses (topotype X) circulating in Nigeria could only be detected by the PanFMD component of the test, but not by the SAT 1 monoclonal specific part of the assay. Sequencing and additional support to NVRI has been provided as part of an OIE twinning project with CODA-CERVA.

Pool 5 Nigeria, FMDV Serology: Dr David Lefebvre, CODA-CERVA

Serological assays were carried out as part of surveillance activities in Nigeria. Samples were collected during 2009-2015 from sheep, goat and wildlife (waterbuck, wildebeest, and African eland). None of the samples reacted with serotype C, SAT 1 and SAT 3. It is unclear at this point as to why SAT 1 was

not detected by serology, since it has been isolated in the area. For sheep and goats (n=300), approximately 20% of the samples were antibody positive. For wildlife less than 50% were positive by antibodies.

Discussion: An observation was that some samples were NSP negative and SP positive. This could have occurred because the NSP levels decrease faster than the SP antibodies or there is a sensitivity problem with the test.

Update from IZSLER: Dr Santina Grazioli, IZSLER

During 2017, IZSLER has received samples from Algeria and Tunisia which were characterised as belonging to the serotype A/AFRICA/G-IV lineage, most closely related to isolates in West Africa (Nigeria, 2015 - ~98% nucleotide identity). There were problems with shipping samples due to incorrect paperwork and labelling. There appears to be a need for training in REMESA countries. Elsewhere, serological testing of 1535 Kenya samples was performed; where antibodies to serotypes A, O and SAT 2 were identified. However, the general conclusion form this work was that the antibody ELISA was not serotype specific. A post vaccination study was also carried out, which highlighted a poor or null response to the first vaccine dose using local vaccine containing serotype O, A, SAT 1 and SAT 2. The number of ELISA kits supplied has increased every year; during 2017, 2135 kits have been supplied to 34 countries.

Discussion – The updated chapter on sample dispatch in the OIE manual may help to provide guidance on how to ship FMDV samples.

ACTION 1 – WRLFMD (with help from the partners) to compile a list of dangerous good couriers that could be used for shipments in the different FMDV pools.

Pool 4 New connections in Burundi: Dr Kris de Clercq, CODA-CERVA

The presentation highlighted a new partnership that has been established in Burundi. The particular focus of the work covered investigation of a possible FMDV epidemic in March 2016 in an area where no vaccination is reported. In total 924 virological samples and a 172 serum samples were collected. Due to cross-reactivity of the serological tests, the dominant serotype was used to assess the most likely (recent) serotype present; using this approach serotype O, A, and SAT 2 were identified. Serotype SAT 2 (IV) and A (AFRICA/G-I) were subsequently isolated and sequenced.

Discussion: Saliva was taken instead of probang samples, as there was no experience of taking probang samples. Also the interest was the acute-phase excretion of FMD virus not the carrier state. The solid phase competition ELISA (in-house and commercial) and VNT were used for this work. The VNT had better specificity however some cross-reactivity was still evident. Several studies have shown that cross-reactivity happens when animals are infected with multiple serotypes. Can use a negative control of a serotype that is not present; for example using Asia 1 tests in Africa to determine cross-reactivity.

West and Central Africa: Dr Labib Bakkali Kassimi, ANSES

Sample received from an FMD outbreak in Guinea-Bissau (in 2016) were characterised as serotype O (O/WA). Samples were also collected from Chad, where the SP ELISA suggested that serotype O, A, SAT 1 and SAT 2 are present; however, in young animals serotype SAT 2 was most dominant. One sample was sequenced (partial VP1) as serotype SAT 2 (topotype VII) which was most closely related to FMD viruses from Libya and Cameroon. A multiplex (gel-based) RT-PCR assay was also evaluated in

collaboration with NVRI, Nigeria, which suggests that serotypes O, A, SAT 1 and SAT 2 circulate in 6 states in the country. Additional SAT 1 viruses will be sequenced with the view to redesigning the RT-PCR (if needed).

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

Samples have been received from South Africa (serotypes SAT 1 and SAT 2), Mozambique (serotypes SAT 1, SAT 2and SAT 3) and Uganda (serotypes O, SAT 1 and SAT 2). Additional samples from UAE and Swaziland were negative. There is no overall change in epidemiological pattern since the samples from South Africa were in the FMD Protective Zone adjacent to the KNP so the outbreak did not impact the OIE status. This presentation also briefly summarised results from FMD transmission studies in an isolated buffalo herd in KNP, South Africa. Using LPBE, the predominant serotype detected in buffalo was serotype SAT 1, followed by a few cases of serotype SAT 2. Maternal antibodies declined between 2-6months and this appears to correlate with the susceptible time for infection of young buffalo.

Pool 4-6 Sub Saharan Africa: Dr Elliot Fana, BVI

During 2017, samples (n=78) have been received from Zimbabwe (SAT 1 and SAT 2), Zambia (SAT 1, SAT 2, and SAT 3), Uganda (O and SAT 2), Namibia (SAT 2), Malawi (negative) and Botswana (SAT 2). In addition, a small number of samples from Zimbabwe, Namibia, Uganda, Malawi, Botswana and Zambia have been tested for NSP antibodies. The recent Botswana outbreak occurred in the 'free with vaccination' zone; and upon investigation it was found that the vaccination schedule had lapsed.

Discussion: Recent experience from ANSES is that negative NSP samples turned positive after storage in the fridge (+5 °C ± 3 °C) for two weeks. This observation is thought to be due to low contamination of bacteria (since the sample became negative after heat inactivation). WRLFMD has also recently observed this phenomenon for a small number of samples sent out as part of an inter-laboratory exercise (using multiple NSP ELISA test kit formats). Canada also observed that NSP negative samples can become positive on re-testing.

ACTION 2 – **ANSES and WRLFMD** to review data from samples that generated inconsistent NSP test results and report back to the Network with these findings

Pool 7 South America: Dr Rossana Allende, PANAFTOSA

FMD-free zones (with and without vaccination) cover large parts of the South American continent. Countries/regions without official OIE status are Venezuela, Surinam and the Amazon region of Brazil. In Colombia (Department of Arauca that neighbours Venezuela) a serotype O outbreak (O/EURO-SA) was identified in June 2017 and immediately after there were three more outbreaks identified in other parts of the country. In the affected herds, one to two years old animals were found that were partially or not vaccinated. The outbreak has been controlled and the vaccination campaign in Colombia has been strengthened. NSP testing is now complete to verify the area is free from active FMD infection. Elsewhere, Surinam is working with PANAFTOSA to apply for OIE recognition of FMD free status and the implementation of a FMDV regional antigen bank has been approved (by PAHO and COSALFA countries).

Pool 7: South America: Dr Andrea Pedemonte, SENASA

SENASA has not received any clinical FMD samples for testing during 2017 and there is no change in Argentina's status. Tetravalent vaccine is used in the region and these have been sold to areas outside of S. America. There are active on-going collaborative projects in Vietnam, South Korea and Paraguay.

Update from Winnipeg: Dr Charles Nfon, NCFAD

Testing has continued to monitor cases of vesicular disease (37 submissions – 789 samples) in Canada due to Senecavirus A. This emerging virus has continued to be a problem for pig industries in Canada and the USA.

Update on Australia - Emergency (high potency) serotype A and O vaccines protect against heterologous viruses: Dr Wilna Vosloo, CSIRO

This presentation reviewed collaborative work undertaken by CSIRO, Wageningen Bioveterinary Research (Lelystad) and WRLFMD to assess the in vivo performance of FMD vaccines against emerging FMDV lineages. The first example covered the A/ASIA/G-VII lineage where *in-vitro* vaccine-matching has yielded poor results. An initial study using a multivalent vaccine (from Merial/BI) containing A-SAU-95 generated a PPG protective result of only 56%. Subsequent pilot studies were carried out using A/MAY/97 (5/7 cattle were protected) and A_{22}/IRQ (2/7 cattle were protected). A full potency test has recently been performed with the A/MAY/97vaccine that showed a PD50 of 6.47. Field viruses from the O/ME-SA/Ind-2001d lineage generally have poor *in-vitro* match to O_1 Manisa and intermediate to good values against the O-3039 vaccine. Studies to evaluate emergency high potency vaccine use have recently been carried out with O_1 Manisa/O-3039 (combination) and O-3039 only. One group was challenged 7 days post vaccination and the other at 21 post vaccination vaccine. At 21 days, both groups were 100% protected; at 7 days 60% were protected when using the monovalent vaccine and 80% were protected when using the bivalent vaccine (this is not statistically significant).

Review of regional FMDV strains and changes in epidemiological patterns - breakout session




Day 2

Breakout session: short summary from each endemic pool and discussion on gaps in surveillance (information to be collated for the Annual Report)

Discussion topic 1: Mapping FMD outbreaks and risk; new ideas to display real-time epi and lab data

Collecting information via EuFMD monthly reports (GMR): Dr Maria Teresa Scicluna, EuFMD

This presentation provided an overview of work undertaken by EuFMD to collate information from Reference Laboratories (as well as OIE and FAO sources) to define patterns of risk for FMD. These data can feed into the tables (within the PRAGMATIST tool) to define which are the most important FMDV serotypes/strains that are circulating in a particular region or country. It is imagined that the PRAGMATIST tool will assist vaccine antigen managers to make decisions about what FMD vaccines are purchased and maintained within antigen banks.

Discussion covered the approaches used to assign risk scores for the circulating FMDV strains – particularly in regions/countries where sampling and testing is very sparse. EuFMD propose to establish a group of regional experts (focal points) to review and analyse the data and help fill in these gaps. Some delegates were uncomfortable with inferences being applied from neighbouring countries where data was missing, since neighbouring countries often have different livestock, practices and trade patterns. With the current extent of lab/epidemiological data available, it is difficult to precisely define these parameters (at a country level) – perhaps starting at the regional level is more sensible (using the data that is generated from the Network breakout sessions). Additional discussion covered the nature of the Global Monthly Report (GMR) and whether these outputs could be integrated into a more dynamic "Network" website that highlighting important epidemiological events (and changes), as well as known trade patterns and livestock densities to help predict likely virus movements.

Update on plans for OIE WAHIS: Dr Min Kyung Park, OIE

OIE is working on improving the maps, which are currently of a low resolution. The High Throughput Sequencing, Bioinformatics and Computation Genomics Group (HTS-BCG) meets to discuss what platform should be used (it will include all genomic data). This group will also take into consideration the Nagoya Protocol. Some of the information is in the Terrestrial manual 1.1.7; however it is an ongoing process. It was decided that FMDV would not to be part of the pilot study to evaluate this platform; bluetongue virus and rabies virus will be included.

Discussion: How will it link to GenBank? The sequence data will not be directly linked. It will be interesting to understand whether endemic sequences will be added to this type of platform or whether it is just "exotic" outbreaks.

Action 3:**Min Kyung Park** will send the report of the last HTS-BCG meeting, which identifies what information will be included in the future.

Discussion Topic 2: FMDV vaccines for Africa

FMDV strains and vaccines: overview of the challenges

Introduction: Dr Anna Ludi, WRLFMD

There are many gaps in our knowledge regarding the performance of vaccines against the FMDV lineages that are present in Africa:

- *In vivo* potency tests are rarely done, particularly those that define cross-protective responses
- Batch serological testing data supplied from manufacturers in Africa is not often reported
- Immunogenicity studies for monovalent or multivalent vaccines are rarely reported
- Reference reagents (such as validated BVS) from vaccines suppliers are not readily available to the Reference laboratory community
- Field vaccine evaluation studies are lacking

Discussion: In addition to the countries highlighted in the presentation, Senegal also produce FMDV vaccine

***In-vitro* and *in-vivo* guidelines to select and assess vaccine performance: Dr David Lefebvre, CODA-CERVA**

An overview of the OIE Terrestrial Manual of Diagnostic Tests and Vaccines was provided which highlighted the requirements for vaccines QA of the final product batch test and the requirements for making a vaccine. The manual states that the post-vaccination sera should come from the manufacturers or OIE Reference Laboratories. At the end of the chapter a method is given for testing fitness for purpose of a vaccine (*in-vivo*).

Data gaps and using data intelligently: Dr Francois Maree, ARC-OVI

For the SATs there is little data for proper vaccine matching using *in vivo* testing. This presentation overviewed serological cross-neutralisation data collected by OVI using a wide range of southern African field strains from SAT 1 and SAT 2 serotypes with representative vaccine sera as well as sera from infected cattle. Two approaches to model these data and estimate likely antigenic phenotype were presented: (i) antigenic cartography and (ii) sequence based antigenic prediction methods. Sequence data (together with serological data) has been used to highlight surface exposed amino acid residues on the FMDV capsid that confer antigenic properties.

Data gaps and using data intelligently: Dr Wilna Vosloo, CSIRO

This presentation reviewed different (yet complementary) approaches that can be used to demonstrate vaccine suitability. Points to consider are (i) do high potency vaccines for SATs protect against heterologous challenge even with poor *in vitro* match as for serotype O, A and Asia 1? – since this might reduce the number of potential vaccine strains required to cover the diversity of FMDVs found in Africa, (ii) are there alternative(i.e., less expensive) approaches that can be used to assess protective responses in target species?, and (iii) how do we determine accurate (i.e., serological) correlates of protection?

What can we learn from existing vaccine QC systems in S. America? Dr Rossana Allende, PANAFTOSA

In South America there is a well-established system to monitor the QA of FMDV vaccines and their use. This presentation reviewed the key "actors" (National Veterinary Authority (NVA), vaccine producers, farmers, stores that sell vaccine, regional political bodies, Reference laboratories and OIE) and their roles and responsibilities in this process. The quality control pathway involves the national veterinary authorities and the vaccine manufacturer. The PANAFTOSA reference centre has the responsibility to collect epidemiological data, harmonise the methods used and coordinate activities with the continental FMD eradication plan (PHEFA). As routine tests performed in the final product of each vaccine batch are innocuity (freedom of infectious virus); sterility, stability of emulsion, purity

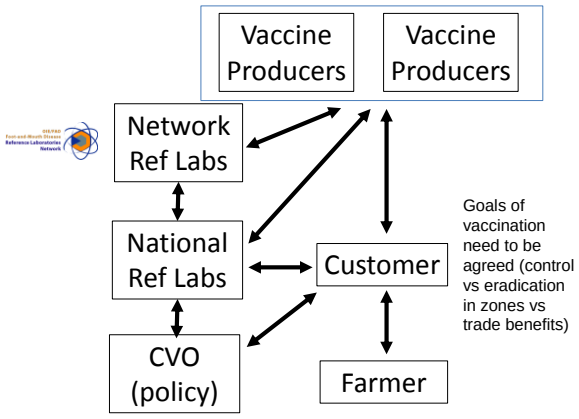
(no induction of NSP antibodies), security (no adverse reactions) and potency. A standardised EPP approach has been heavily validated as the method used to verify the potency on the final product of the vaccine batches. Additional tests of duration of immunity are required for licencing and also after licensed they are aleatory performed over time. All tests are done by the NVA. PVM studies are generally performed annually to monitor the efficiency of the vaccination programs.

FMD vaccination and post vaccination monitoring guidelines: Dr Samia Metwally, FAO

The PVM document (http://www.fao.org/3/a-i5975e.pdf) provides practical guidance on how to evaluate the effectiveness of vaccination campaigns that is tailored to the requirements of countries at different stages of the PCP. The plan is to have (a) vaccine quality centres, (b) ELISA kits for the most common commercially available vaccines and (c) training. It is anticipated that a pocket guide for field veterinarians will be produced shortly, together with training sessions (on [i] design of field studies and [ii] lab ELISA methods).

Using the Network to validate a pipeline? Future prospects: Dr Don King, WRLFMD

The "actors" and their interactions:



A table (see next page) was proposed by WRLFMD to highlight the responsibilities of each of these "actors" including the vaccine producers and role that could be undertaken by the OIE/FAO reference laboratories. It was noted that such a generic table has limitations since different regions/countries adopt different approaches with respect to vaccine potency and safety testing. This table has been circulated for comments from the Network Partners and may be subject to revisions.

Discussion to agree priorities for the Network: *It is anticipated that the vaccine producer will undertake studies to define the homologous potency of the vaccine, as well as produce data to support the safety and batch agreement of these products (black boxes). Some countries use registration dossiers to validate the vaccine batch, while in others this work is undertaken by the Reference Laboratories. Key roles for Network laboratories (highlighted in green) include: (i) continued review of regional epidemiological risks via testing of field samples and exchange of data, (ii) generation of tailored and harmonised diagnostic tools (to cover post-vaccination responses of specific vaccines), (iii) generation, collation and exchange of reference sera for vaccines (including "validated" BVS), coordination and implementation of immunogenicity studies and (iv) contribution to efforts to define correlates of protection for the vaccines. Specific activities are indicated in the footnote of the table. The OIE has expressed an interest in developing improved capacity for FMDV vaccine Quality control in Africa – via PanVac (under the auspices of the African Union). Key priority activities are highlighted in the dark red and pale red boxes including the generation and testing of reagents (including BVS) and capacity to perform immunogenicity studies in targeted populations. In addition, inocuity testing to confirm that products are fully inactivated is important and may need to be addressed.*

Activity	Vaccine Producer	National Ref labs	Customer	Farmer	OIE/FAO Network labs
Homologous potency testing	++	+/-	Performance defined by the NVA[7]		
Safety testing Inc. innocuity	++	+/-			
Batch testing Potency, 146s assessment, stability oil emulsion, purity	++	+/-			+/-
Defining regional risks (and identifying gaps)	+	++	+	+	++[1]
Providing relevant diagnostic tools	+	+			++[2]
Generation and validation of BVS	++	+			++[3]
Immunogenicity studies (in target populations)	+	++		+	++[4]
Defining correlates of protection (in different species)	++	+			++[5]
PVM: population immunity[8] (extent and degree of immunity)	+	++	+	+	+[6]
PVM: Investigation of cases of vaccine breakdown	+	++	+	++	+
PVM: measuring the impact of vaccination campaigns (disease clinical cases and infection - NSP)		++	++	+	+

Footnotes defining priorities for Network (and associated Working Groups):

[1] Via exchange of field and laboratory data and presentation via Website (and PRAGMATIST)

[2]Work to assess vaccine matching approaches in different laboratories and future development of "tailored" ELISAs to measure post-vaccination serological responses

[3] Network to prepare a list of available reagents and to highlight gaps that should be prioritised for the generation of new BVS (possibly seek funding from vaccine suppliers for this work?)

[4]Focus of Network Woking Group

[5] Focus of Network Working Group

[6] via contribution to training initiatives (led by FAO and EuFMD?)

[7] NVA: National Veterinary Authority

[8] PVM serology determined using homologous vaccine strains or representative field viruses

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