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

Annual Report 2018

Editors:

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and Dr Mark Henstock,

The Pirbright Institute, UK

Contents

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 2018 - 31st December 2018

1.3 Collated input from

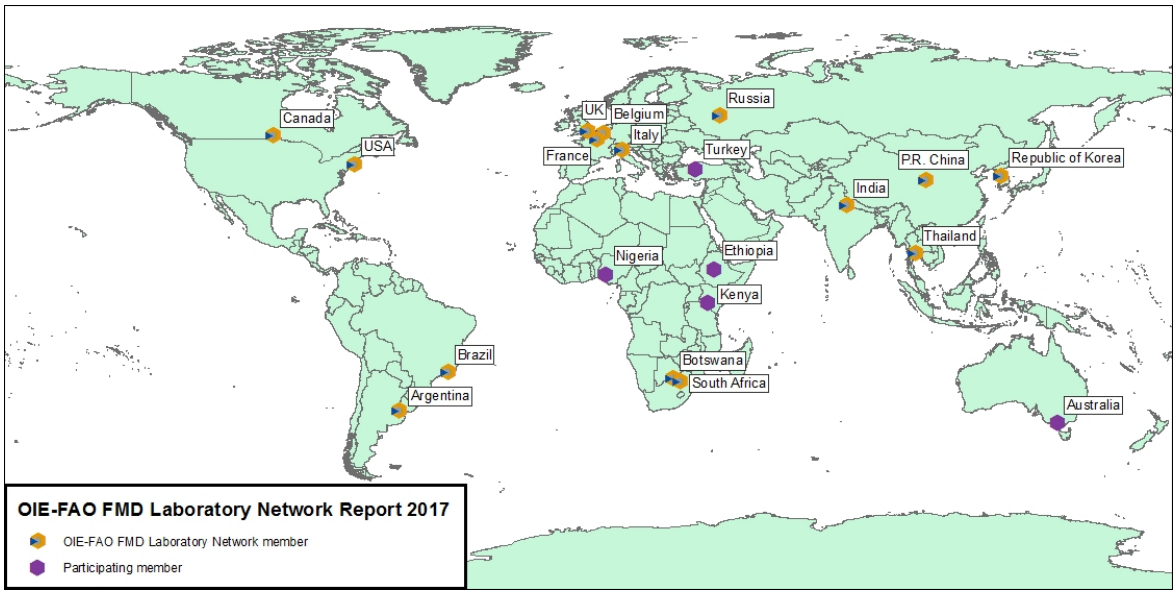


Figure 1.1: Participating laboratories

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

SENASA, Argentina

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

BVI, Gaborone, Botswana

FAO FMD Reference Laboratory

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

OIE FMD Reference Laboratory

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

OIE/FAO FMD Reference Laboratory

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

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

Sciensano, Ukkel, Belgium

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

Rio de Janeiro, Brazil

OIE and China National FMD Reference Laboratory

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

FAO Reference Centre for FMD in South Asia

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

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

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

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

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

Department of Livestock Development, Pakchong, Thailand

FAO World Reference Laboratory and OIE FMD Reference Laboratory

The Pirbright Institute Pirbright, Surrey, United Kingdom

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

Additional input kindly supplied by:

Australian Animal Health Laboratory (AAHL)

Geelong, Australia

NATIONAL Animal Health Diagnostic & Investigation Center (NAHDIC)

Sebeta, Ethiopia

Foot and Mouth Disease Laboratory

Embakasi, Kenya

National Veterinary Research Institute

Vom, Plateau State, Nigeria

ŞAP INSTITUTE (and WELNET FMD)

Ankara, Turkey

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

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

Global surveillance for FMD is necessary to identify the current hazards and to predict heightened risk so that appropriate diagnostic tools and vaccines are available for detection and control. This requires sustained effort directed towards the monitoring of FMD outbreaks and ideally also of FMDV circulation and persistence, along with collection and characterisation of FMD viruses and integration of findings with associated epidemiological intelligence. Such an extensive effort requires a coordinated approach encompassing national and international disease laboratories of the **OIE/FAO FMD Laboratory Network** along with commercial vaccine and diagnostic providers. The worldwide distribution of the different serotypes and variants of FMD virus (as compiled in 2018) 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	Western Asia with spill over into North Africa
Pool 4	Eastern Africa with spill over into North Africa
Pool 5	Western Africa
Pool 6	Southern Africa
Pool 7	South America

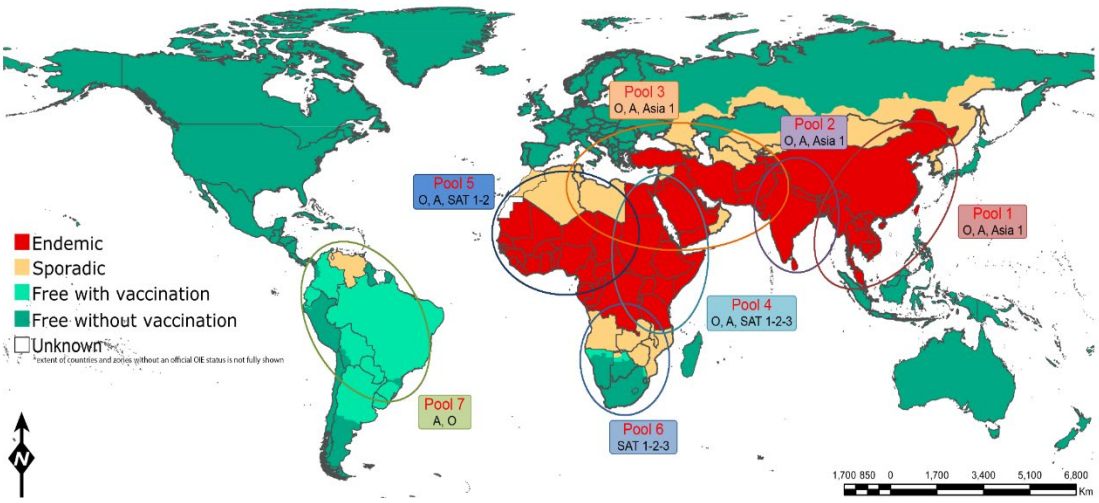


Figure 2.1: Distribution of the seven endemic pools of FMD showing conjectured status of FMD in countries during 2018. Periodically, viruses spread between pools and to free regions, and countries at the interfaces between pools (such as in North Africa and Central Asia) often experience FMD outbreaks 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).

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 2018

Headline events are highlighted in Figure 2.2. During the past year, particular attention has been focussed on the interconnected and on-going FMD situation in West Africa and North Africa. New field outbreaks due to the O/EA-3 topotype have been widely reported to the OIE in a number of West African countries, and by the end of 2018, outbreaks due to this lineage had been confirmed in Burkina Faso, the Gambia, Guinea, Senegal and Sierra Leone. The O/EA-3 topotype originates from East Africa (countries such as Sudan, Ethiopia and Eritrea) and has previously spread to Egypt in 2012 (where it has persisted), Libya in 2012 (only one report), Palestine (Gaza & the West Bank; 2017) and Israel (2017). The new outbreaks in West Africa appear to be due to FMD viruses most closely related to those introduced into the region and detected in Nigeria (during 2007 and subsequently in 2009, 2011, 2014 and 2016). In addition to what appears to be an upsurge in the FMD cases in West Africa, this viral topotype has spread during 2018 to the Maghreb (confirmed in Algeria and Mauritania, and is suspected as causing outbreaks reported in Tunisia and Morocco). In many ways, these FMD virus movements parallel the earlier introduction of the A/AFRICA/G-IV into North Africa during 2017 (see Pezzoni et al., 2019); raising obvious questions about increased trans-Saharan connectivity between countries and the precise routes by which FMD viruses are being spread (for an example see: https://en.wikipedia.org/wiki/Trans-Sahara_Highway).

This report also describes the FMD situation in other parts of the world including the continued spread of the O/ME-SA/Ind-2001 lineage which has been detected for the first time in Malaysia. This lineage has emerged from South Asian countries (Pool 2) on many occasions since 2013 from South Asian countries to cause outbreaks in the Gulf State States of the

Middle East, North Africa and Southeast/East Asia. Endemic and established FMD viruses continue also circulate with Southeast/East Asia (Pool 1), and during 2018 new cases due to A/ASIA/Sea-97 were reported in South Korea have raised the greatest concerns and have occurred over the same period that outbreaks due to serotypes O and A have been reported in China. Elsewhere, the National Veterinary Laboratory and FAO in Pakistan has collected serotype O viruses that when tested at WRLFMD appear to be antigenically distinct to previous strains found in the region (see Bachanek-Bankowska et al., 2019). These viruses show no cross-neutralisation with serotype O vaccines from two commercial suppliers (Boehringer-Ingelheim and MSD). The spread of antigenically similar viruses needs to be closely monitored in order to understand any potential impacts upon FMDV vaccination campaigns in the region.

Eastern Mediterranean countries represent an interface between two endemic pools. This region has recently experienced FMD outbreaks due to lineages acquired from East Africa (Pool 4: such as O/EA-3 reported in 2017) while during 2018, cases due to the O/ME-SA/PanAsia-2^{QOM} strain were detected in Israel (arising from Pool 3). Within Africa, the O/EA-2 topotype has also been detected in new locations in central Zambia. In South America, reports to the OIE also include new FMD outbreaks (serotype O) in Columbia (in the centre of the country and close to the border with Venezuela).

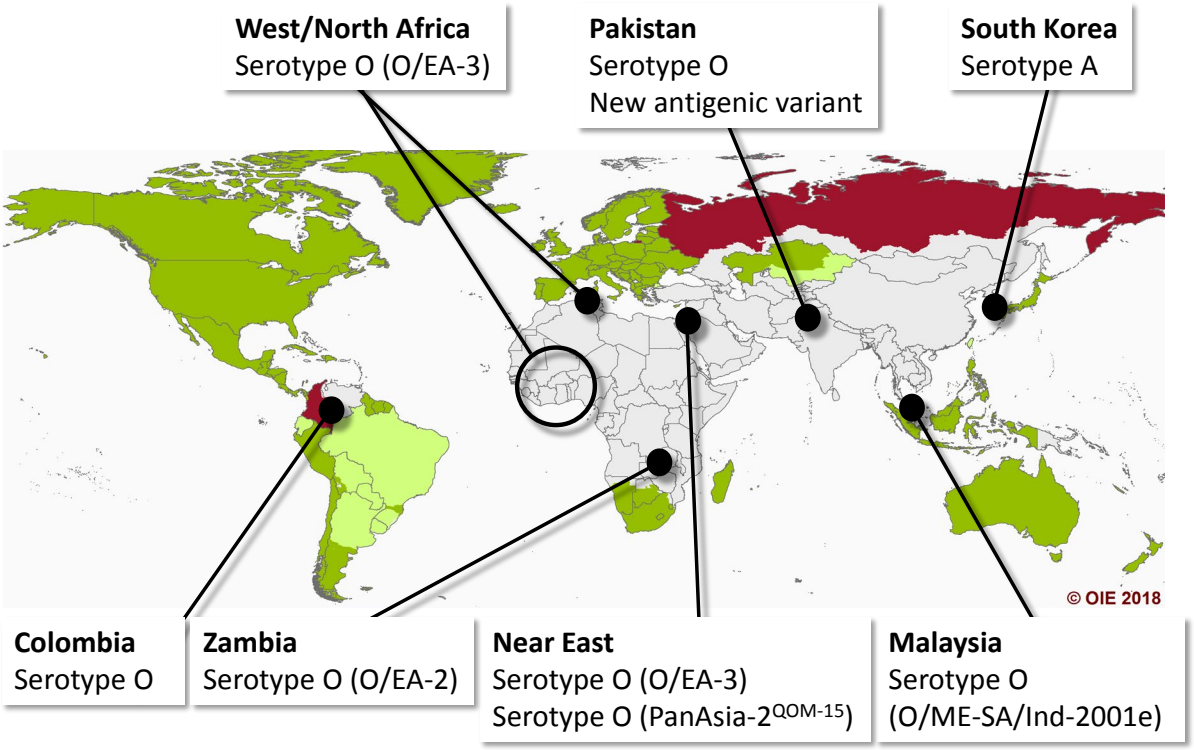


Figure 2.2: Headline FMD events for 2018

Bachanek-Bankowska K., Wadsworth J., Henry E., Ludi A. B., Bin-Tarif A., Staham B., King D. P., Afzal M., Hussain M., Manzoor S., Abubakar M. and Knowles N. J. (2019) Genome sequences of antigenically distinct serotype O foot-and-mouth disease viruses in Pakistan. *Microbiology Resource Announcements* 17: e01397-18

Pezzoni G., Bregoli A., Grazioli S., Barbieri I., Madani H., Omani A., Sadaoui H., Bouayed N., Wadsworth J., Bachanek-Bankowska K., Knowles N. J., King D. P. and Brocchi E. (2019) Foot-and-mouth disease outbreaks due to an exotic virus serotype A lineage (A/AFRICA/G-IV) in Algeria in 2017. *Transboundary and Emerging Diseases* 66: 7-13.

Specific 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 2018, 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 2018 (data collated in Table 2-1).*

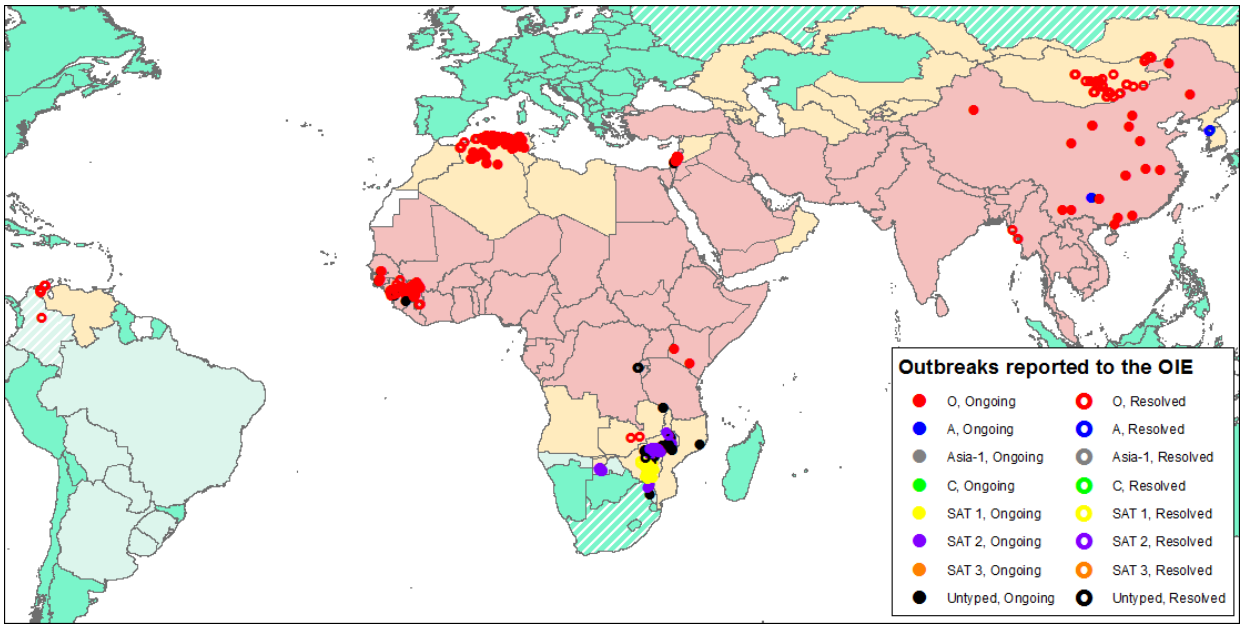


Figure 2.3: Map indicating the location of significant epidemiological events and disease outbreaks reported to OIE in immediate notifications or follow-up reports in 2018 (data available from: http://www.oie.int/wahis_2/public/wahid.php/Diseaseinformation/Immsummary.

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 2018 (data retrieved from WAHIS on www.oie.int on 21st January 2019). 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	3	5	8	7	16	11							50
Bangladesh			+										+
Bhutan			4										4
Botswana						8							8
Burkina Faso	2	6	2	11	19	4							44
Cambodia	7	3	6	3	14	5							38
Cent. Afric. Rep.			+..										+..
Cote D'Ivoire	2	2	6	2	9	5							26
Egypt	1	11	4	4	5	5							30
Eritrea	2	4	2		1								9
Hong Kong		1	2										3
Iraq	3	7	14	9	11	7							51
Israel				6	3								9
Kenya	27	9		1									37
Laos			15	9	22								46
Mali				2	7	8							17
Mongolia	10	11	2		2								25
Nepal		5	10	6	7	7							35
Niger			?										0
Nigeria	5		1	1	3	3							13
Russia		5											5
Saudi Arabia			+										+
Senegal	1				3	1							5
Somalia			17										17
South Africa					1								1
Sudan		1		1									2
Tanzania	1	1	1	2	1	1							7
Thailand	10	10	4	4	3	6							37
Turkey	86	106	69	50	24	11							346
Uganda	1	3		3	2	4							13
U.A.E.	2												2
Vietnam	1												1
Zimbabwe	23	19	17	4		1							64

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 Overview of the activities of the OIE/FAO FMD Laboratory Network during 2018

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.

Almost 2500 clinical samples from suspect cases of FMD were tested by laboratories in the Network (and associated laboratories) during 2018. These samples were collected from 46 countries from all seven FMD endemic pools 1 to 6 (Figure 2-4). **However, sampling within these pools is not equivalent:** and efforts are currently underway with the Network to improve sample collection in regions where sampling is particularly under-represented.

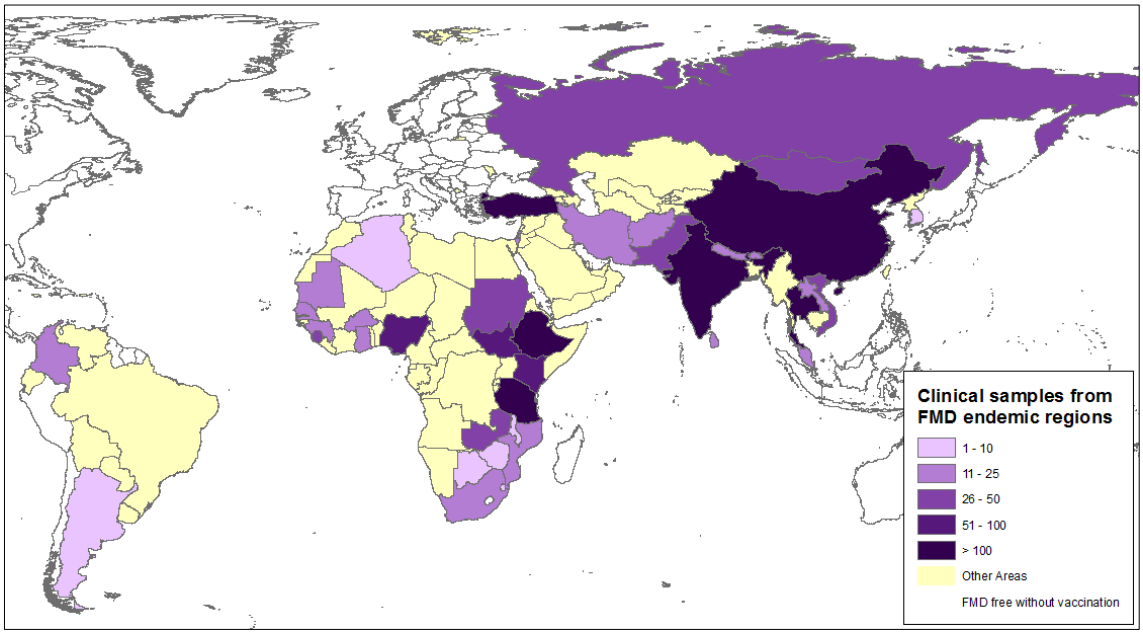


Figure 2.4: Distribution of samples collected from suspect cases of FMD (highlighted in purple) and tested by the OIE/FAO FMD Laboratory network during 2018. Areas recognised as FMD free without vaccination are shaded white, all other areas (including FMD free with vaccination) are shaded pale yellow.

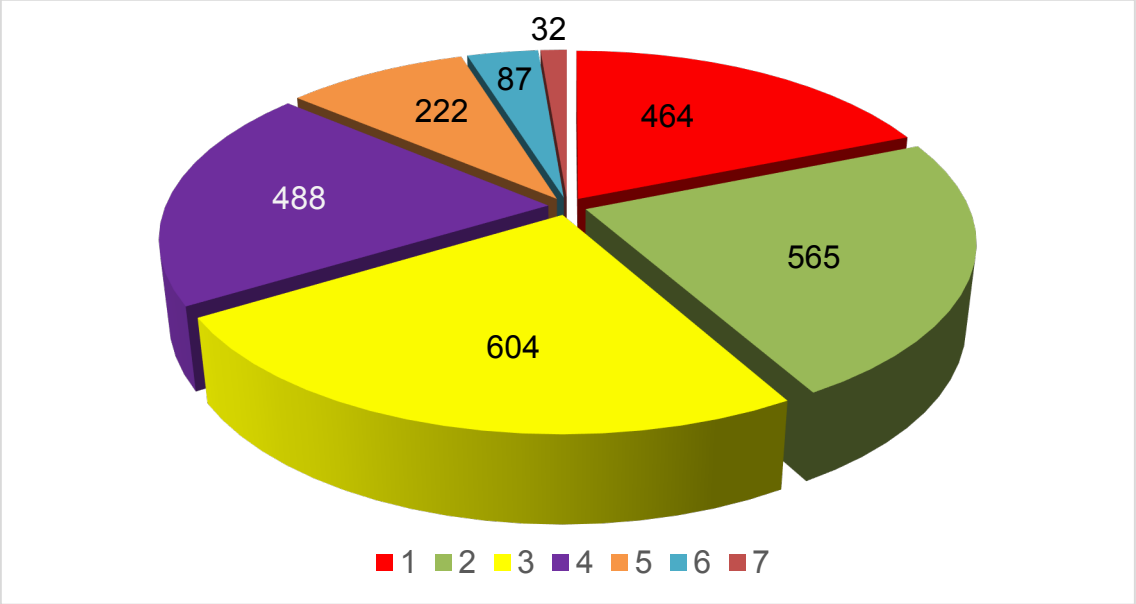


Figure 2.5: Clinical samples (n=2462) tested for FMD investigation (virology) by the OIE/FAO FMD Laboratory Network from FMD endemic countries during 2018 and their distribution across the seven FMD endemic pools (see Figure 2-1)

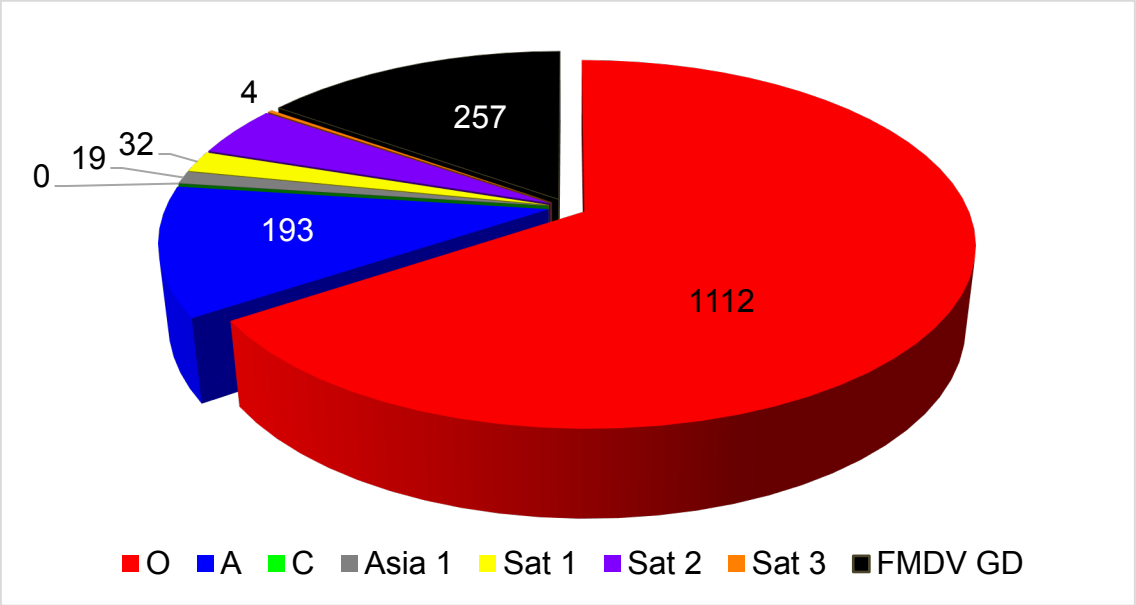


Figure 2.6: Summary of results for characterised isolates (n=1693) from FMD endemic countries were reported by the Network during 2018. FMDV GD denotes samples that were only positive using molecular (RT-PCR methods), while a further 769 samples were tested but found to be negative for FMDV using all diagnostic methods.

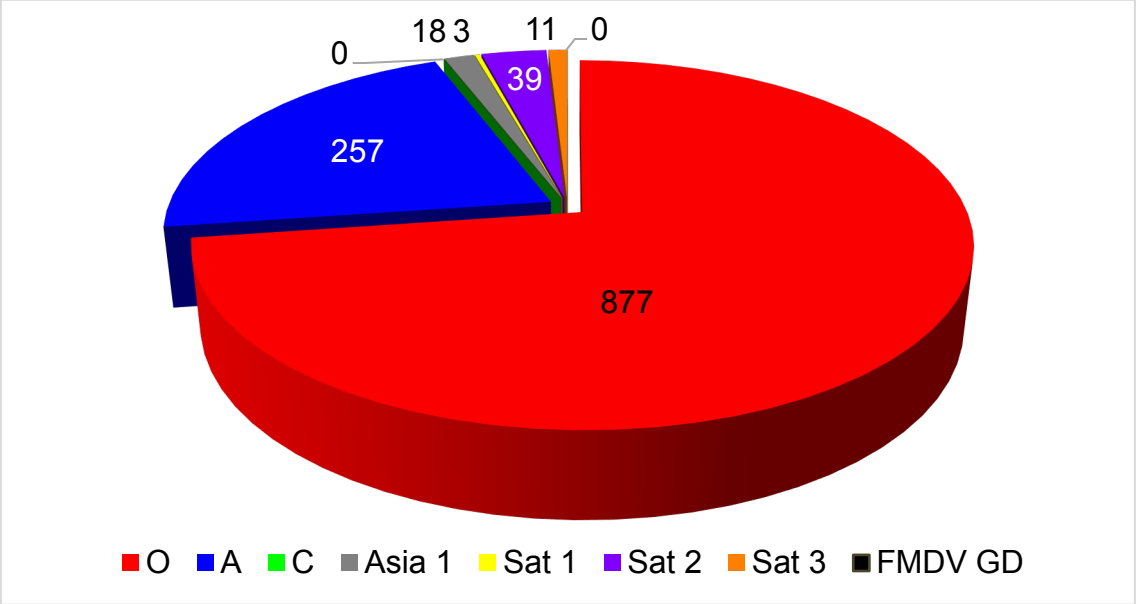


Figure 2.7: Summary of 1259 samples (viruses and field isolates) that were sequenced (VP1/capsid/complete genome) during 2018 (see Appendix 3).

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.

2.3 Regional distribution of different FMD viral lineages

In regions where FMD is endemic, continuous evolution of the virus generates geographically discrete lineages that are genetically distinct from FMD viruses found elsewhere. The conjectured global status for FMD (see Figure 2-1) masks the underlying complexity of FMDV virus distribution in the different pools (at serotype, topotype and lineage levels). This report showcases a new format to display how different FMD lineages 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	10	80	-	-	-	-
O/EA or O/WA	3	-	55	-	55	70	-	-
O/EURO-SA	-	-	-	-	-	-	-	80
O/CATHAY	-	10.5	-	-	-	-	-	-
A/ASIA/Sea-97	-	25	-	-	-	-	-	-
A/ASIA/Iran-05	25.5	-	-	-	-	-	-	-
A/ASIA/G-VII	17.5	-	-	16	-	-	-	-
A/AFRICA	-	-	25	-	22	15	-	-
A/EURO-SA	-	-	-	-	-	-	-	20
Asia-1	12.5	1.5	-	4	-	-	-	-
SAT 1	-	-	-	-	8	5	27	-
SAT 2	0.5	-	10	-	14	10	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-2001, O/ME-SA/PanAsia, O/ME-SA/PanAsia-2, O/SEA/Mya-98, O/EA-3, A/ASIA/G-VII, A/ASIA/Iran-05, A/ASIA/Sea-97 and SAT 2/VII.

The current known and conjectured distribution of these different FMD viral lineages are represented in the maps below: The extent of current distribution for each of the viral lineages is represented within the black lines, while the location of individual outbreaks (dots) and affected countries (shaded colours, according to dates) are shown. NB: Arrows are drawn to highlight the regions that are now threatened by these lineages and text boxes highlight some of the headline events and changes that have occurred during 2018

FMDV O

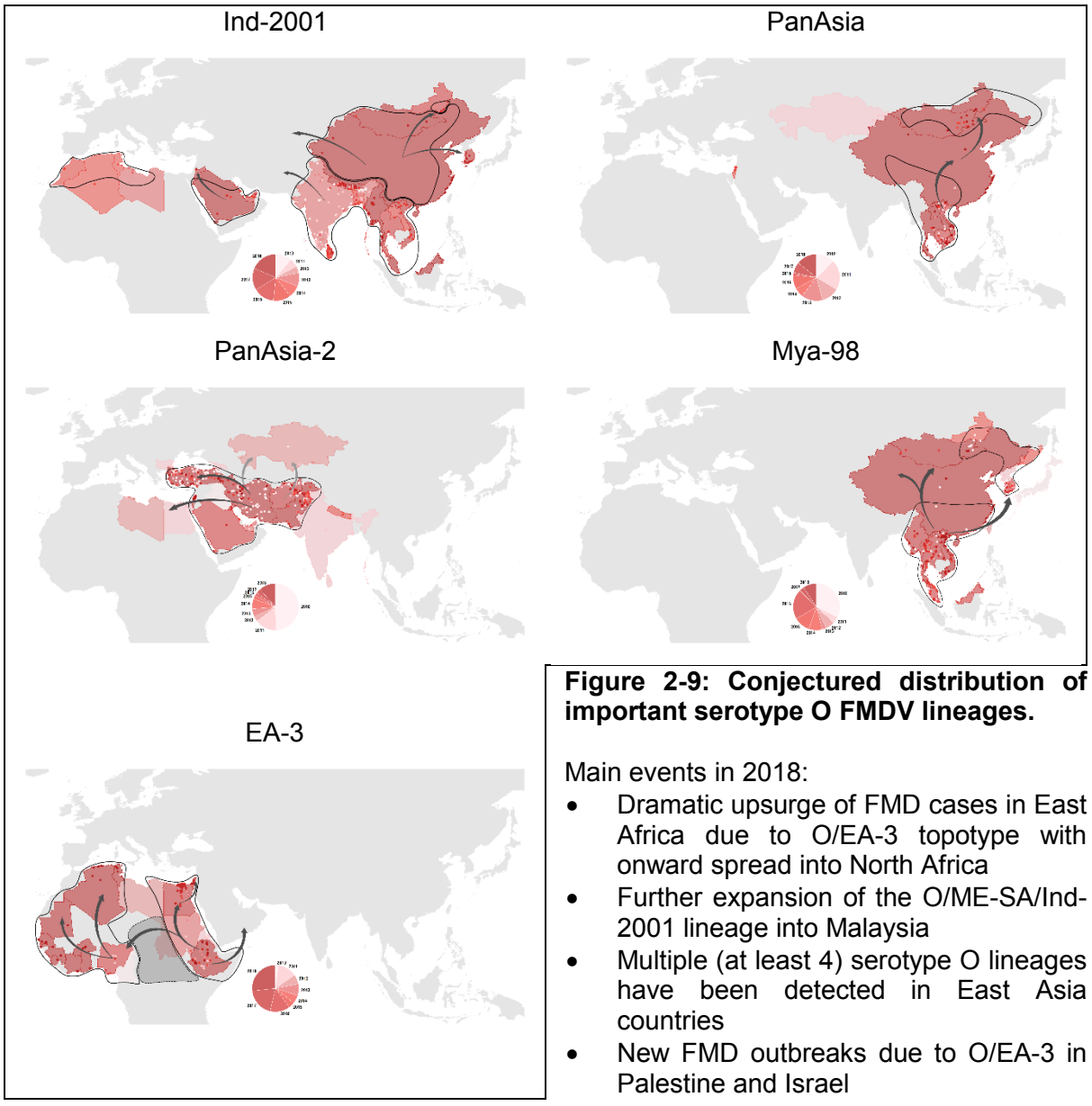


Figure 2-9: Conjectured distribution of important serotype O FMDV lineages.

Main events in 2018:

- Dramatic upsurge of FMD cases in East Africa due to O/EA-3 topotype with onward spread into North Africa
- Further expansion of the O/ME-SA/Ind-2001 lineage into Malaysia
- Multiple (at least 4) serotype O lineages have been detected in East Asia countries
- New FMD outbreaks due to O/EA-3 in Palestine and Israel

FMDV A

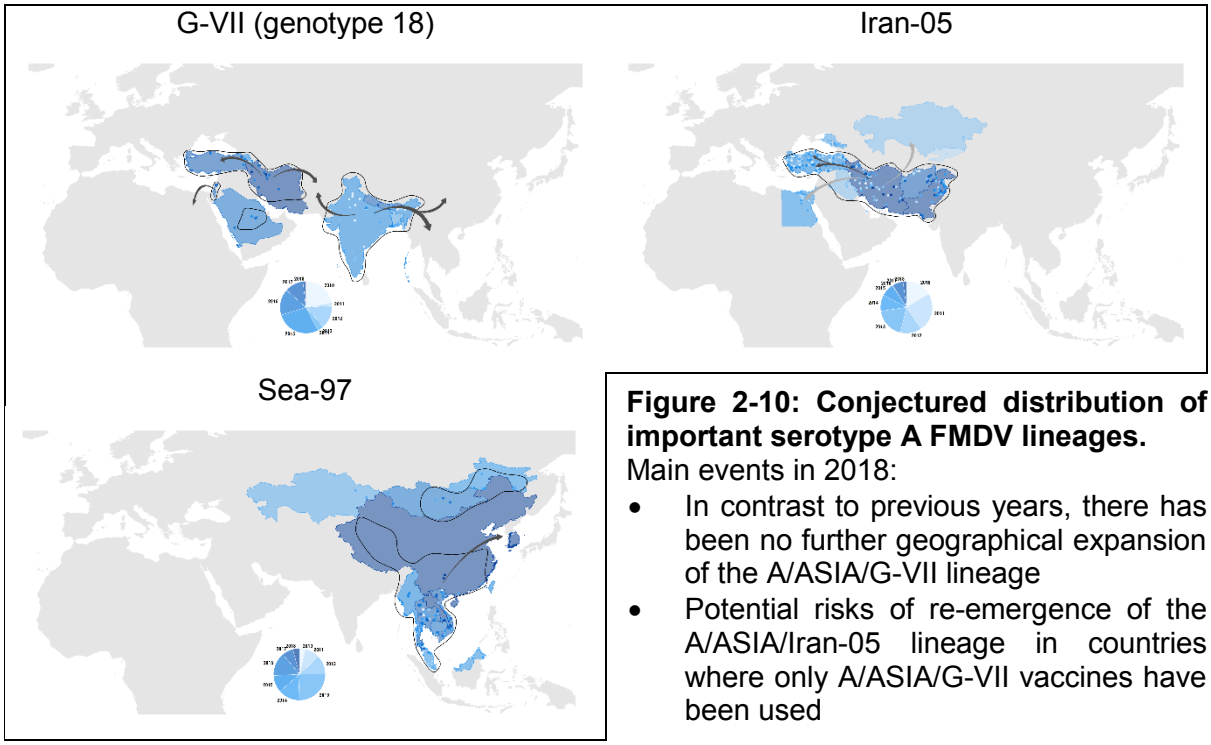


Figure 2-10: Conjectured distribution of important serotype A FMDV lineages.
Main events in 2018:

- In contrast to previous years, there has been no further geographical expansion of the A/ASIA/G-VII lineage
- Potential risks of re-emergence of the A/ASIA/Iran-05 lineage in countries where only A/ASIA/G-VII vaccines have been used

FMDV Asia 1

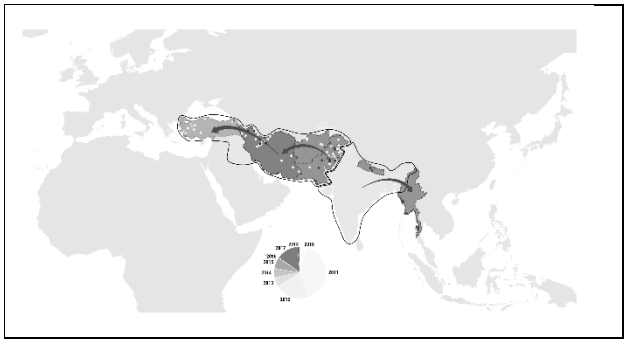


Figure 2-11: Conjectured distribution of serotype Asia 1.
Main events in 2018:

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

FMDV SAT 2

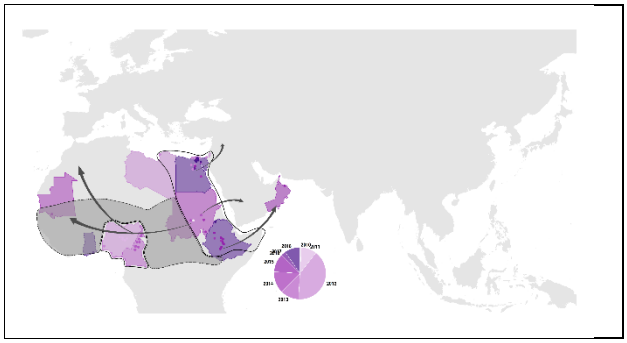


Figure 2-12: Conjectured distribution of serotype the SAT 2 (topotype VII) FMDV lineage.

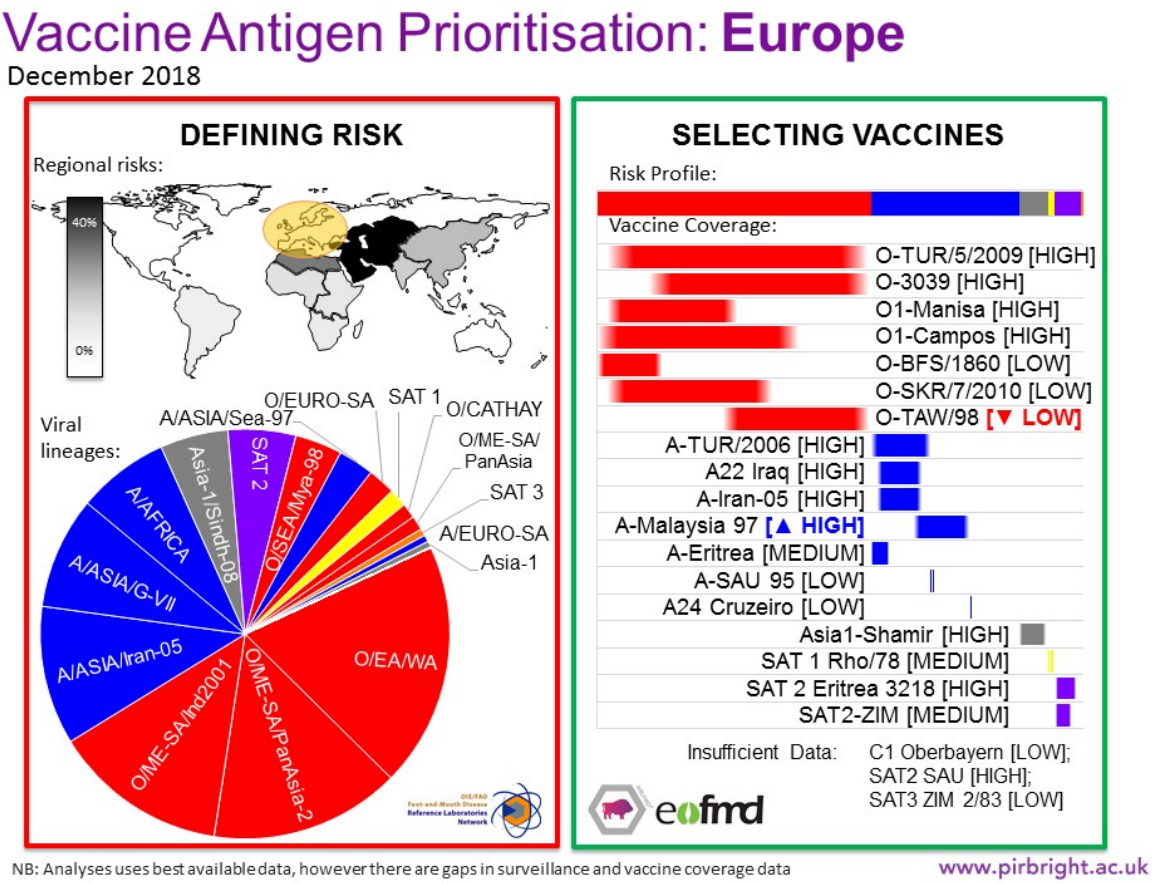
- Potential for this serotype to spread from West Africa into North Africa (paralleling the incursions of A/AFRICA/G-IV (in 2017) and O/EA-3 (in 2018).

2.4 Vaccine matching and recommendations

These take two forms: regional recommendations and details of locally produced vaccines for each of the FMD endemic pools are summarised later in this report, whilst the WRLFMD recommendations for FMD free countries are given in Table 2-3 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.

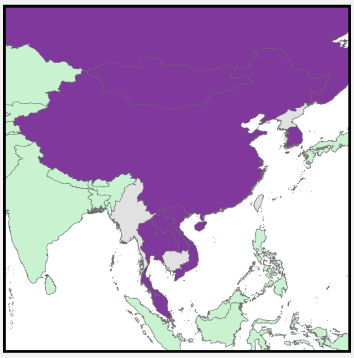
3 Overview of Network surveillance activities in each of the regional endemic pools

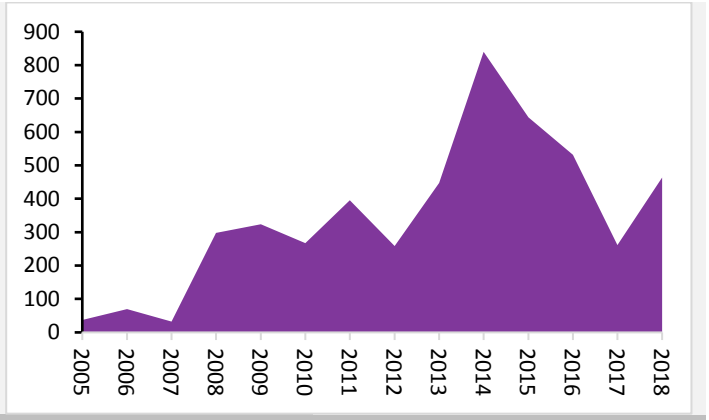
3.1 Pool 1 Regional synopsis

3.1.1 Conjectured circulating FMD viral lineages in Pool 1 during 2018

- Serotype O:
  - SEA/Mya-98
  - ME-SA/PanAsia
  - ME-SA/Ind2001d
  - ME-SA/Ind2001e
  - CATHAY
- Serotype A:
  - ASIA/Sea-97
- Serotype Asia-1 (no outbreaks detected since 2017, Myanmar)

Table 3-1: Overview of clinical samples collected and tested from Pool 1 in 2018 (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	139	5280
APQA, Republic of Korea	Republic of Korea	2	610102
FGBI ARRIAH, Russia	Mongolia, Russia	60	0
RRL SEA Pakchong, Thailand	Lao PDR, Thailand	135	7179
WRLFMD, UK	Hong Kong, SAR of PRC, Republic of Korea (South), Laos, Malaysia, Mongolia, Thailand, Vietnam	130	0
FADDL, USA	Vietnam	0	405

Pool 1 headlines: Changes to FMD status in 2018:

- Since 2015, the O/ME-SA/Ind-2001 lineage has **rapidly** spread from South Asian countries into mainland Southeast Asia. In 2018, this lineage was detected for the first time in Malaysia
- No new cases of serotype Asia 1 have been detected in the region (beyond the two outbreaks reported in Myanmar in 2017). Sero-surveillance studies are underway in Myanmar to determine whether undisclosed spread of this serotype has occurred
- Endemic FMDV strains normally found in mainland Southeast Asia continue to be detected:
    - Serosurveillance studies in Thailand demonstrate that ~21% cattle have FMDV NSP-specific antibodies
    - Complex epidemiological pattern of serotype O lineages in China (O/CATHAY, O/SEA/Mya-98, O/ME-SA/PanAsia (and O/ME-SA/Ind-2001e) detected in 2018 in addition to A/ASIA/Sea-97 (See Appendix 4)
    - New A/ASIA/Sea-97 outbreaks reported in South Korea (see Appendix 4)
    - New serotype O outbreaks in Russia (O/ME-SA/PanAsia - see Appendix 4)

3.1.2 Vaccine recommendations for Pool 1

- Internationally produced vaccines:
    - O: Campos, Manisa, Nakornpathom, Primosky, 3039
    - A: Malaysia/97, Zabaikalsky, Iraq/64 & A22-IRQ.
    - Asia 1: Shamir
- Locally produced vaccines (at RRL SEA):
    - O: 189/87 (Udornthani/87)
    - A: Lopburi/12, Sakolnakorn/97
    - Asia1: Petchaburi/85
- Locally produced vaccines (at FGBI ARRIAH):
    - O: Ind-2001d, Mya-98, PanAsia, PanAsia-2
    - A; G-VII, Iran-05, Sea-97
    - Asia1: Shamir, Sindh-08
- Locally used vaccine strains (by Chinese manufactures):
    - O/Mya-98 (O/Mya98/BY/2010 and Re-O/Mya98), 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

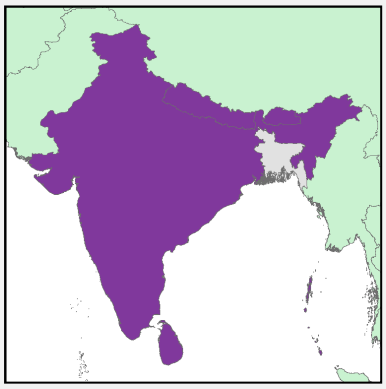
3.2.1 Conjectured circulating FMD viral lineages in Pool 2 during 2018

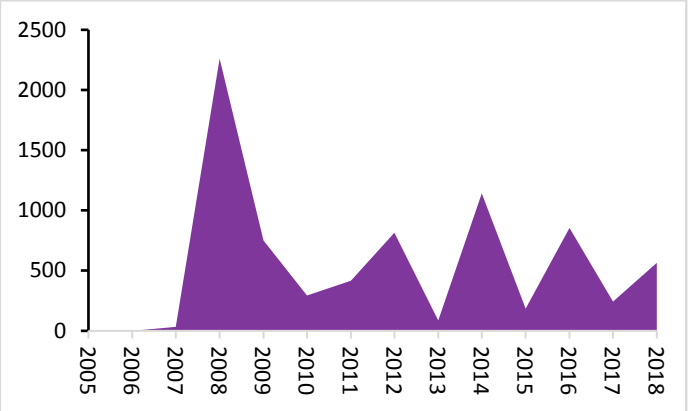
- Serotype O:

- 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 clinical samples collected and tested from Pool 2 in 2018 (countries highlighted in purple; graph represents clinical submissions since 2005)





Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
PDFMD, India	India	520	42010
WRLFMD, UK	Bhutan, Nepal, Sri Lanka	45	0

Pool 2 headlines: Changes to FMD status in 2018:

- Serotype O continues to be the most dominant FMD serotype in India. Most viruses represent the O/ME-SA/Ind-2001e clade however, three viruses collected during 2017 were from the O/ME-SA/Ind-2001d sub-lineage (see Appendix 4)
- Using full genomic data a collaborative team has reconstructed the global space-time transmission history of the O/ME-SA/Ind-2001 lineage (which normally circulates in Pool 2) providing evidence of at least 15 independent escapes during 2013-2017 that have led to outbreaks in North Africa, the Middle East, Southeast Asia, the Far East and the FMD-free Islands of islands of Mauritius (see Bachanek-Bankowska et al., 2018).
- Outbreaks in Sri Lanka have also been due to serotype O, while FMD cases in Bhutan and Nepal have also included A and Asia-1, respectively
- There appear to be large genetic gaps for FMD viruses sequenced – findings that are consistent with a large number of unsampled FMD cases in the region

Bachanek-Bankowska et al., (2018) Reconstructing the evolutionary history of pandemic foot-and-mouth disease viruses: the impact of recombination within the emerging O/ME-SA/Ind-2001 lineage. *Scientific Reports* **8**(1): 14693.

3.2.2 Vaccine recommendations for Pool 2

- Internationally produced vaccines:

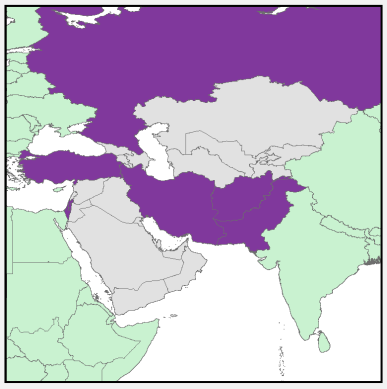
- O/ME-SA/PanAsia-2 (or suitable alternative). *In vitro* vaccine matching data for O/ME-SA/Ind2001 provides evidence for an antigenic match with O/TUR/09 vaccine (MSD) and O-3039 (Boehringer Ingelheim).
- Locally produced vaccines (by Indian suppliers):
  - O/IND/R2/1975
  - A/IND/40/2000
  - Asia1/IND/63/1972

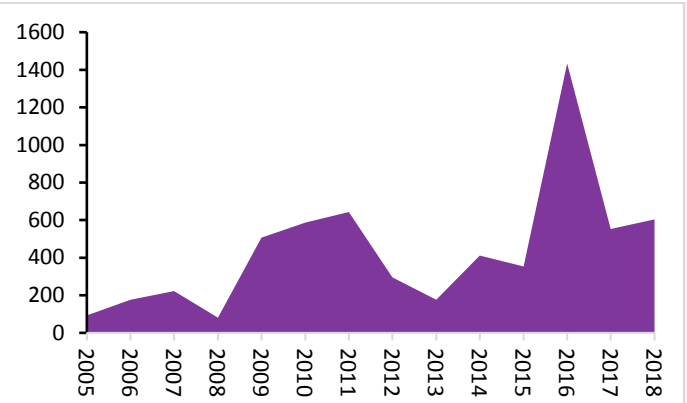
3.3 Pool 3 Regional synopsis

3.3.1 Conjectured circulating FMD viral lineages in Pool 3 during 2018

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

Table 3-3: Overview of clinical samples collected and tested from Pool 3 in 2018 (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	Pakistan	40	0
ŞAP Institute, Turkey	Turkey	491	42823
WRLFMD, UK	Afghanistan, Iran, Israel, State of Palestine	73	0

Pool 3 headlines: Changes to FMD status in 2018:

- No further spread of the A/ASIA/G-VII lineage has occurred during 2018
- Experimental studies demonstrate that A/ASIA/G-VII and A/ASIA/Iran-05 are antigenically distinct; since there is no cross-protection provided by commercial A/Iran-05 (and related vaccines) to field viruses from the A/ASIA/G-VII lineage, and tailored A/G-VII vaccines do not confer protective responses against A/ASIA/Iran-05 field viruses
- The O/ME-SA/PanAsia-2^{QOM-15} lineage has become established in Israel and has been responsible for the majority of FMD cases in Turkey (see Appendix 4)
- A new antigenic variant of serotype O (within the O/ME-SA/PanAsia-2^{ANT-10} lineage) has been detected in Pakistan (see Appendix 4) that is not neutralised by any of the international vaccines provided by MSD or BI.

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
  - A/G-VII (from BI)
- 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:
  - O/PanAsia-2/QOM-15
  - A/Iran05/SIS-13
  - A22 Iraq
  - A/Asia/G-VII
  - Asia 1/TUR 15 (Sindh-08)
  - Asia1/Shammir
- Locally produced vaccines (other suppliers in the region):
  - Vetal
  - MEVAC

3.4 Pool 4 Regional synopsis

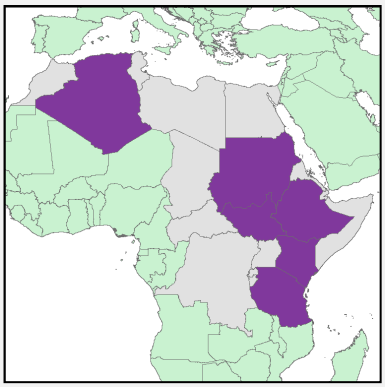
3.4.1 Conjectured circulating FMD viral lineages in Pool 4 during 2018

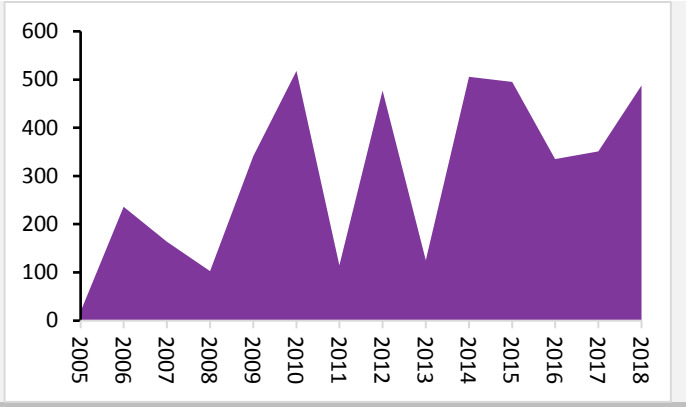
- Serotype O:
  - EA-2 (Kenya, Tanzania, DR Congo, Uganda)
  - EA-3 (Egypt, Ethiopia, Eritrea, Sudan)

- 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 2013)

- **Table 3-4:** Overview of clinical samples collected and tested from Pool 4 in 2018 (countries highlighted in purple; graph represents clinical submissions since 2005)





Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
NAHDIC, Ethiopia	Ethiopia	105	3385
FMD Laboratory, Kenya	Kenya, South Sudan, Tanzania	265	1190
WRLFMD, UK	Algeria, Ethiopia, Kenya, South Sudan, Sudan	118	0
FADDL, USA	Uganda	0	8354*

** Additionally FADDL tested 13,400 serum and 2,000 oropharyngeal fluid samples collected from Uganda between 2014 and 2018. From this project 300 sequences were deposited in Genbank.*

Pool 4 headlines and status in 2018:

- FMD virus distribution support the idea that there are two separate sub-regional pools of endemic virus circulation:
  - O/EA-3 is present in countries in the northern part of East Africa (such as Ethiopia and Sudan) and that this lineage has spread from this region to affect countries in West Africa (Nigeria), North Africa (Egypt), and beyond (Israel and Palestine)
  - A second topotype (O/EA-4) is also detected in Ethiopia. In contrast, countries in the southern part of the East Africa region maintain different serotype O topotypes, including O/EA-2 (currently very active), which has the widest distribution (Kenya, Uganda, Tanzania, Zambia), while O/EA-1 appears to be restricted to Kenya (last detected in 2009).
  - This observed segregation between viruses found in the northern and southern parts of the East Africa region is mirrored for serotype A, SAT 1 and SAT 2 FMD viruses
- O/EA-2 has been detected in Central Zambia (Chisamba) representing increased spread of this topotype in a south-westerly direction.
- In Ethiopia SAT2/ V-II^{ALX-12} has been detected for the first time in the far north of the country
- Novel SAT genotypes have been detected using retrospective full genome analyses highlighting the extent of un-sampled viral diversity that may exist within African wildlife parks (Lasecka-Dykes et al., 2018)

NB: Outbreaks in Algeria described below (see Pool 5)

Lasecka-Dykes et al., (2018) Full genome sequencing reveals new South African Territories genotypes bringing us closer to understanding true variability of foot-and-mouth disease virus in Africa. *Viruses* **10**(4): E192

3.4.2 Vaccine recommendations for Pool 4

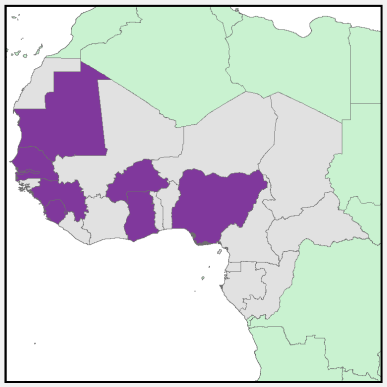
- Internationally produced vaccines:
  - O/Manisa
  - O/PanAsia-2 (or equivalent)
  - A/Eritrea
  - SAT2/Eritrea
- Locally produced vaccines from KEVIVAPI (Kenya):
  - O: K 77/78 – EA1
  - A: K5/80 –G1
  - SAT1: T155/71- NWZ
  - SAT2: K52/84 – IV
- Locally produced vaccines from Ethiopia:
  - Serotype O
  - Serotype A
  - Serotype SAT 2
- Locally produced vaccines from BVI (Botswana) and ME-VAC (Egypt)

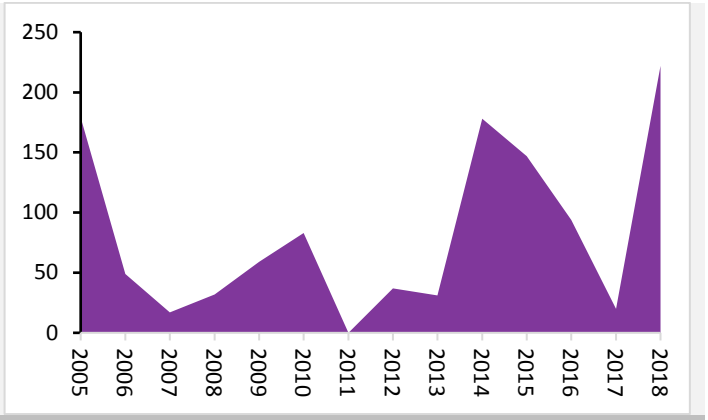
3.5 Pool 5 Regional synopsis

3.5.1 Conjectured circulating FMD viral lineages in Pool 5 during 2018

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

Table 3-5: Overview of clinical samples collected and tested from Pool 5 in 2018 (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, Sierra Leone	49	4
NCFAD, Canada	Ghana	23	715
ANSES, France	Guinea, Mauritania	41	60
Sciensano, Belgium	Nigeria	44	0
WRLFMD, UK	Burkina Faso, Gambia, Nigeria, Senegal, Sierra Leone	114	0

Pool 5 headlines: Changes to FMD status in 2018:

- Network laboratories have provided coordinated support to understand the emergence and spread of the O/EA-3 topotype in West Africa and North Africa
- Sequence data demonstrates very close genetic identity (>99%) between FMD viruses collected in West African countries and North Africa (see Appendix 4)
- Collection of good-quality samples remains an important challenge and Network laboratories have implemented novel approaches using nucleic acid recovery from lateral-flow devices as well as RNA transfection methods to characterise FMD viruses causing these outbreaks
- The emergence of O/EA-3 and A/AFRICA/G-IV (in 2017) in the Maghreb is a significant change of epidemiological status which may substantiate new trans-Saharan connections between North and West Africa which raise the onward risks to FMD-free countries in Europe.

3.5.2 Vaccine recommendations for Pool 5

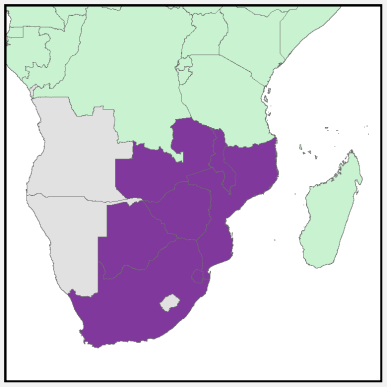
- Internationally produced vaccines:
  - O/Manisa
  - O/Maghreb
  - O/PanAsia-2 (or equivalent)
  - O: 3039
  - A: Eritrea
  - SAT 2: Eritrea & Zimbabwe
- Locally produced vaccines
  - O: NIG 04/14
  - O: WA and EA-3 topotypes
  - A: NIG 07/13
  - A: West Africa (G-IV lineage)
  - SAT 1: Topotype X
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

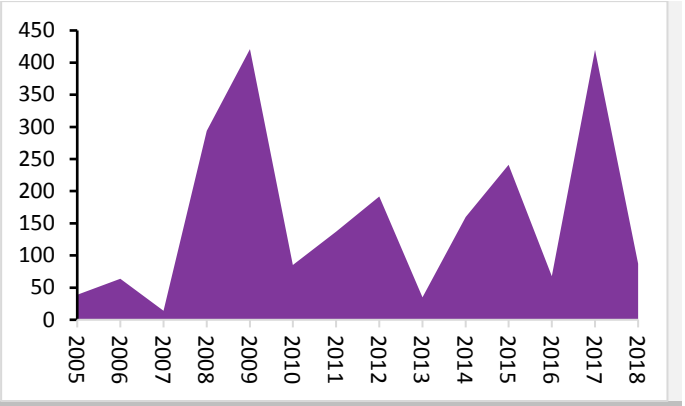
3.6 Pool 6 Regional synopsis

3.6.1 Conjectured circulating FMD viral lineages in pool 6 during 2018

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

Table 3-6: Overview of clinical samples collected and tested from Pool 6 in 2018 (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, Malawi, Mozambique, Zambia, Zimbabwe	55	207
ARC-OVI, South Africa	Mozambique, Namibia, South Africa, Eswatini, Zimbabwe	26	34418
WRLFMD, UK	Swaziland, Zambia	6	0

Pool 6 headlines: Changes to FMD status in 2016:

- Outbreaks due to two serotypes (SAT 2 and SAT 3) have occurred and no outbreaks due to serotype SAT 1 were reported from countries in the region during 2018
- In 2018 network laboratories have identified:
  - SAT 2 from Botswana, Malawi, South Africa (see Appendix 4), Zambia, Zimbabwe
  - SAT 3 from Mozambique, Zambia

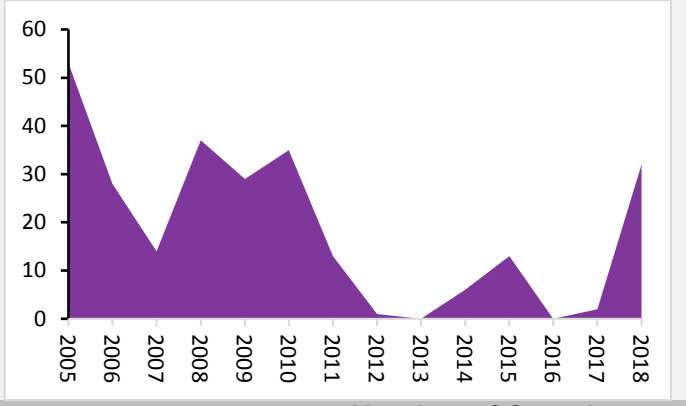
NB: O/EA-2 outbreaks in Zambia are described in Pool 4

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

Table 3-7: Overview of clinical samples collected and tested from Pool 7 in 2018 (countries highlighted in purple; graph represents clinical submissions since 2005)



Laboratory	Countries of Origin	Number of Samples	
		Clinical Field Cases	*Surveillance Activities*
SENASA, Argentina	Argentina	9*	14000
PANAFTOSA, BRAZIL	Colombia	23	0
FADDL, USA	Colombia (from 2017)	0	4

Pool 7 headlines: Changes to FMD status in 2018:

- During 2018, new FMD outbreaks have been reported in Colombia (see Appendix 4)
- Sequence analyses place these viruses within the O/EURO-SA/cluster 6 (described in 2011) and are 90% identical to outbreaks in Andean Region of South America
- Affected species are cattle and swine; evidence indicates that partially immunized cattle (mainly 1-2 years old) have been infected and moved into the affected region via illegal trade from Venezuela

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 *
- * will be withdrawn from the vaccine in Brazil, Paraguay and Bolivia in 2019

4 Improving the quality of laboratory tests from FMD reference laboratories

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

China

- A national PT for major animal diseases funded by MARA was organized by CADC and FMD RL jointly in April 2018.
    - FMD and SVV (Seneca Valley virus) coded samples were prepared and provided by FMDRL for real-time RT-PCR.
    - 32 provincial labs were invited to participate.

Italy

- PTS organised for 10 regional laboratories in Italy
    - Goal: To practise the regional laboratories in the use of serological tests for preparedness in case of national emergency
- Supplied panel of 22 sera (naïve and FMDV serotypes O and A) and SPCE kits to detect antibodies for FMDV O and A.

Republic of Korea

APQA organises a national scheme for regional Diagnostic Centers (8) for FMD antigen and antibody test (twice a year)

Thailand

- 5th Round / 2017 : 16 Participating laboratories;
    - 7 FMD laboratories within Thailand
    - 9 SEAFMD laboratories ; Cambodia, Lao PDR, Brunei, Malaysia, Myanmar, Singapore, Vietnam (Hanoi), Vietnam (Ho Chi Minh) and Thailand
- 6th Round / 2018: In process of distributing the Inter-lab samples to all participating laboratories
    - 7 FMD laboratories within Thailand had already received samples and also completed in testing of inter-lab samples
    - All SEAFMD laboratories are contacting courier companies to organise the shipping and document process

United Kingdom

	Phase XXX (2017)		Phase XXXI (2018)	
Total invited laboratories[1]	81		94	
Total number of shipments[1]	70		76	
EURL funded participants				
Participants from European Union (funded by EURL for FMD)	27 (EU member states)		26 (EU member states)	
% of labs meeting target performance[4]	Cat-1 Cat-2 Cat-3 Cat-4	0 % 0 % 44.44 % 55.56 %	Cat-1 Cat-2 Cat-3 Cat-4	0 % 3.85 % 46.15 % 50 %
EUFMD funded participants				
Participants from Global Network Labs[2]	Argentina, Botswana, Brazil, Canada[3], Ethiopia, Kenya, Nigeria Russia, South Africa, Thailand, USA[3].		Argentina, Botswana, Brazil, Canada[3], China, Ethiopia, Kenya, Nigeria Russia, South Africa, Thailand, USA[3].	
% of labs meeting target performance[4]	Cat-1 Cat-2 Cat-3 Cat-4	0 % 0 % 72.73 % 27.27 %	Cat-1 Cat-2 Cat-3 Cat-4	0 % 7.69 % 69.23 % 23.08 %
Participants from EuFMD Member states (non-EU)	Albania, Israel, FYR Macedonia, Norway, Georgia, Serbia, Switzerland, Turkey.		Albania, North Macedonia, Norway, Georgia, Serbia, Switzerland, Turkey.	
% of labs meeting target performance[4]	Cat-1 Cat-2 Cat-3 Cat-4	0 % 0 % 75 % 25 %	Cat-1 Cat-2 Cat-3 Cat-4	0 % 0 % 42.86 % 57.14 %
Participants from neighbourhood countries	Algeria, Armenia, Azerbaijan, Egypt, Jordan, Kosovo, Lebanon, Moldova, Morocco, Tunisia.		Algeria, Armenia, Azerbaijan, Iran, Lebanon, Moldova, Montenegro, Morocco, Tunisia, Egypt, Jordan, Kosovo	
% of labs meeting target performance[4]	Cat-1 Cat-2 Cat-3 Cat-4	0 % 0 % 70 % 30 %	Cat-1 Cat-2 Cat-3 Cat-4	9.09 % 0 % 63.64 % 27.27 %
Summary of EUFMD funded participants				
Invited			25	
Panels shipped	Panel 1	22	Panel 1	20
	Panel 2	23	Panel 2	20
	Panel 3	25	Panel 3	20
	Panel 4	15	Panel 4	19
	-	-	Panel 5	6
Total number of participants funded by EUFMD	**25**		**22**	
Self-funded participants				
Participants	Australia, Kazakhstan, Namibia, Pakistan, Senegal, Singapore, Swaziland, UAE, & Zambia		Australia, Namibia, Nepal, New Zealand, Republic of Korea, Senegal, Singapore, Taiwan, UAE	
% of labs meeting target performance[4]	Cat-1 Cat-2 Cat-3 Cat-4	0 % 0 % 44.44 % 55.56 %	Cat-1 Cat-2 Cat-3 Cat-4	0 % 0 % 55.56 % 44.44 %

*[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

- 2018 FMD real time RT-PCR for the National Animal Health Laboratories Network (NAHLN)
  - 47 participating laboratories; 275 PTs shipped to NAHLN Labs
  - 233 Individuals' PTs Evaluated
  - 115 New Trainees
- 2018 VI PT for vesicular diseases
  - 1 national, with 6 states
- 2018 FMD exercises
  - 1 vaccine matching exercise
  - 1 interstate FMD "outbreak" exercise

4.2 Supply of reagents

Argentina

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
Hyper immune guinea pig sera A24 Cruzeiro-A arg 2001-O1 Campos-C3 Indial	63 vials x 1 ml	Paraguay
FMD challenge viral suspension for PGP test A24 Cruzeiro – A Arg 2001-O1 Campos	1500 vials x1 ml	Argentina
Typing ELISA	20 x 5 plates	Argentina
3 ABC ELISA	20 x 10 plates	Uruguay
3ABC Protein	10 vials x1 ml	Paraguay
3D Protein/3B Protein	5 vials x 1ml each	Argentina

Brazil

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV Kits for detection of antibodies against nonstructural protein (NSP): *Kit NCP-Panaftosa System (Elisa 3ABC and EITB)*	643	• Argentina (Senasa) • Bolivia (Lidivet and Senasag) • Brazil (Lanagro, Biogenesis, Biovet, Merial, Ourofino, Vallee, Inova, IB/SP and Vet Lab) • Colombia (ICA and Vecol) • Ecuador (Agrocalidad) • Korea (Jayon) • Paraguay (Senacsa and Lauda) • Peru (Senasa) • Uruguay (Dilave,Di Santi, Potimor) • Venezuela (Insai and C.A. Laboratorios
FMDV Kits for detection of antibodies against structural protein: • Lp-ELISA FMD "O" • Lp-ELISA FMD "A" • Lp-ELISA FMD "C" kits for PVM (post vaccination monitoring) purposes	436	
FMDV antigen kits *FMDV/VSV*	40	• Argentina (Senasa) • Colombia (ICA) • Ecuador (Agrocalidad) • Paraguay (Senacsa) • Peru (Senasa) • Uruguay (Dilave) • Venezuela (Insai)
Positive controls for PCR *BHK-21 and IB RS-II cell lines*	7	• Paraguay

Botswana

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	40ml Each SAT1-3 ELISA reagents and controls	BNVL/ Botswana

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antigen kits	50ml Each SAT1-3 ELISA reagents and controls	CVL/Zimbabwe

Canada

Type of reagent	Recipient of the reagent (Laboratories / Countries)
FMDV 3ABC ELISA kit reagents	PANAFTOSA
Two FMDV serotype A monoclonal antibodies	BioStone Animal Health, USA
Monoclonal antibody F1412SA	Tiba Biotech, USA; Moredun Institute, UK
FMDV RRT-PCR reagents	National Veterinary Lab, Ghana

China

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
LPBE-O	57233	Veterinary laboratories and large scale breeding companies (China)
LPBE-Asia1	2220	
LPBE-A	3562	
NSP-3ABC-ELISA	2134	
Antigen ELISA	0	
Conventional Multi-RT-PCR	147	Provincial veterinary laboratories in China
Real-time RT-PCR	1034	
Typing real-time RT-PCR	381	

France

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
Primers for FMDV RT-PCR detection and typing	200 rx	NRVI (Nigeria)
LFD (extraction and Ag detection)	1 kit	ONARDEL (Mauritania)
Primers for FMDV RT-PCR detection and typing	200 rx	LNERV (Senegal)
Primers and probes for FMDV rtRT-PCR detection	200rx	PI (Guinea)

India

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	NSP = 42, 010 samples SP= 159, 700 samples	FMD Regional Centers and Collaborating units, India. National Dairy Development Board (NDDB)
FMDV antigen kits	2000 samples	FMD Regional Centers and Collaborating units, India

Italy

Country or Organisation		FMDV antigen detection ELISA *(O,A,C,Asia1, SAT1-2)*	NSP Ab ELISA kit 3ABC	SP antibody ELISA kit O	A	Asia 1	SAT 2	SAT 1
FAO (training)		4		1	1	1		
Asia	Nepal	5						
	Myanmar	10	3	6				
	Rep. Korea	15		2	14	1		
	China	15		450	100			
	Sri Lanka	4		2				
	Mongolia	2		11	10			
Central Asia & West Eurasia	Iran	31		2	2	2		
	Kazakhstan			963				
	Georgia	3	43	1	3	9		
	Afghanistan	5	9	7	6	6		
	Russia	310						
	Pakistan		15	5	5	5		
Middle East	Jordan	2						
	UAE	5	1					
	Bahrain	6						
	Kuwait	4		1	1			
	Oman			2	2	1		
	Saudi Arabia		3	8	7	7	7	
Africa	Egypt	6						
	Ethiopia	17						
	Morocco		1	2	2			
	Kenya	4	5	2	2	2	2	2
	Botswana	3						
	Zambia	1	1	2				
	Libya	1	1	1	1			
	Algeria	2	2	3	3	3	3	3
South America	Argentina	5		3	3	3		

	Brazil	1						
FMDV-free countries	Austria	10						
	Belgium	6						
	Cyprus	8						
	Czech Rep.	2						
	Estonia	2		1	1	1	1	
	France	1						
	Greece	4				1		
	Kosovo	1		1	1	1		
	Lithuania			1	1	1	1	
	New Zealand				1	1	1	
	Poland	1		1	1	1	1	
	Slovenia			1				
	Sweden			1	1	1		
	Switzerland	2						
Totals		201	84	1480	168	48	16	5

Republic of Korea

Type of Reagent	Product name	Details	Quantity	Recipient of the reagent (Lab/Countries)
Antigen Test	VDRD FMDV 3Diff/PAN Ag Rapid kit	FMDV Ag Rapid kit	100	Myanmar
	RT-PCR kit for Universial	RT-PCR kit for Universial	144	
	RT-PCR kit for serotype O, A,Asia1	RT-PCR kit for serotype O,A,Asia1	144	
Antibody Test	VDpro FMDV NSP Ab ELISA(MedianDiagnostic)	NSP Ab ELISA	1440	
	FMDV NSP(3ABC) Antibody ELISA(Bionote)	NSP Ab ELISA	1440	
Antigen Test	VDRD FMDV 3Diff/PAN Ag Rapid kit	FMDV Ag Rapid kit	100	Vietnam
Antigen Test	VDRD FMDV 3Diff/PAN Ag Rapid kit	FMDV Ag Rapid kit	50	Cambodia
Antigen Test	VDRD FMDV 3Diff/PAN Ag Rapid kit	FMDV Ag Rapid kit	50	LAO PDR

Russia

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMDV antibody kits	220	Pakistan, Kyrgyzstan, Republic of Korea, Russia, Syria, Vietnam
FMDV antigen kits	7	Kyrgyzstan, Russia

Thailand

Type of reagents	Supplied nationally and own lab	Myanmar and Lao PDR	Remarks
Rabbit trapping antibody for type O, A and Asia1	Type O = 31 sets Type A = 38 sets Type Asia1 = 28 sets	Type O = 3 sets Type A = 6 sets Type Asia1 = 4 sets	Providing of complete set of ELISA reagents for interlaboratory comparison testing round 6/2018. Total 16 sets (7 sets - FMD labs in Thailand, 9 sets - SEA Labs)
Guinea pig detecting anibody for type O, A and Asia1	Type O = 37 sets Type A = 40 sets Type Asia1 = 30 sets	Type O = 3 sets Type A = 6 sets Type Asia1 = 4 set	
Inactivated & concentrated antigen (50X) for type O, A and Asia1	Type O = 66 ml Type A = 73 ml Type Asia1 = 73 ml	Type O = 6 ml Type A = 12 ml Type Asia1 = 8 ml	
Control serum for C++, C+ and C-	C++ = 263 ml C+ = 242 ml C- = 192 ml	C++ = 35 ml C+ = 35 ml C- = 35 ml	

United Kingdom

Country	Number of vials	Serotype	Reagent type
Argentina	18	Asia 1	
Australia	99	O, A, Asia 1	Antisera
Botswana	486	O, A, SAT 1-3	Antigens, antisera, controls
Colombia	12	O	Controls
Croatia	41	NSP	control
Czech Republic	84	O, A, C, Asia 1, SAT 1-3	Antigens, antisera, controls
Denmark	4	SAT 2	Antisera
Estonia	10	O, A, C, Asia 1, SAT 1-3	
France	7	SAT 1-3	Antigens, antisera, controls
Iraq	41	O, Asia 1	Antigen, antisera, controls
Poland	102	O, A, C	
Romania	1	SAT 2	Antigen
South Korea	199	O, A, C, Asia 1, NSP	Antigens, antisera, controls, NSP
Switzerland	9	NSP	
UK	7	O, A	Antigens, antisera
USA	66	O, A, Asia 1	Antigens, controls
Vietnam	893	O, A, Asia 1	Antigens, antisera, controls
Zambia	14	O, A, C, Asia 1, SAT 1-3	
Total	2116		

FMD viruses provided to other FMD labs and commercial companies:

Country	volume	Serotype	Reagent type
Argentina	5.4 ml		Viral isolate
Czech Republic	1.8 ml		Viral isolate
Germany	7.2 ml		Viral isolate
Netherlands	3.4 ml		Viral isolate
Spain	9 ml		Viral isolate
USA	3.6 ml		Viral isolate
Commercial companies	195.4 ml		Viral isolate
Total	225.8 ml		

USA

Type of reagent	Quantity	Recipient of the reagent (Laboratories/Countries)
FMD PT/Reference Panels	300	FADDL and NAHLN Labs / U.S.
ASF/FMD/CSF Combo PT	500	NAHLN Labs / U.S.
CSF/FMD PCR Controls (PAC)	400	NAHLN Labs / U.S.
Vesicular Exanthema of Swine IFA PT	8	FADDL-NVSL
Purified Ag for Vesicular Ag kit	17	FADDL-NVSL
Antisera for Vesicular Ag kit	34	FADDL-NVSL

4.3 Training courses organised by Network partners

Argentina

- Vesicular Disease Diagnosis
  - March 2018, Senacsa (Paraguay)
- Genetic characterization; PCR, q-PCR, sequencing
  - October 2018, Senacsa (Paraguay)

Belgium

In the framework of the OIE Twinning programme:

- Laboratory training of 3 scientists of NVRI (Nigeria) visiting Sciensano in October 2018
- Assistance with the organisation of a regional hands-on laboratory workshop at NVRI (Nigeria)

Botswana

- FMD isolation and characterization undergraduate student – Botswana International University of Science and Technology (BIUST).
- Investigation susceptibility of different cells to FMD virus undergrad-student - BUIST.
- Training is planned for field sampling and preservation of samples to reduce negative submissions.

Brazil

- 8th to 19th October 2018 - Training of RT-PCR and RT-qPCR for FMD and other vesicular diseases.
    - Request from Suriname for technical cooperation to maintain the status of FMD free without vaccination, recognized by the OIE in 2018
- 6th to 10th October 2018 – Ilhéus, Bahia, Brazil
    - for Brazilian veterinarians of the official service responsible for attending suspected vesicular diseases.

Canada

- Foreign Animal Disease Recognition course (for Canadian veterinarians)
- Training of CAHSN lab analyst on FMDV RRT-PCR
- FMDV 3ABC ELISA and FMDV RRT-PCR panels provided to the Canadian Animal Health Surveillance Network (CAHSN) laboratories

China

- About 25 seminars and presentations were given at workshops or conferences.
- 11 series of Training Courses jointly organized by FMDRL and Diagnosis Center, LVRI.
- A National Animal Experimental Biosafety Workshop held in LVRI on 26th-27th September 2018
- Field training courses during active surveillance
- An “International Training workshop on Major Transboundary Animal Diseases FMD, PPR and Sheep/Goat Pox Diagnosis Technology” has been held in Lanzhou Veterinary Research Institute on 11th-25th November 2018.
    - Sponsored by the Department of International Cooperation of MOST, China.
    - 23 scientists from 8 countries including Bangladesh, Democratic People's Republic of Korea, Egypt, Ethiopia, Nepal, Nigeria, Pakistan and The Republic of Sudan participated in this training workshop

France

- Two Scientists from LDV, Madagascar (5th to 16th March 2018) hosted at ANSES.
- One scientist from LNERV, Senegal (13th to 30th April 2018) hosted at ANSES.
- Training provided at ONARDEL, Mauritania (4th to 6th October 2018).
- Training provided at PI, Guinea (22nd to 26th October 2018).
- Workshops:
    - Fièvre aphteuse: Surveillance pour la détection précoce et confiance en l’absence de circulation virale (Tunis, Tunisia. 27th Feburary to 1st March 2018)
    - Atelier régional “Analyse qualitative et cartographique des risques pour l’optimisation de la surveillance de la fièvre aphteuse et ds maladies prioritaires” (CIRAD, France. 23rd to 27th April 2018).

- PRODEL: Workshop on the completion of data collection tools for basic surveys of animal priority diseases (Mbalmayo, Cameroon. 26th to 29th June 2018)

Italy

- Laboratory training on FMD diagnostic tests (ELISAs for antigen and antibody detection and RT-PCRs)
  - 17th to 28th September 2018
  - One scientist from Botswana, two scientists from Libya

Republic of Korea

- Scientific and Technical Training for Asian Countries, 6th Workshop (designed for Rabies, JE, CWD, ND, Brucellosis, FMD)
  - FMD diagnosis and surveillance, and vaccine evaluation
  - 6th to 14th September 2018
  - 12 participants from Mongolia, Vietnam, Indonesia and Kazakhstan.
- KOICA Global Training Program: Surveillance and Diagnosis Development of Foot-and-Mouth Disease in Myanmar (by APQA)
  - Training in Myanmar by KOICA (Animal and Plant Quarantine Agency)
    - FMD diagnosis and surveillance
    - 29th July to 12th August, 2018
    - 11 Participants from LBVD Myanmar
  - Training in Korea by KOICA (Animal and Plant Quarantine Agency)
    - FMD diagnosis and surveillance
    - 11th October to 2nd November, 2018
    - 7 Participants from LBVD Myanmar (Management level(4), Working level(3))
- Dr. Alfonso Clavijo (Executive Director, National Centres for Animal Disease (NCAD, Canadian Food Inspection Agency)
  - To discuss on evaluation of antibody test (SP and NSP Ab) of FMD
  - 22nd May to 25th May, 2018

Nigeria

- Regional hands-on laboratory workshop organised in Nigeria in December 2018 by NVRI with the assistance of Sciensano, Belgium

South Africa

Training on the diagnosis of Transboundary diseases were provided to 3 veterinarians from Eritrea. Training was focused on the diagnosis of FMD and PPR using molecular tests, virus isolation, virus typing and virus isolation.

Thailand

- Mr. Chattouphone Keokhamphet, from Lao PDR.
  - Training on FMD diagnosis and vaccine matching under IAEA support.

- 8th January to 2nd February 2018.
- Participated in the 2nd Scientific Meeting on FMD between RRLFMD, Pakchong and Exotic Disease Research Station, National Institute of Animal Health, NARO, Japan.
  - 15th-16th February 2018; Kodaira, Tokyo, Japan.
- Participated in the 21st SEACFMD National Coordinators Meeting.
  - 17th-19th July 2018; Penang, Malaysia.
- Coordination Meeting with Veterinary Laboratories in Africa and Asia Supported by the African Renaissance Fund and the Peaceful Uses Initiative.
  - 6th-10th August 2018; Vienna, Austria.
- 5th Meeting of SAARC Laboratory Directors' Forum.
  - 1st-3rd October 2018; Bangkok, Thailand.
- The 2018 Regional Animal Health Laboratory Technical Advisory Group (Lab-TAG) Meeting and 6th Meeting of ALDF.
  - 29th October- 2nd November 2018; Singapore.
- The 6th Joint meeting of NIAH Japan and NIAH Thailand.
  - 20th-21st November 2018; Tsukuba, Japan.
- The 24th Meeting of the OIE Sub-Commission for foot and mouth disease in South East Asia China and Mongolia.
  - 28th-30th November 2018; Ho Chi Minh City, Vietnam.
- Japan Asia Youth Exchange Program in Science.
  - 7th-16th December 2018; Miyazaki, Japan.

Turkey

- Training provided on diagnosis of FMD, techniques of vaccine quality control and vaccine production
  - 8 participants from Pakistan and 1 participant from Azerbaijan
- 3 phase outbreak investigation training courses provided for Turkish vets
  - 70 participants
- An Online outbreak investigation course (with technical assistance of EuFMD) for Turkish and Azeri participants
  - 157 participants

United Kingdom

- August 2018, Technical visit and training on FMD: UVAS, Pakistan
- Seminars provided to delegations from Vietnam, Republic of Korea, Ukraine
- Hands-on training courses covering FMD diagnostics at Pirbright: Ethiopia, Latvia, New Zealand, Thailand, Ethiopia, USA
- WRLFMD hosted a visiting scientist from Kazakhstan to develop tailored diagnostic methods for Central Asia
- Ethiopia - (WRLFMD and NAHDIC are currently collaborating on an OIE Twining project) training missions to Ethiopia reciprocal visits to the UK

USA

- FADD School (Ames and Plum Island Centers, USA)
  - 12th – 16th February 2018, 26 participants
  - 9th – 13th February 2018, 18 participants
  - 3rd – 7th December 2018, 35 participants
- UGANDA: Project funded by the DoD's Threat Reduction Agency (DTRA) through their Cooperative Biological Engagement Program (CBEP), included University of Minnesota, ARC of South Africa, Makerere University and UVRI, Ben Gurion University of Israel, and the Uganda Ministry of Agriculture
  - APHIS-USDA Training to support development of a Laboratory Quality Management Program in Uganda, 2018
    - Provided training to a network of laboratories in Uganda to develop or refine their quality management program in support of a long-term goal of becoming ISO-accredited. Personnel sent: Two (2) NVSL-FADDL scientists. Subject: quality assurance topics, calibration, and validation, and documentation, implementation of new assays, proper necropsy technique, and sample collection.
  - ARS-USDA: international collaboration for surveillance of FMD
    - Capacity building included training and technological transfer of a nanobody-based FMD 3ABC competitive ELISA for detection of antibodies against FMD non-structural proteins
    - Different training modules included: field sample collection, real time RT-PCR, ELISA, and sequencing

4.4 Collaborative projects

Argentina

Collaborators	Purpose of collaboration	Outcomes
SENACSA (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
Republic of Mongolia	FMD project Argentina fund for horizontal cooperation (FO.AR)	Strengthening laboratory´s capabilities and FMD epidemiological surveillance

Belgium

Collaborators	Collaborative project	Outcomes
NVRI, Nigeria	OIE Laboratory Twinning Program for capacity building	• Personnel training • Implementation of SOPs • Sample characterisation including phylogenetic analysis
LNV, Burundi	Bilateral collaboration	Sample characterisation including phylogenetic analysis
BVI, Botswana	Bilateral collaboration	• Personnel training • Sample characterisation including phylogenetic analysis • Participation of Sciensano in PT organised by BVI

Botswana

Collaborators	Purpose of collaboration	Outcomes
University of Botswana Keck Graduate Institute	Multivalent SAT FMD Vaccine	Plant based produced FMD vaccine for SATs
BITRI Canadian Food Inspection Agency	Develop and validate LFD for detection of FMD Antigen in the field	Serotype specific detection of outbreak strain
Pirbright Institute, UK	ILC, PTs, and Genotyping	Improve capacity
CODA-CERVA	ILC	Improved capacity

Brazil

- Validation of the lateral flow device kit for identification of foot-and-mouth disease virus and senecavirus A
    - 8th to 13th July 2018: Meeting for technical discussions
    - Nine professionals from the Animal and Plant Quarantine Agency - APQA (FMD diagnosis Division) from South Korea

Collaborators	Purpose of collaboration	Outcomes
COSALFA	Review the definition and role of the information system continental of the differential diagnoses of foot-and-mouth disease (SivCont-Continental Epidemiological Surveillance System - SivCont – Panaftosa)	15th – 17th October 2018, PANAFTOSA-OPS/OMS Meeting on Differential Diagnoses of Foot-and-Mouth Disease and the SIVCONT - Continental Epidemiological Surveillance System. The document will be submitted for discussion and approval at the next COSALFA (46th) in April 2019 in Colombia.
COSALFA	Advice to COSALFA´s Regional Commission for Biorisk Management in Laboratories handling FMDV and/or its derivatives.	Constitution of COSALFA´s Regional Commission of Biorisk Management in Laboratories handling FMDV and/or its derivatives.
Department of Animal Production and Health Veterinary Service, Suriname	Support in differential diagnosis of vesicular diseases Training of human resources	Training of Suriname laboratory staff *RT-PCR for strengthening the FMD diagnostic capacity as part of the early detection system*

Canada

Collaborators	Purpose of collaboration	Outcomes
PANAFTOSA	Validation of the FMD enzyme linked immunoblot assay (EITB) for multiple species	An EITB as a confirmatory test for sera from multiple species positive for antibodies to FMDV NSP
PANAFTOSA	Full genome sequencing of archived FMDV isolates in South America	Deep sequence data for South American FMDV isolates
APQA, QIA, South Korea	FMD diagnostic kit comparisons	More knowledge on available diagnostic tests
North American FMD Vaccine Bank	Use of monoclonal antibodies for Vaccine matching and antigenic cartography	Tools for FMD vaccine matching

Collaborators	Purpose of collaboration	Outcomes
Kansas State University	Multi-Antigen Print Immunoassay (MAPIA) as an alternative to EITB for confirmation of FMDV NSP antibodies	An improved confirmatory test for sera positive for antibodies to FMDV NSP
Iowa State University	Validation of assays for FMDV 3ABC ELISA for antibody detection in swine oral fluids	FMDV 3ABC ELISA for swine oral fluids
Botswana Institute for Technology Research / Botswana Vaccine Institute	Development of strip tests for SAT1,2 3 antigen; and NSP antibody detection	Field deployable FMDV diagnostic tests

China

Collaborators	Purpose of collaboration	Outcomes
Korea Atomic Energy Research Institute/Prof. Seo HoSeong	Research and development of an attenuated edible FMD vaccine using salmonella as the vector	LVRI collaborators visited Korea
Korea Atomic Energy Research Institute/Prof. Seo HoSeong	Research and development of FMD viral like particle (VLP) fused with the specific DC targeting domain	Constructed the recombinant plasmids.
Kazakh National Agrarian University, Kazakhstan/Prof. Gulnaz Ilgekbayeva	Cooperative creation and application studies of new products for prevention and control of major transboundary animal diseases	Constructed the FMD marker vaccines Established the platform for expression and in vitro assembly of FMD VLPs
The University of East Anglia(UEA), UK/Professor Tom Wileman	Exchange of vaccine technology for the development of oral vaccines for FMD and other viral diseases	Prof. Tom Wileman and other 5 people from UEA visited LVRI in October 2018

- 2nd East Asia NCP Meeting and 2018 SEACFMD Epidemiology Network Meeting.
  - 5th-6th April 2018; Yogyakarta, Indonesia.
- The Symposium on Prevention and Control of FMD & AI.

- 21st-22nd June 2018; Seoul, Republic of Korea.
- 21st SEACFMD NCP Meeting.
  - 17th-19th July 2018; Penang, Malaysia.
- 2018 ASEAN Regional Animal Health Laboratory Technical Advisory Group (Lab-TAG) Meeting, FAO.
  - 29th-31st October 2018; Singapore.
- The 13th OIE/FAO FMD Reference Laboratories Network Annual Meeting.
  - 6th-8th November 2018; UK.
- The 24th OIE SEACFMD Sub-Commission Meeting.
  - 27th-30th November 2018; Ho Chi Minh City, Vietnam.

Ethiopia

Collaborators	Collaborative project	Outcomes
WRLFMD (UK)	OIE twining project	Building the capacity of NAHDIC in different areas: • FMD antigen detection • Molecular test • Serotyping • Vaccine matching

France

Collaborators	Purpose of collaboration	Outcomes
LNERV (Senegal), NRVI (Nigeria)	Validation of 6-plex RT-PCR for FMDV detection and typing	One-step 6-plex RT-PCR for detection and typing O, A, SAT 1 & SAT2 in West Africa
DTU, NRVI, SAP, UM, BI	Field validation of LFD inactivation protocol	Protocol for safe and low cost shipment of FMD samples
INRA, SLU, FLI, Sciensano, MERIAL, ANSES	Host response gene signatures associated with FMDV infection, vaccination and persistence	Cellular model Transcriptomic Proteomic

Italy

Collaborators	Purpose of collaboration	Outcomes
The Pirbright Institute	Continuous validation and improvement of new diagnostic kits (ELISA)	• Recombinant products (Integrin, VLPs) in ELISA kits • New mAbs investigations Cross-reactivity of SP Ab-ELISAs
University of Tripoli, NCAH - Libya	1. New Country serosurvey Collection of suspect samples (or OP samples) to characterize FMD circulating viruses	Samples should be shipped to IZSLER
North Africa, OIE, EuFMD	Field vaccination trials for evaluation of vaccines currently used in Maghreb region	ELISA and VNT performed on sera from Morocco and Tunisia, waiting sera from Algeria
Kenya, ILRI	1. Evaluation of vaccine used in Kenya by field vaccine trials Investigation of virus serotype diversity by serology	Analysis of serological results at ILRI
University of Glasgow	To time outbreaks of specific serotypes and inform epidemiological models of disease spread in the context of pastoralist and agro-pastoralist livestock movements in FMD endemic settings	Sera testing ongoing

Kenya

Collaborators	Purpose of collaboration	Outcomes
• Kenya Wildlife Service • US Department of Agriculture-Plum Island Animal Disease Center University of Minnesota	Evaluating cross-species transmission of FMD in rangelands shared by buffalo and cattle in Kenya	Improved understanding of FMD transmission dynamics in Kenya

Collaborators	Purpose of collaboration	Outcomes
• Tanzania Veterinary Laboratory Agency • Dar es Salaam • Pan African University Institute of Science and Technology Innovation, Nairobi	Characterization of circulating FMDV serotypes detected from cattle populations in eight geographical areas of Tanzania – student work	Contribution to understanding of FMD distribution in Tanzania and the student's graduation

Republic of Korea

Collaborators	Purpose of collaboration	Outcomes
National Center for Veterinary Diagnosis, Department of Animal Health, Hanoi, Vietnam	To carry out comparative studies of avian influenza virus and foot-and-mouth disease virus between Korea and Vietnam	Data and materials (2016-2024)
1. National Animal Health and Production Research Institute, General Directorate of Animal Health and Production Phnom Penh, Cambodia 2. National Animal Health Laboratory, Ban Sithan Nua, Luang Prabang Rd Km 2., Sikhottabong District, Vientiane Lao PDR	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)	Data and materials (2018-2022)
Ministry of Livestock, Fisheries & Rural Development Livestock Breeding and Veterinary Department or other relevant departments, Myanmar	Surveillance and Diagnosis improvement of foot-and-Mouth Disease in Myanmar (KOICA project)	Professional (Human resources) in FMD diagnosis in Myanmar (2018-2020)

Nigeria

Collaborators	Purpose of collaboration	Outcomes
Sciensano, Belgium	OIE Laboratory Twinning Program for capacity building	• Personnel training • Implementation of SOPs • Sample characterisation including phylogenetic analysis

Collaborators	Purpose of collaboration	Outcomes
ANSES, France	Rapid on site diagnosis of FMD and safe and cost-effective shipment of samples using lateral flow devices for laboratory diagnostics	Personnel training on the use and shipment of LFD and 20 samples shipped for further characterisation

Russia

Collaborators	Purpose of collaboration	Outcomes
Agreement on Transboundary Trade and Mitigation of Transboundary Animal Disease Spread Risk between China, Mongolia and Russia	Cooperation in case of dangerous animal disease emergency, including FMD	Joint FMD control, disease freedom
Immunity level assessment in animals vaccinated against FMD and identification of possible virus circulation in vaccination zones of Mongolia	Improvement of Mongolian livestock animal health status in relation to highly dangerous diseases, including FMD	FMD freedom in the zones where vaccination is practiced

South Africa

Collaborators	Purpose of collaboration	Outcomes
Dr B. Charleston – The Pirbright Institute Dr A. Jolles – Oregon State University	NSF-EID funded project investigating persistence of FMD in African buffalo	
Dr R. Reeve – University of Glasgow	Tracking the antigenic evolution of foot-and-mouth disease virus	Genetic basis of antigenic variation of SAT3 viruses
ARS, USDA, USA UVRI, Uganda Makerere University, mUganda ARC, SA	***Novel Countermeasures Designed for the Progressive Control of FMDV in Uganda*:** To conduct surveillance of FMDV in Uganda and identify the serotype, subtype and genetic makeup of FMDV circulating in Uganda. To carry out serological studies of FMDV circulating in Uganda in support of vaccine matching studies.	High seroprevalence for O (80%) and A (40%), SAT1 and SAT2 (15%) correlates with isolated and sequenced viruses from project. However exposure to SAT3 seen in 2 areas (4 herds) even though population seroprevalence is low. Wide distribution of antibodies to 4 serotypes across the country.

Thailand

Collaborators	Collaboration project	Outcomes
National Institute of Animal Health (NIAH), Japan	1) Research topic: FMDV Complete Genome Sequencing (continued) 2) Joint the Scientific Meeting on FMD research between RRL, Pakchong and NIAH, Kodaira. Japan, 15-16 Feb 2018 3) The 5th Thailand-Japan Joint Conference on Animal Health, 20-21 November 2018 at National Institute of Animal Health NARO, Tsukuba, Japan	- Scientific information on Molecular epidemiology of FMDV and genomic variation - Sharing and updating FMD information and researches - Exchange FMD viruses for research collaboration under the MOU and specific MTA - To interchange of researches friendship and cooperation on animal health
National Institute of Animal Health (NIAH), Japan	Validation of pen-side kit to distinguish serotype O, A and Asia 1	To improve and rapid detection of FMDV in field outbreak
Australian Animal Health Laboratory (AAHL) OIE-SRR, Bangkok	1) Enhancing of laboratory capacity on FMDV diagnosis, molecular epidemiology and others 2) On process drafting the project proposal	Enhance the diagnostic techniques and human resource development

Turkey

Collaborators	Collaboration project	Outcomes
Pakistan	Technical support for vaccine production	-

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	New ELISAs for FMD diagnosis

Collaborators	Collaborative project	Outcomes
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
INTA (Argentina)	Development of new vaccine matching tests for FMD	Generate validation data for field tests

USA

Collaborators	Collaborative project	Outcomes
APHIS-ARS-Uganda Gov. (DTRA)	FMD Surveillance	• >13,400 FMDV sera from 2014 up to early 2018 (+ and -) • 22 FMD isolates representing the main FMDV lineages in Uganda (topotypes of serotypes A, SAT1 and SAT2) isolated from probing samples, field samples collected between 2014-2017 • >300 genome sequences deposited in GenBank
CDC-APHIS/Select Agent Services (Federal Select Agent Program) (FADDL)	Validation BEI inactivation SOP	4 FMDV, 2 VSV, and 1 SVDV tested under different conditions of inactivation using BEI
IZSLER (FADDL)	SVV Monoclonal Ab production	• Virus was sent and amplified • Antigen preparation for inoculations
WRLFMD (FADDL)	SVV molecular epidemiology analysis and production of diagnostic reagents	• Virus was sent • Full length sequence and preliminary phylogeny was done • Production of reagents is pending
Interagency agreements US Department of Agriculture-APHIS with the US Department of Homeland Security (DHS)	Evaluation of a pen-side PCR assay for FMD Evaluation and Methods Comparison of the commercially available	All projects initiated in late 2018, outcomes are pending

Collaborators	Collaborative project	Outcomes
	version of the VMRD 3B ELISA kit with the Prionics PrioCheck ELISA kit currently in use at FADDL.	
	Evaluation of a swine FMD vaccine	
	Evaluation of a bovine FMD vaccine	
	Validation of a Pen-Side Multiplex Platform (PanNAT) for the detection of FMDv and BPSv.	
	Validation of a pen-side multiplex platform (MRI Global) for the detection of FMDv SVAv and SVDv.	

Appendix 1 - Details of clinical samples from field cases from countries in FMDV endemic regions tested during 2018

Laboratory	Samples from	Total	O	A	C	Asia 1	Sat 1	Sat 2	Sat 3	Untyped	NVD	Comments
ANSES	Guinea	21	6	-	-	-	-	-	-	2	13	
	Mauritania	20	8	-	-	-	-	-	-	7	5	
APQA	Republic of Korea	2	-	2	-	-	-	-	-	-	-	
BVI	Botswana	5	-	-	-	-	-	3	-	-	2	
	Malawi	3	-	-	-	-	-	1	-	-	2	
	Mozambique	12	-	-	-	-	-	-	-	-	12	
	Zambia	28	9	-	-	-	-	-	3	-	16	
	Zimbabwe	7	-	-	-	-	-	4	-	-	3	
FGBI ARRIAH	Mongolia	14	5	-	-	-	-	-	-	-	9	
	Pakistan	40	18	2	-	3	-	-	-	-	17	
	Russia	46	8	-	-	-	-	-	-	-	38	
FMD laboratory, Kenya	Kenya	77	38	2	-	-	2	2	-	-	33	
	South Sudan	38	1	-	-	-	-	-	-	-	37	
	Tanzania	150	5	46	-	-	29	28	-	-	42	
LVRI	China	139	37	1	-	-	-	-	-	60	41	
NAHDIC	Ethiopia	105	30	20	-	-	-	15	-	-	40	
NCFAD	Ghana	23	-	-	-	-	-	-	-	23	-	
NVRI	Nigeria	49	10	-	-	-	-	10	-	29	-	
OVI	Mozambique	1	-	-	-	-	-	-	1	-	-	
	South Africa	25	-	-	-	-	-	5	-	-	19	
PANAFTOSA	Colombia	23	11	-	-	-	-	-	-	10	2	
PD FMD	India	520	364	-	-	3	-	-	-	-	153	More than one sample per case were collected (from 169 cases, with 146 serotype O diagnosis)
RRLSEA	Lao PDR	24	3	4	-	-	-	-	-	-	17	
	Thailand	111	55	38	-	-	-	-	-	-	18	
ŞAP Institute	Turkey	491	323	1	-	-	-	-	-	33	134	
Sciensano	Nigeria	44	19	8	-	-	-	1	-	16	-	samples from late 2017, tested in 2018
SENASA	Argentina	9	-	-	-	-	-	-	-	-	9	
WRLFMD	Afghanistan	22	3	4	-	1	-	-	-	10	4	
	Algeria	2	2	-	-	-	-	-	-	-	-	
	Bhutan	11	4	3	-	-	-	-	-	2	2	
	Burkina Faso	18	7	-	-	-	-	-	-	5	6	
	Ethiopia	28	11	7	-	-	-	1	-	7	2	
	Gambia	2	2	-	-	-	-	-	-	-	-	
	Hong Kong	27	14	-	-	-	-	-	-	4	9	
	Iran	25	11	9	-	4	-	-	-	-	1	
	Israel	14	8	6	-	-	-	-	-	-	-	
	Kenya	21	3	3	-	-	1	1	-	11	2	
	Republic of Korea	5	-	2	-	-	-	-	-	3	-	

Laboratory	Samples from	Total	O	A	C	Asia 1	Sat 1	Sat 2	Sat 3	Untyped	NVD	Comments
	Laos	1	1	-	-	-	-	-	-	-	-	
	Malaysia	12	11	-	-	-	-	-	-	-	1	
	Mongolia	24	17	1	-	-	-	-	-	4	3	One sample positive for serotypes O and A
	Nepal	18	3	-	-	8	-	-	-	2	5	
	Palestine	12	12	-	-	-	-	-	-	-	-	
	Senegal	11	6	-	-	-	-	-	-	3	2	
	Sierra Leone	34	1	-	-	-	-	-	-	2	31	
	South Sudan	29	-	-	-	-	-	-	-	7	22	
	Sri Lanka	16	9	-	-	-	-	-	-	2	5	
	Sudan	38	6	13	-	-	-	5	-	6	8	
	Swaziland	3	-	-	-	-	-	-	-	-	3	
	Thailand	19	8	8	-	-	-	-	-	3	-	
	Vietnam	40	20	13	-	-	-	-	-	6	1	
	Zambia	3	3	-	-	-	-	-	-	-	-	

* Additionally FADDL tested 13,400 serum and 2,000 oropharyngeal fluid samples collected from Uganda between 2014 and 2018.

Appendix 2 - Vaccine matching studies undertaken by Network partners during 2018

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.

Brazil

Virus Strain	EPP "O" VN
O/Boyaca/Colombia/2018 (Field isolate)	79.03 **
O1 Campos Br/58 (Vaccine strain)	98.20

*Percentage of expectancy of protection (EPP)

**Use of Panaftosa reference cattle sera panel - standard panel serum (n=32) composed of cattle sera collected 30 days post booster vaccination (DPR), with a bivalent commercial vaccine (O1 Campos Br/58 and A 24 Cruzeiro), were analyzed by virus neutralization against vaccine and field strains.

China

Field isolate	Lineage	Animal	Vaccine strain O/MYA98/BY/2010	Methods used
17016	Mya-98	pig	0.25*	VNT
18001	CATHAY	pig	0.13*	VNT
18035	PanAsia	cattle	0.50	VNT
18054-1	PanAsia	cattle	0.35	VNT
18056	PanAsia	cattle	0.50	VNT
18053	Ind-2001	cattle	0.5	VNT
18012	Mya-98	cattle	1	VNT

* The heterologous challenge experiments have been performed and the results showed that the O/MYA98/BY/2010 vaccine could provide protection against these prevalent O/Mya 98 and O/Cathay field isolates.

Ethiopia

Field Isolate	Vaccine strain							
	A IRN/2005	A TUR/20/2006	A22 IRQ/24/64	O33039	O Manisa	OtUR5/09	SAT2 ERI	SAT2 ZIM
A/ETH/2/2018	0.29	0	0.29					
A/ETH/6/2018	0.45	0	0.45					
O/ETH/13//20018				0.34	0.21	0.38		
O/ETH/16/2018				0.21	0.15	0.31		
SAT 2/ETH/11/2018							0.58	0.35

* Vaccine matching completed at WRLFMD

India

Samples	Name of Vaccine strain	Result
Field isolates (n= 50)	O IND R2/1975	44 out of the 50 isolates having r-value > 0.3

Kenya

Name of Field isolate	Vaccine strain	
	O K77/78	Test Used
K27/17	0.1	VNT
K34/17	0.3	VNT
K40/17	0.1	VNT
K42/17	0.1	VNT
NBG 11*	0.3	VNT

* South Sudan Isolate

Republic of Korea

VNT	Type A Vaccine strains							
	A Iran/05	A MAY97	A Tur 20/06	A/GVII	A22 IRAQ	A24 Cruz(1)	A24 Cruz(2)	A Zabaikalsky
A/SKR/5/2018 (WRLFMD)	0.45	0.12	0.00	0.47	0.43	0.19	0.35	-
A/SKR/2018 (APQA)	-	-	-	-	0.48-0.78	-	-	0.77-1.00

(1) PANAFTOSA vaccine,

(2) BI Merial vaccine

Russia

Serotype O

FMDV isolate	Vaccine strain						
	O1 Manisa	O Russia/ 2000 (PanAsia)	O PanAsia2	O TWN/ 3/97	O Russia/ SEA/2010	O Russia/ 2012 (PanAsia)	O Russia/ SEA/2014
O/Zabaikalsky/2018	0.37	0.29	0.46	0.08	0.19	0.58	0.21
O/Mongolia/03/2018	0.51	0.18	0.11	0.006		0.72	0.15
O/Pakistan (PK)/18/2	0.19	0.2	0.53	-	-	0.2	-
O/PK/18/08	0.2	0.2	0.72	-	-	0.2	-
O/PK/18/21	0.2	0.2	0.63	-	-	0.13	-

O/PK/18/25	0.2	0.15	0.41	-	-	0.12	-
O/PK/18/32	0.22	0.2	0.39	-	-	0.11	-
O/PK/18/40	0.2	0.2	0.83	-	-	0.12	-

Serotype A

FMDV isolate	Vaccine strain			
	A22 550	A/IRN/97	A/TUR/06	A/RUS/2013 (Sea-97)
A/PK/18/23	0.28	0.11	0.33	0.19
A/PK/18/38	0.38	0.14	0.64	0.26

Serotype Asia 1

FMDV isolate	Vaccine Strain	
	Asia1 Shamir 3/89	Asia1 Sindh/08
Asia1 /PK/18/14	0.09	0.3
Asia1 /PK/18/35	0.26	0.38
Asia1 /PK/18/36	0.23	0.7

Thailand

Serotype O

Field strain	r-value Vaccine strain O/189/87 (Thai vaccine strain)			
	by LP ELISA	by VNT	Topotype/strain	Remarks
TA I139/17	1.0	nd	PanAsia	Good match
TAI 1/18	0.69	nd	PanAsia	Good match
TAI 6/18	0.75	1.0	PanAsia	Good match
TAI 7/18	1.0	nd	IND2001e	Good match
TAI 10/18	1.0	nd	IND2001e	Good match
TAI 12/18	1.0	nd	nd	Good match
TAI 14/18	1.0	nd	IND2001e	Good match
TAI 17/18	1.0	nd	nd	Good match
TAI 20/18	1.0	1.0	IND2001e	Good match
TAI 30/18	1.0	1.0	IND2001e	Good match
TAI 39/18	1.0	1.0	IND2001e	Good match
TAI 42/18	1.0	1.0	PanAsia	Good match
TAI 43/18	1.0	nd	PanAsia	Good match
TAI 53-1/18	1.0	nd	nd	Good match
TAI 58/18	1.0	1.0	nd	Good match
Lao PDR 9/18	1.0	1.0	PanAsia	Good match

Serotype A

Country	No. of Samples	r-value by LP ELISA Serotype A/Thai Vaccine Strain						
		A118/87		A/Sakolnakom/97		A/Lopburi/2012		
		0.2 - 0.39	≥ 0.4	0.2 - 0.39	≥ 0.4	< 0.19	0.2 - 0.39	≥ 0.4
Thailand	8	Low binding reaction (n = 8)		Low binding reaction (n = 4)	4 *	-	-	8
Thailand	17	ND		5	12	-	1	16
Lao PDR	3	ND		-	3	-	-	3

* 1 sample gave r-value> 0.3 by VNT using A/Sakolnakorn/97 as vaccine strain

Turkey

	Vaccine strain	
	O/TUR 07	O/TUR 16
OTUR/35/2018 *[O/PanAsia-2/QOM-15]*	1	0.77

	Vaccine strain			
	A/TUR 15 (G-VII)	A/TUR 16 (G-VII)	A22 Iraq	A/TUR 06
A/TUR/236/2017 *[A/Asia/G-VII]*	0.36	0.07		
A/TUR/205/2017 *[A/Asia/G-VII]*	0.19	0.390		
A/TUR/44/2017 *[A/Asia/G-VII]*	n.d.	0.81		
A/ASIA/Iran 05 *[Vaccine Strain]*			0.294	
A/ASIA/A22Iraq *[Vaccine Strain]*	0.089			1

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	O1 Manisa	O/TUR/5/2009
HKN/8/2017	O	CATHAY	-	0.09	0.15	0.13
HKN/11/2017	O	CATHAY	-	0.09	0.15	0.14
HKN/12/2017	O	CATHAY	-	0.1	0.07	0.12
HKN/4/2018	O	CATHAY	-	0.11	0.1	0.14
HKN/5/2018	O	CATHAY	-	0.13	0.14	0.13
HKN/13/2018	O	CATHAY	-	0.11	0.09	0.11
VIT/21/2017	O	CATHAY	-	0.17	0.11	0.2
KEN/4/2017	O	EA-2		0.25	0.41	0.56
KEN/6/2017	O	EA-2		0.32	0.41	0.5
KEN/11/2017	O	EA-2	-	1	1	0.81
KEN/15/2017	O	EA-2	-	0.5	0.52	0.47
ZAM/3/2018	O	EA-2	-	0.4	0.28	0.37
ETH/13/2018	O	EA-3		0.34	0.21	0.38
ISR/15/2017	O	EA-3		0.52	0.47	0.58
ISR/18/2017	O	EA-3		0.62	0.42	0.5
PAT/11/2017	O	EA-3		0.6	0.62	0.93
PAT/22/2017	O	EA-3		0.4	0.37	0.63
ALG/1/2018	O	EA-3	-	0.51	0.37	0.46
ALG/2/2018	O	EA-3	-	0.45	0.34	0.59
ETH/16/2018	O	EA-3	-	0.21	0.15	0.31
GAM/1/2018	O	EA-3	-	0.45	0.3	0.52
SEN/2/2018	O	EA-3	-	0.38	0.3	0.49
SEN/11/2018	O	EA-3	-	0.63	0.39	0.54
SUD/3/2017	O	EA-3	-	0.49	0.28	0.45

Sample	Serotype	Topotype	Strain	O 3039	O1 Manisa	O/TUR/5/2009
SUD/15/2017	O	EA-3	-	0.25	0.26	0.49
NEP/33/2017	O	ME-SA	Ind-2001d	0.35	0.23	0.76
NEP/35/2017	O	ME-SA	Ind-2001d	0.35	0.26	0.56
SRL/7/2016	O	ME-SA	Ind-2001d	0.46	0.51	0.87
SRL/3/2017	O	ME-SA	Ind-2001d	0.49	0.71	0.66
SRL/5/2018	O	ME-SA	Ind-2001d	0.13	0.07	0.32
BHU/24/2017	O	ME-SA	Ind-2001e	0.48	0.48	0.55
BHU/2/2018	O	ME-SA	Ind-2001e	0.29	0.42	0.6
MAY/1/2018	O	ME-SA	Ind-2001e	0.5	0.4	0.4
MAY/5/2018	O	ME-SA	Ind-2001e	0.6	0.4	0.72
MOG/2/2018	O	ME-SA	Ind-2001e	0.55	0.37	0.66
SRL/1/2018	O	ME-SA	Ind-2001e	0.32	0.35	0.47
VIT/9/2017	O	ME-SA	Ind-2001e	0.35	0.26	0.63
MOG/10/2018	O	ME-SA	PanAsia	0.62	0.44	0.51
VIT/1/2018	O	ME-SA	PanAsia	0.68	0.44	1
AFG/44/2017	O	ME-SA	PanAsia-2	0.44	0.36	0.65
AFG/52/2017	O	ME-SA	PanAsia-2	0.36	0.31	0.42
IRN/1/2018	O	ME-SA	PanAsia-2	0.58	0.37	0.34
IRN/12/2018	O	ME-SA	PanAsia-2	0.85	0.48	0.63
ISR/2/2018	O	ME-SA	PanAsia-2	0.32	0.3	0.48
ISR/4/2018	O	ME-SA	PanAsia-2	0.18	0.24	0.5
PAK/10/2016	O	ME-SA	PanAsia-2	0	0	0
MAY/12/2016	O	SEA	Mya-98	0.56	0.35	0.59
MOG/7/2018	O	SEA	Mya-98	0.4	0.19	0.46
VIT/5/2017	O	SEA	Mya-98	0.22	0.1	0.34

Sample	Serotype	Topotype	Strain	A/IRN/05	A/TUR/20/06	A22 IRAQ	A/ERI/3/98	A/ASIA/GVII	A MAY 97	A24 Cruz Merial	A24 Cruz PANAFTOSA
ETH/2/2018	A	AFRICA	G-I	0.29	0.02	0.29					
ETH/6/2018	A	AFRICA	G-I	0.45	0.02	0.45					
KEN/14/2017	A	AFRICA	G-I	0.05	0	0.21	0.2				
KEN/17/2017	A	AFRICA	G-I	0.03	0	0.3	0.1				
SUD/9/2018	A	AFRICA	G-IV	0.06	0.02	0.17	0.39				
SUD/10/2018	A	AFRICA	G-IV	0.2	0.12	0.25	0.26				
BHU/26/2017	A	ASIA	G-VII	0.04	0	0.17		0.78			
BHU/28/2017	A	ASIA	G-VII	0.05	0	0.11		0.79			
IRN/25/2018	A	ASIA	G-VII	0.01	0.01	0.14		0.71			
ISR/9/2017	A	ASIA	G-VII	0	0	0.11					
ISR/13/2017	A	ASIA	G-VII	0	0	0.24					
AFG/50/2017	A	ASIA	Iran-05	0.1	0.36	0.2		0			
IRN/10/2018	A	ASIA	Iran-05	0.48	0.22	0.45		0.02			
IRN/23/2018	A	ASIA	Iran-05	0.19	0.36	0.33		0.02			
PAK/25/2016	A	ASIA	Iran-05	0.26	0.17	0.33					
SKR/5/2018	A	ASIA	Sea-97	0.45	0.01	0.43		0.47	0.12	0.35	0.19
VIT/6/2017	A	ASIA	Sea-97	0.52	0.14	0.87	0.14				
VIT/19/2017	A	ASIA	Sea-97	0.06	0.13	0.36	0.23				

Sample	Serotype	Topotype	Strain	Asia 1 Shamir
AFG/56/2017	Asia-1	ASIA	Sindh-08	0.33
IRN/7/2018	Asia 1	ASIA	Sindh-08	0.48
IRN/19/2018	Asia 1	ASIA	Sindh-08	0.39
NEP/42/2017	Asia-1	ASIA	G-VIII	0.83
NEP/45/2017	Asia-1	ASIA	G-VIII	0.51

Sample	Serotype	Topotype	Strain	SAT 1/RHO/12/78
KEN/8/2017	SAT 1	I (NWZ)	-	0.25

Sample	Serotype	Topotype	Strain	SAT 2 ERI	SAT 2 ZIM
ETH/11/2018	SAT 2	VII	-	0.58	0.35
SUD/14/2017	SAT 2	VII	Alx-12	0.76	0.32
KEN/19/2017	SAT 2	IV	-	0.5	0.31

USA

2dVNT	Serum from Bovine Vaccinated with											
FMDV strain	A22 IRQ	A24 Cruz	A IRN 05 / A Turkey 06	A IRN 99	A SA 95	A May 97	A ARG 01	O1 Campos	O ECU 2010	O1 Manisa	SAT2	TOTAL
A22 IRQ-bank	4	1	1	1	2	4	1					14
A24 Cruz	4	1	1	1	2	4	1	1		1		16
A IRN 05/ A Turkey 06	2	1	1	1	2	2	1					10
A IRN 99	2	1	1	1	2	2	1					10
A SA 95	4	1	1	1	8	4	1					20
A May 97	4	1	1	1	3	3	1					14
A Arg 01	2	1	1	1	2	2	1					10
O1 Campos								21	4	3		28
O ECU 2010								21	4	3		28
O Taiwan								1		1		2
O1 Manisa								15		1		16

A Egypt	2	2		2	2							8
O Egypt										4		4
SAT-2 Egypt											2	2
TOTAL	24	9	7	9	23	21	7	59	8	13	2	

Appendix 3 - Nucleotide sequence analysis

FMDV nucleotide sequence data for phylogenetic analysis (1363 sequences)

** From FADDL repository*

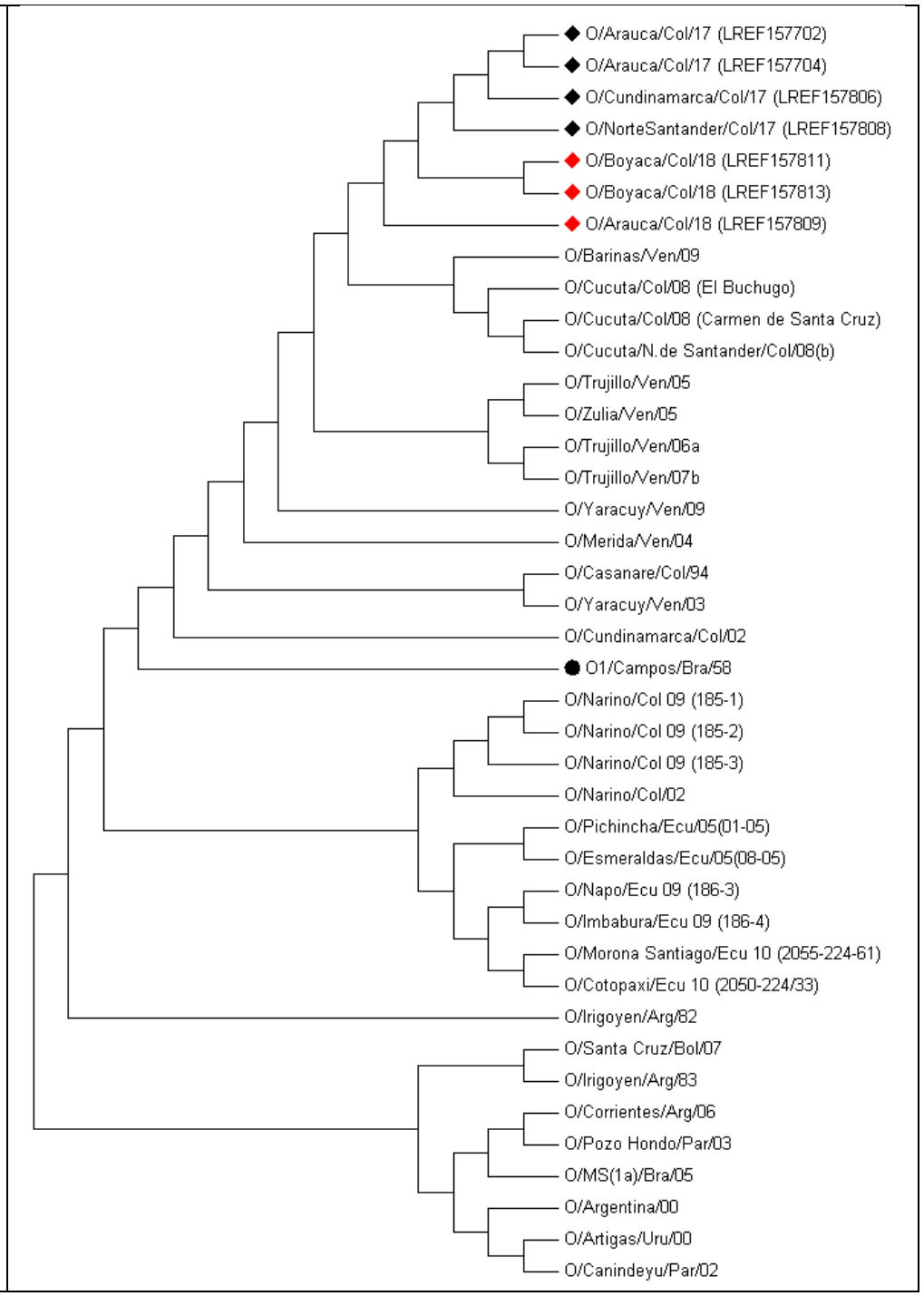
† North American FMD Vaccine Bank

Laboratory	Samples from	Region	Total	O	A	C	ASIA-1	SAT 1	SAT 2	SAT 3	FMDV GD
ANSES	Guinea	VP1	4	4							
	Mauritania	VP1	7	7							
APQA	Republic of Korea	VP1	2		2						
		capsid	2		2						
		Complete genome	2		2						
BVI	Botswana	VP1	4						3		
	Malawi	VP1	3						1		
	Zambia	VP1	18	9						3	
	Zimbabwe	VP1	5						4		
FADDL	USA *	Complete Genome	129	33	42						8
	Colombia 2017	Complete Genome	4	4							
	Uganda	Complete Genome	8	5							
		P1	47	40							
		VP1	83	67							
	NAFMDVB†	Complete Genome	19	4	9		12	10	14	9	1
	Vietnam	VP1	274	171	103				2	1	8
FGBI ARRIAH	Russia	VP1	8	8							
	Mongolia	VP1	11	11							
	Pakistan	VP1	33	25	3		5				
FMD Lab., Kenya	Kenya	VP1	11	6	3			1	1		
ICAR	India	VP1	84	84							
LVRI	China	VP1	95	90	5						
	China	Complete Genome	7	7							
NAHDIC	Ethiopia		19	11	7				1		
OVI	South Africa	VP1	3						3		
PANAFTOSA	Colombia	VP1	5	5							

Laboratory	Samples from	Region	Total	O	A	C	ASIA-1	SAT 1	SAT 2	SAT 3	FMDV GD
RRLSEA	Thailand	VP1	81	34	47						
	PDR Lao	VP1	6	2	4						
ŞAP Institute	Turkey	VP1	116	115	1						
Sciensano	Nigeria	VP1	12	6	5				1		
WRLFMD	Afghanistan	VP1	8	3	4		1				
	Algeria	VP1	2	2							
	Bhutan	VP1	7	4	3						
	Burkina Faso	VP1	7	7							
	Ethiopia	VP1	19	11	7				1		
	Gambia	VP1	2	2							
	Hong Kong	VP1	14	14							
	Iran	VP1	25	11	10		4				
	Israel	VP1	14	8	6						
	Kenya	VP1	12	6	3			2	1		
	Korea, Republic Of (South)	VP1	2		2						
	Laos	VP1	1	1							
	Malaysia	VP1	11	11							
	Mongolia	VP1	18	17	1						
	Nepal	VP1	11	3			8				
	Palestine, State of	VP1	12	12							
	Senegal	VP1	6	6							
	Sierra Leone	VP1	1	1							
	Sri Lanka	VP1	9	9							
	Sudan	VP1	25	7	13				5		
	Thailand	VP1	16	8	8						
	Vietnam	VP1	33	20	13						
	Zambia	VP1	6	3	3						

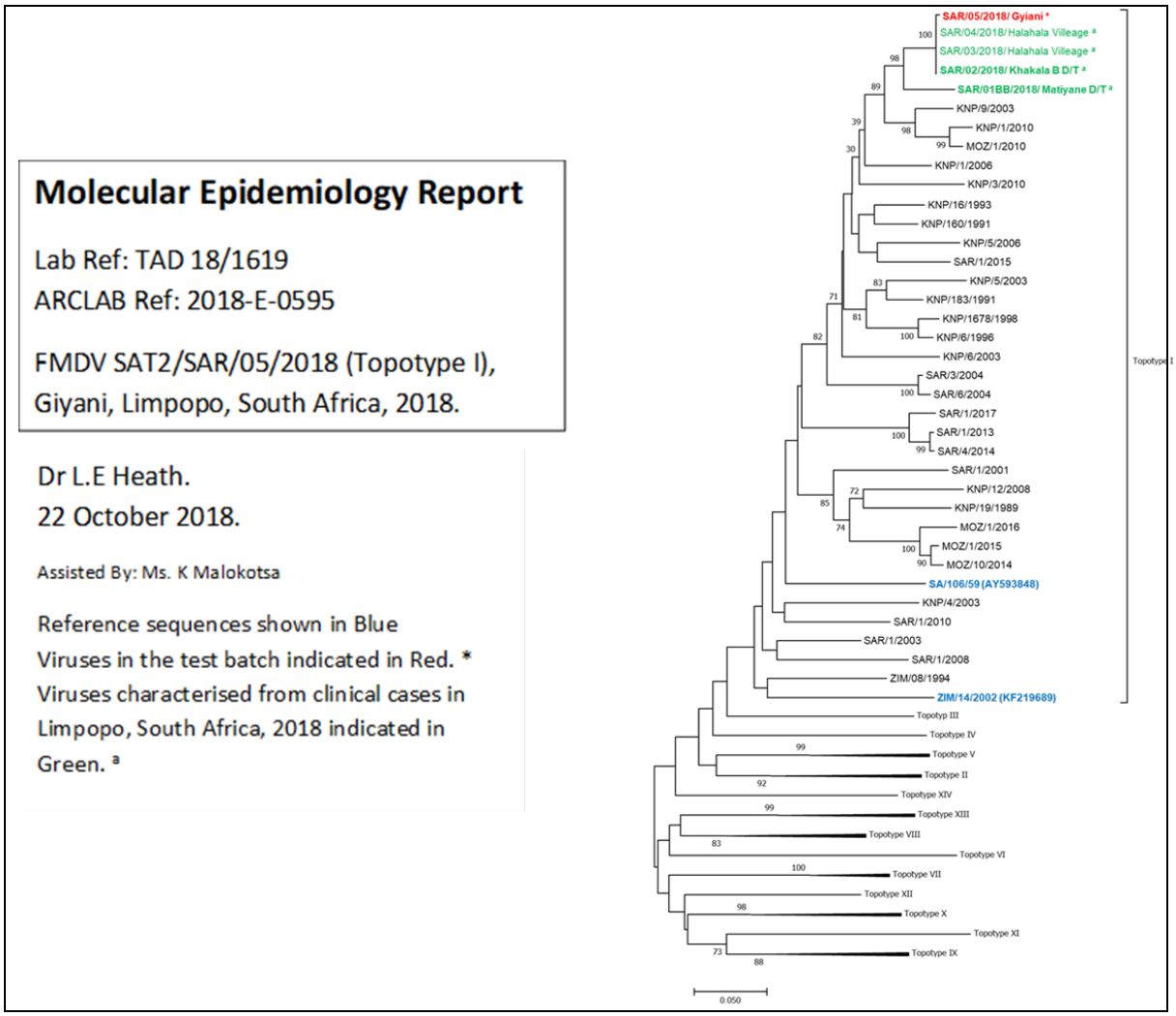
Appendix 4 - Selected phylogenetic trees for 2018

Phylogenetic tree from PANAFTOSA, Brazil:

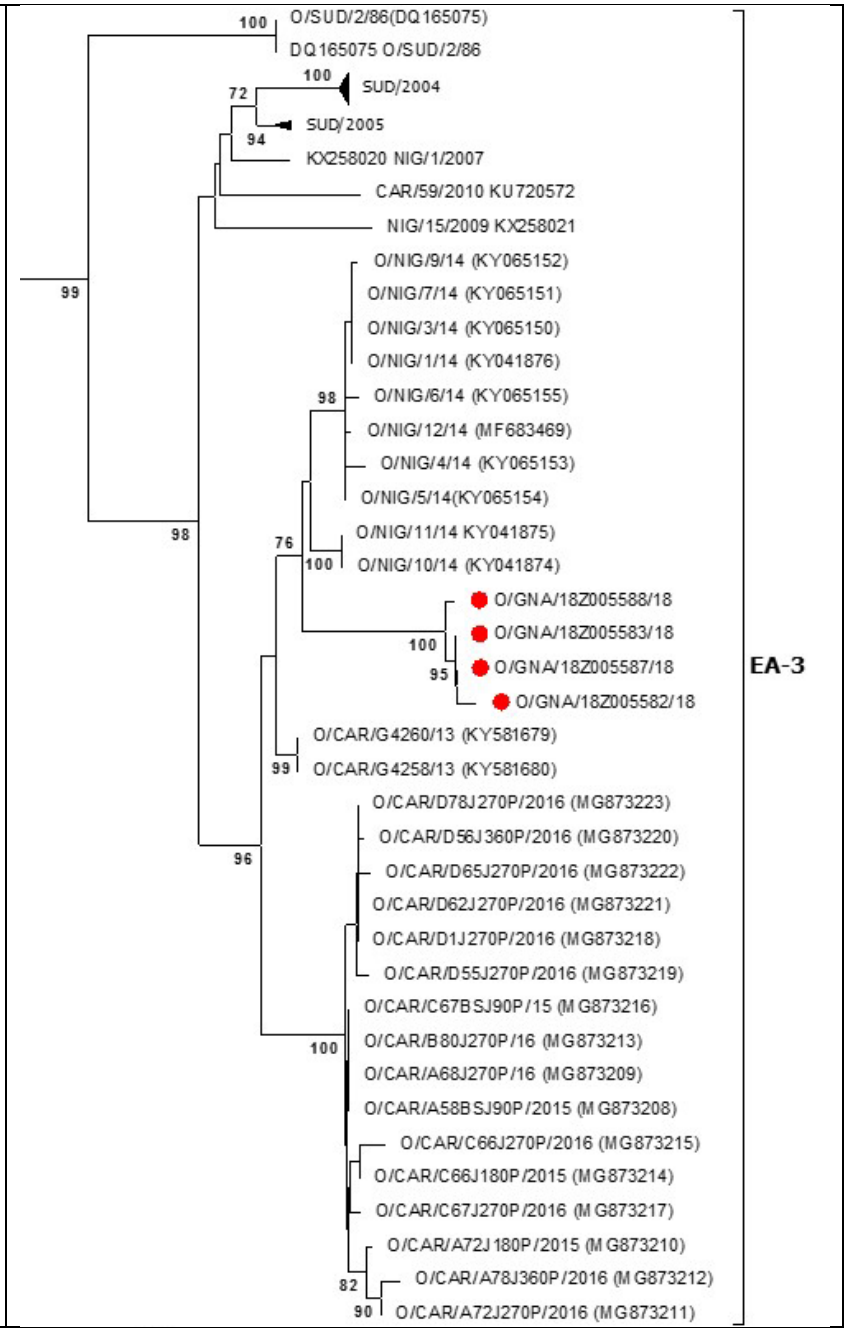
FMDV type O in Colombia, 2018	

Phylogenetic tree from OVI, South Africa

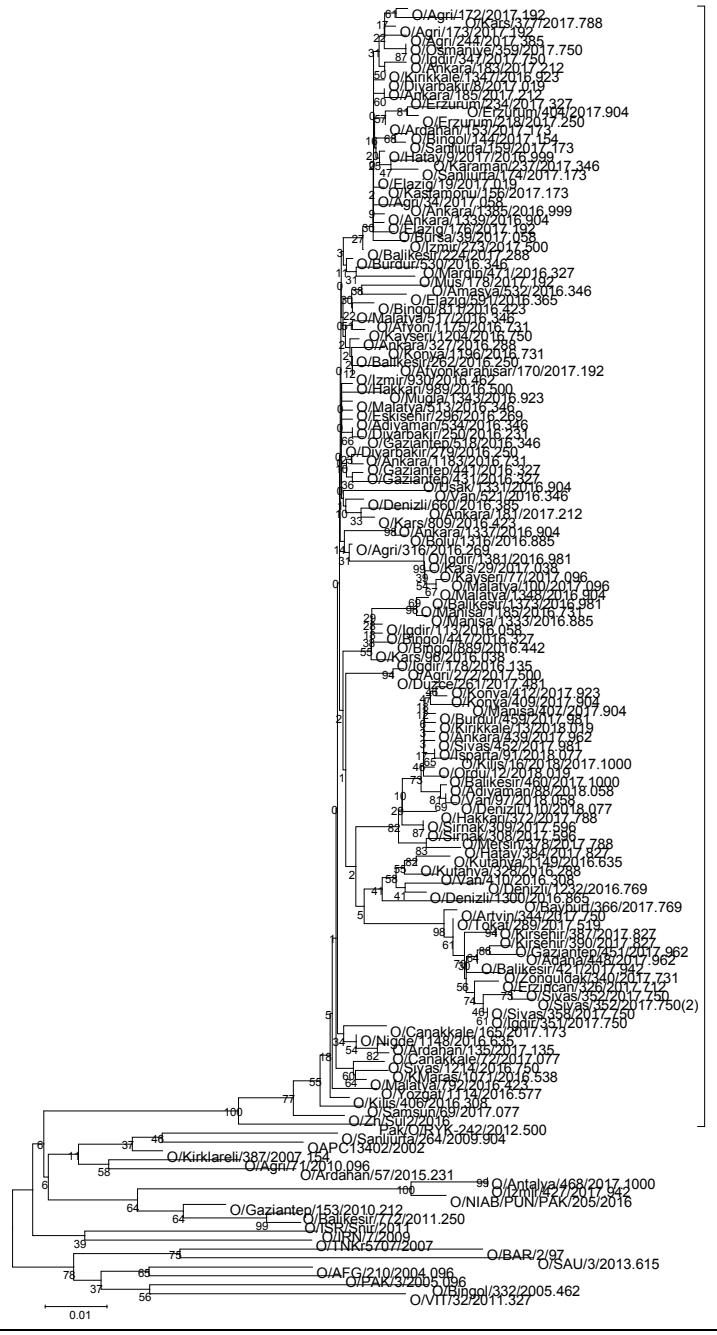
SAT 2 – 2018 in South Africa



Phylogenetic tree from ANSES, France:

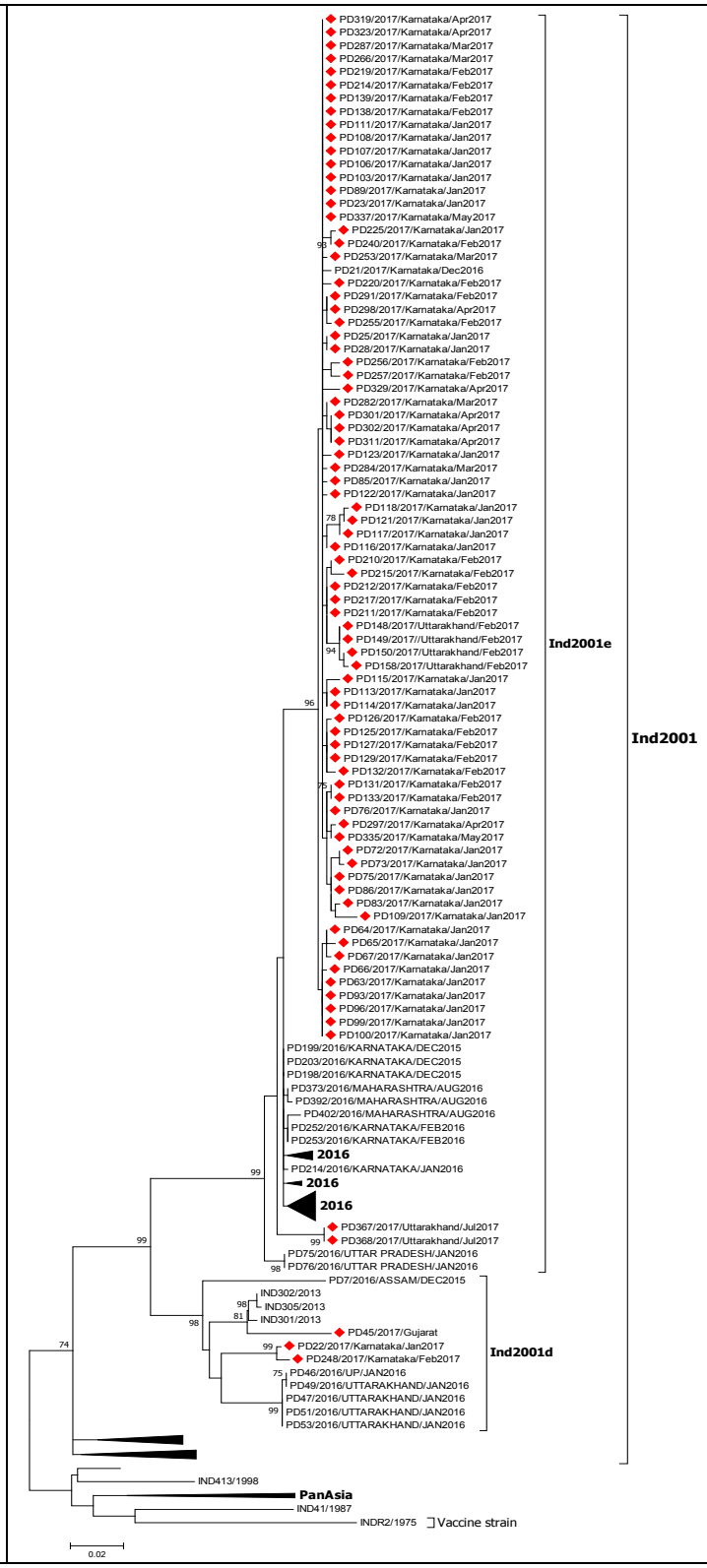
FMDV type O in Guinea, 2018	

Phylogenetic tree from SAP Institute, Turkey

FMDV type O in Turkey, 2018 **(O/ME-SA/PanAsia-2)**	

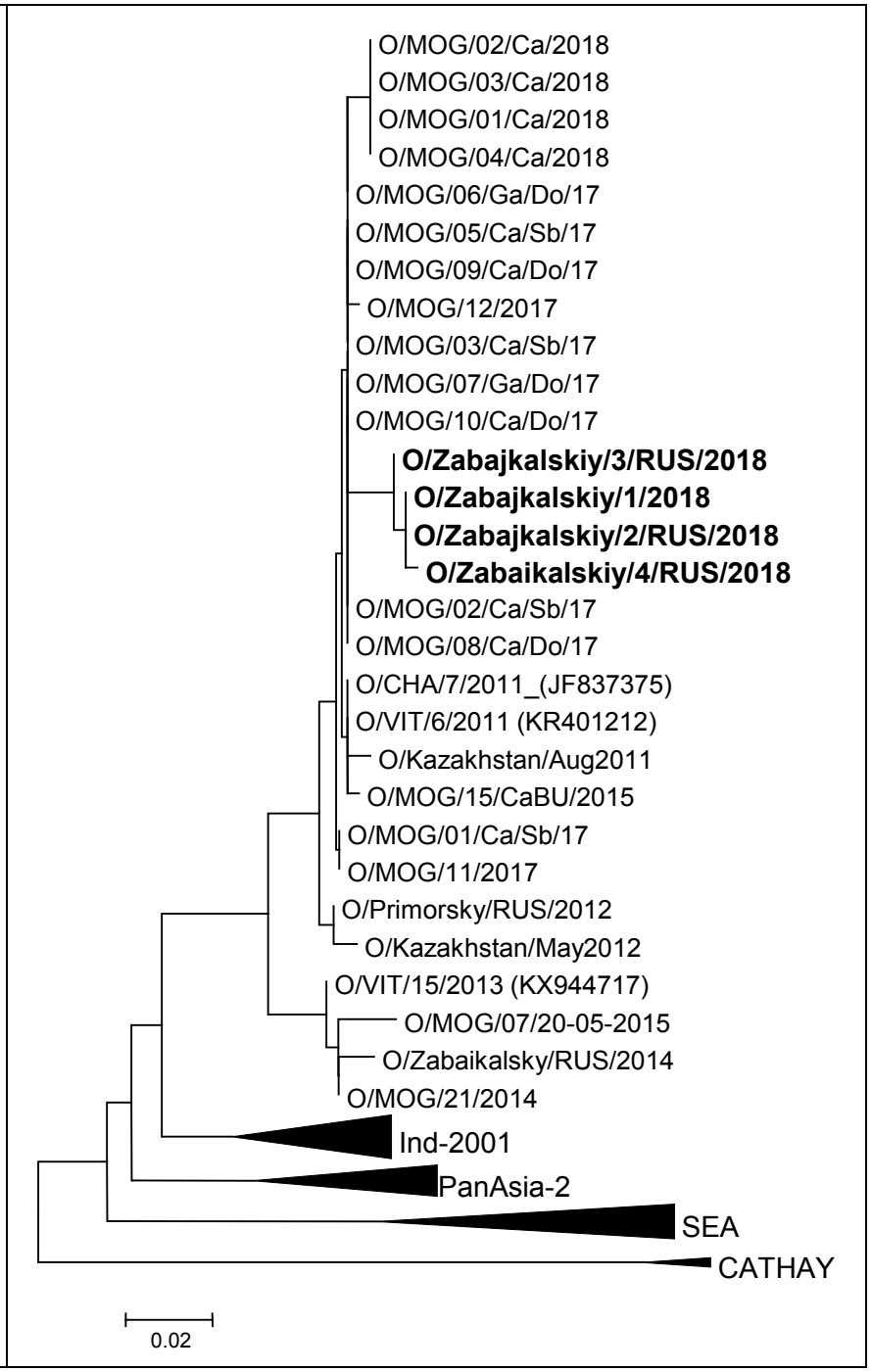
Phylogenetic tree from ICAR-DFMD, India

FMDV type O in India
(O/ME-SA/Ind-2001)

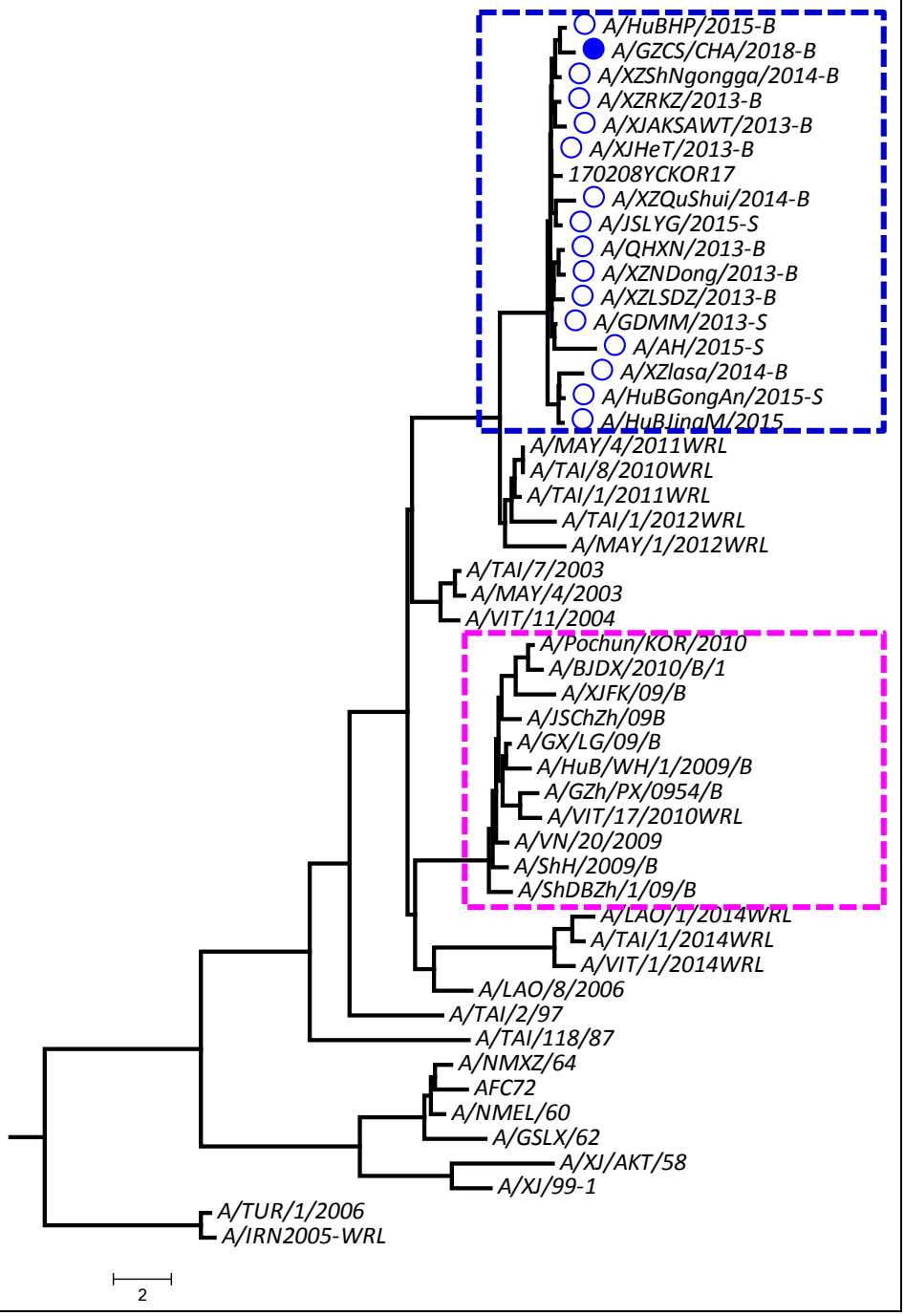


Phylogenetic tree from FGBI-ARRIAH, Russia

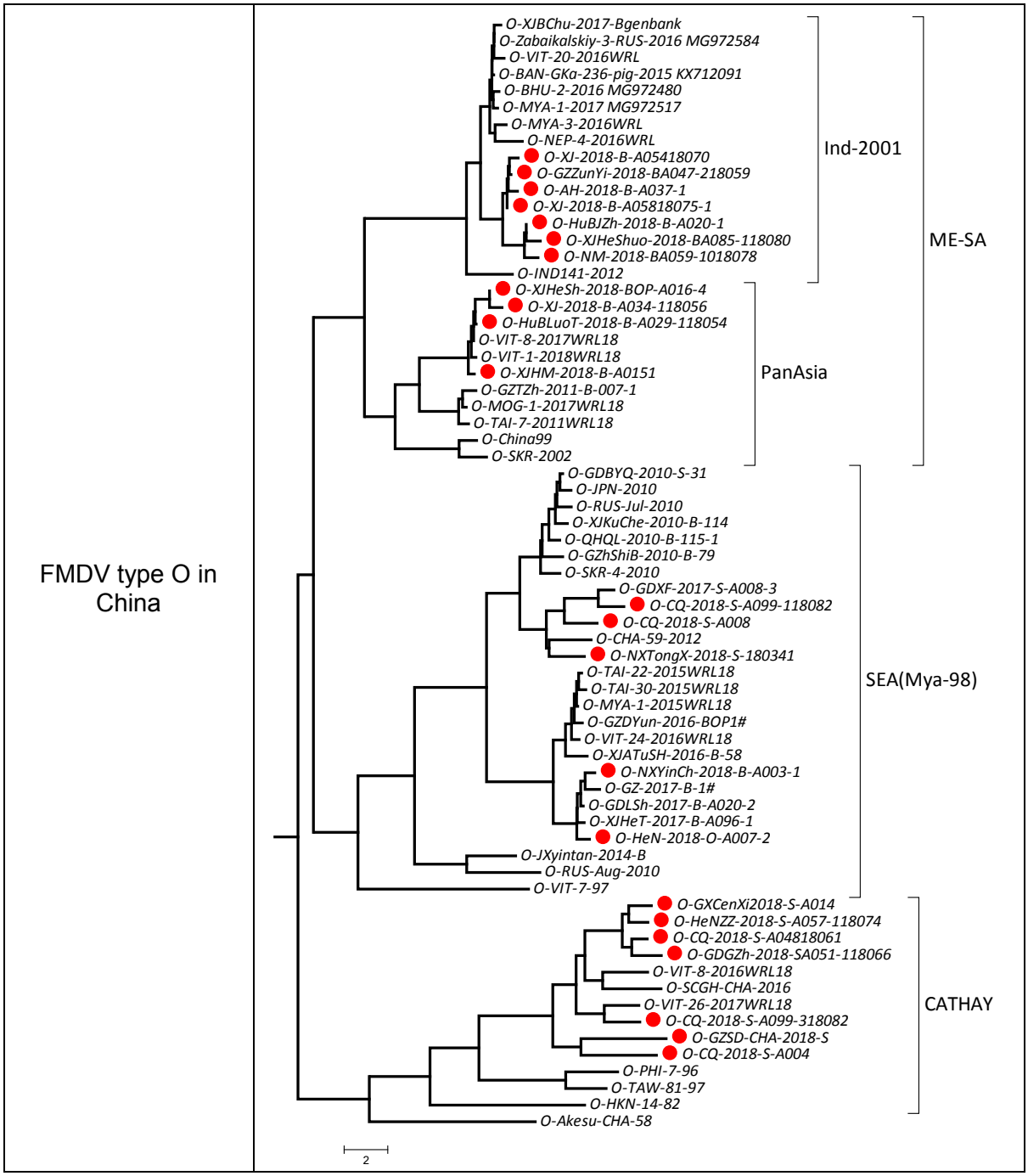
FMDV type O in Russia **(O/ME-SA/PanAsia)**



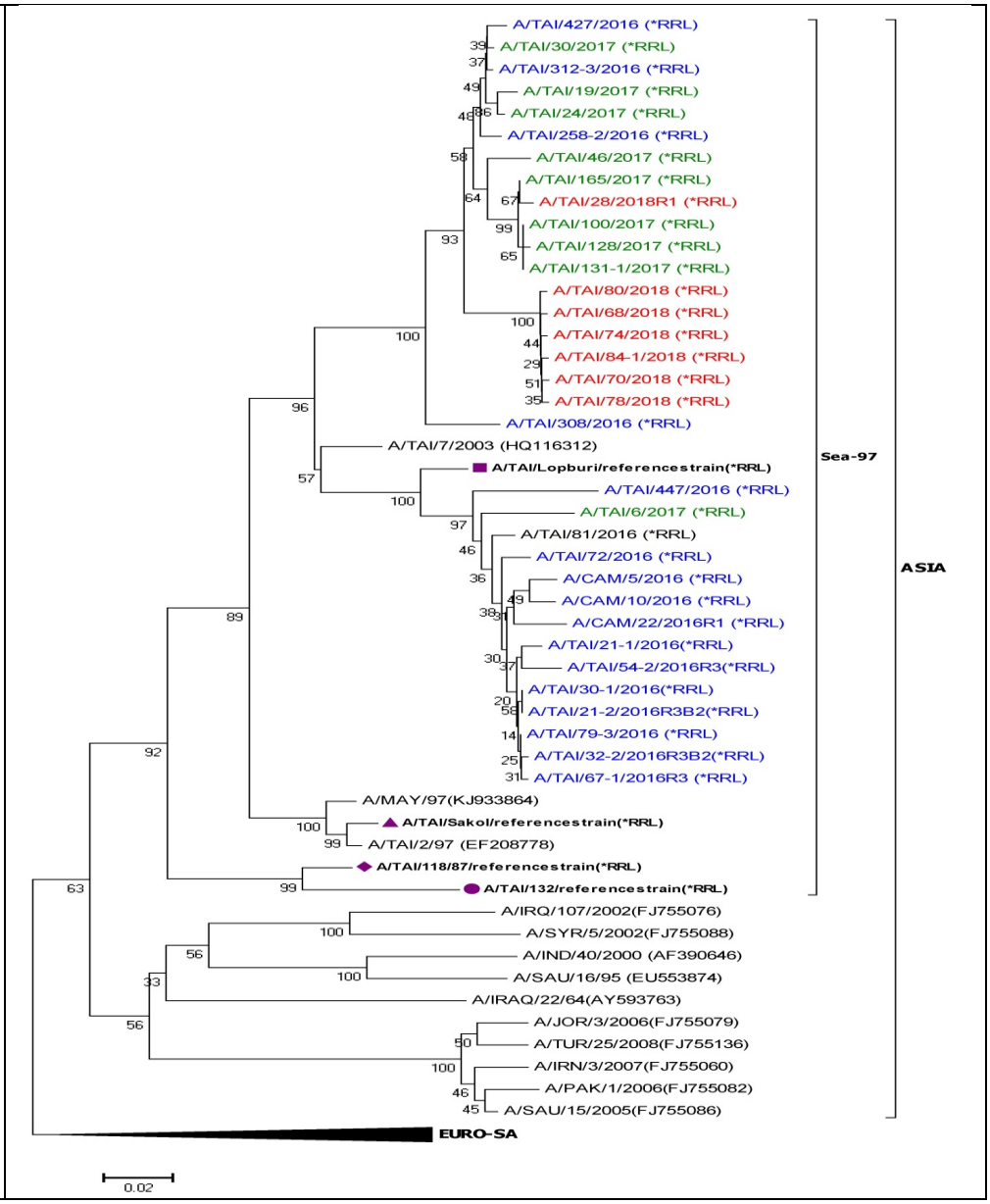
Phylogenetic tree from LVRI, China

FMDV type A in China	

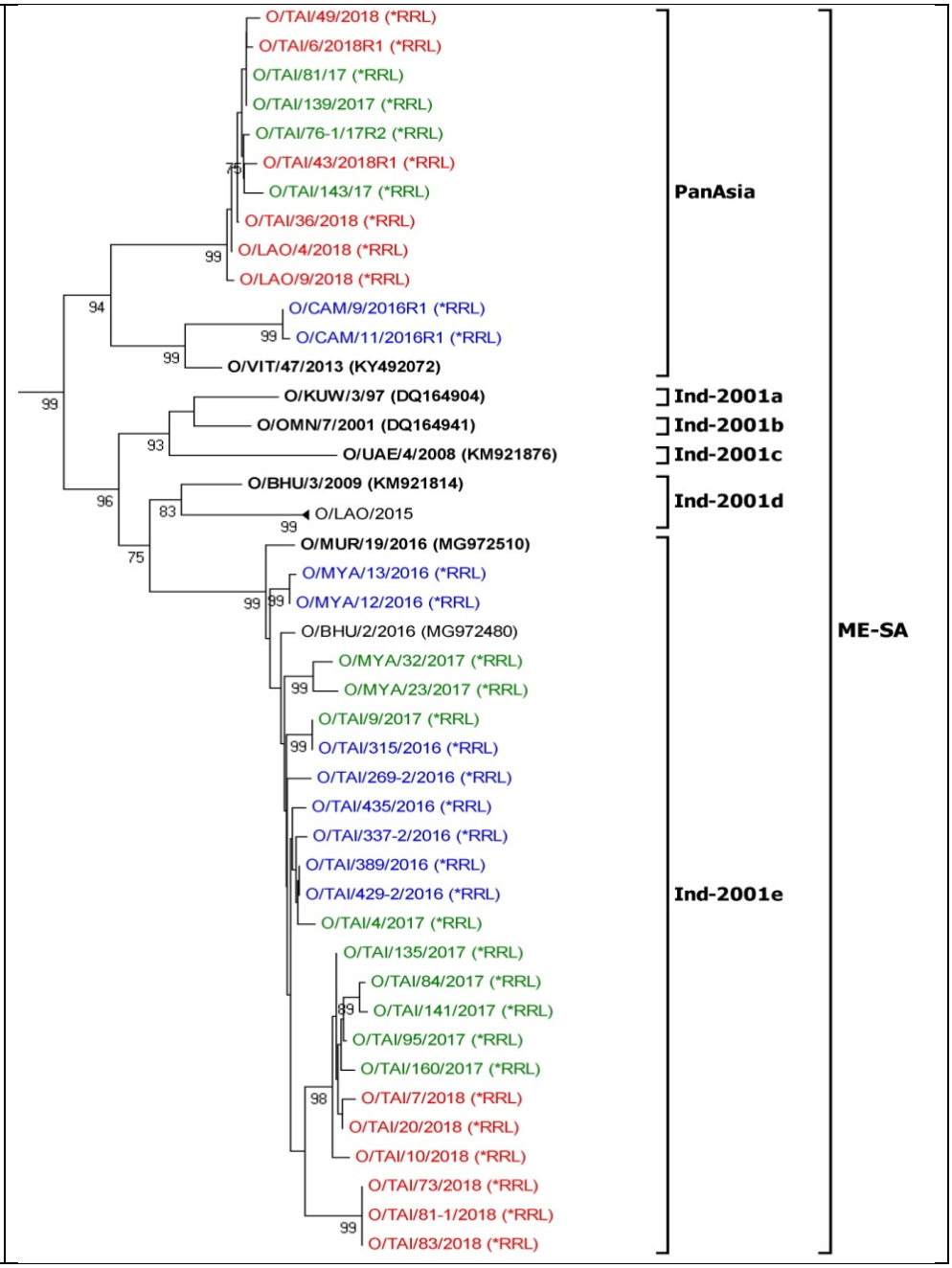
Phylogenetic tree from LVRI, China



Phylogenetic tree from RRLSEA, Pakchong, Thailand

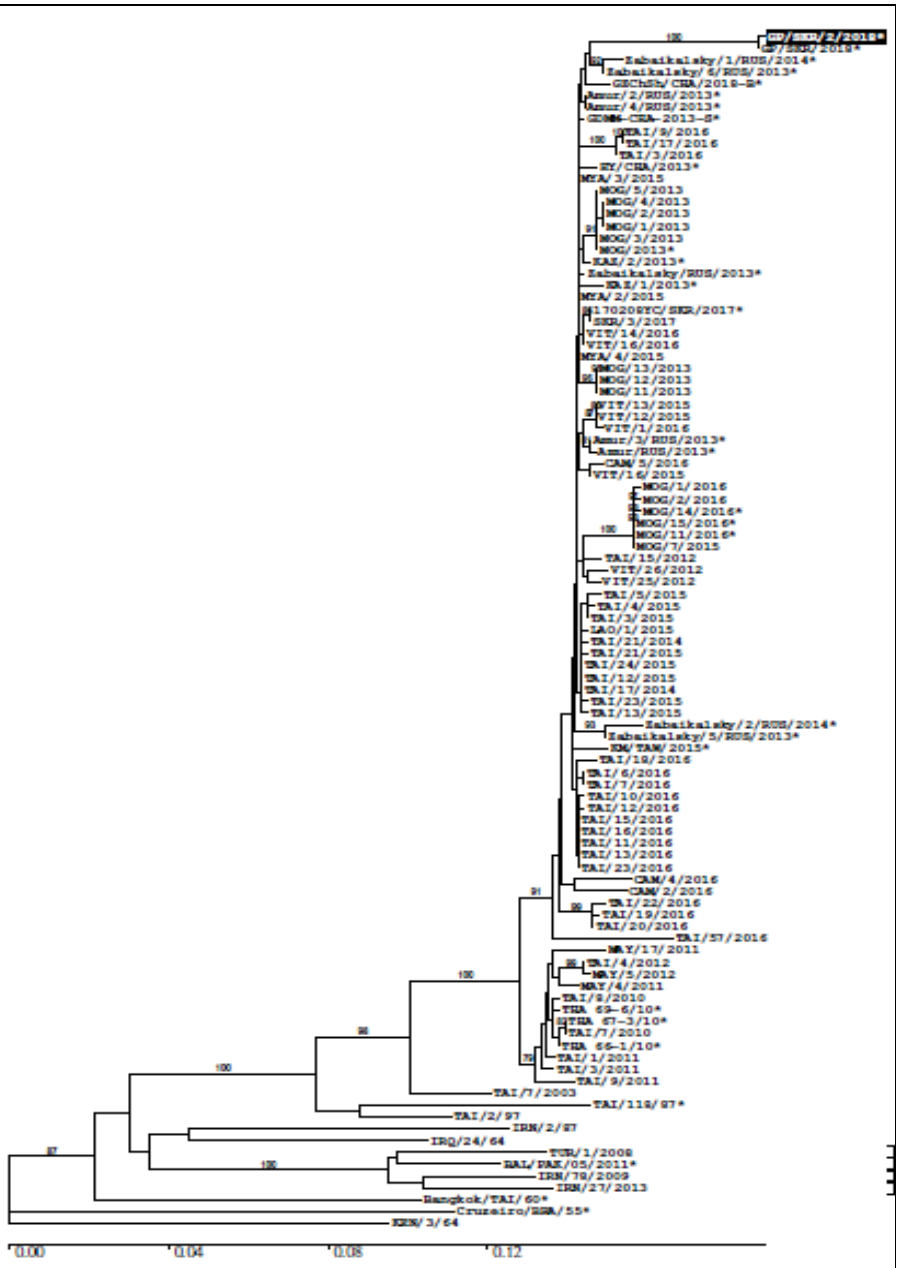
FMDV type A in Southeast Asia	

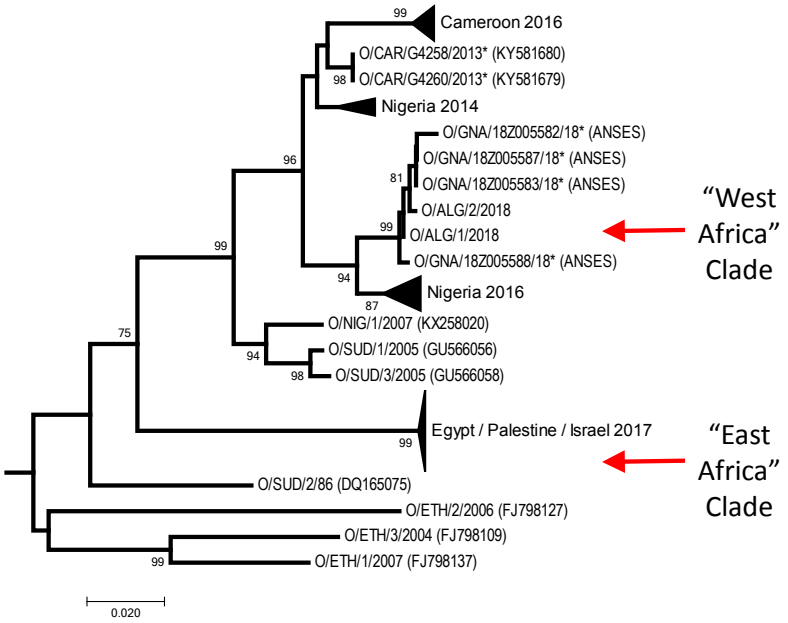
Phylogenetic tree from RRLSEA, Pakchong, Thailand

FMDV type O in Southeast Asia	

Phylogenetic trees from WRLFMD, UK

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

Republic of Korea A/ ASIA/Sea-97	

Serotype O (O/EA-3) distinct clades in West and East Africa	

Serotype O from Pakistan (new antigenic variant) Isolates PAK/4/2017 and PAK/10/2016	

Appendix 5 - The 13th Annual Meeting of the OIE/FAO FMD Reference Laboratories Network
7th – 8th November 2018
Gorse Hill Hotel, Woking, UK – hosted by The Pirbright Institute, UK

Global Headlines (WRLFMD)

Over the last ten years, long-distance trans-pool movement of FMD viral lineages has been a common theme of reports generated by laboratories within the Network. An example is represented by the O/ME-SA/Ind-2001 lineage, where viral genetic data has been shared between the Network to show that this lineage has "escaped" from the South Asian countries (Pool 2) on many occasions to now become an important endemic virus lineage in the Gulf States of the Middle East (Pool 3) and Southeast/East Asia (Pool 1). Based on data presented by PD-FMD and WRLFMD at last year's meeting, this lineage has been divided into two sublineages (O/ME-SA/Ind-2001d and O/ME-SA/Ind-2001e). O/ME-SA/Ind-2001e appears to now dominate the situation in Pool 1 where the O/ME-SA/IND-2001d has not been reported since 2015. Other recent trans-pool movements out of Pool 2 include the spread of A/ASIA/G-VII to countries to the West (most recently causing outbreaks in northern Israel in 2018) and serotype Asia 1 causing outbreaks in Myanmar in 2017.

During 2017/18, attention has been focussed on the emerging situation in North Africa where outbreaks due to serotypes O and A have been reported. During 2018, FMDV causing outbreaks in Algeria has been characterised as belonging to the O/EA-3 topotype, most closely related to viruses circulating in West African countries (>99% with sequences collected by ANSES in Guinea), where there appears to have been upsurge in cases due to FMD. These O/EA-3 sequences collected from West Africa are phylogenetically distinct from the O/EA-3 strains seen in Egypt, Palestine and Israel. A lineage specific real-time RT-PCR developed by WRLFMD via a twinning project with NAHDIC (Ethiopia) is now available. Vaccine matching tests have been reported; but, there is a lack of in vivo evidence to support the use of vaccines for O/EA-3 viruses, since no potency tests have been performed, and filling this gap should now become a priority for the Network. Taken together with the outbreaks that have recently occurred in Algeria and Tunisia due to A/AFRICA/G-IV (reported in 2017), the emergence of these new FMD lineage in Maghreb is a significant change of epidemiological status which may substantiate new trans-Saharan connections between North and West Africa which raise the onward risks to FMD-free countries in Europe.

Elsewhere, in Southern Africa there has been a southwest spread of serotype O/EA-2. In Zambia, this lineage is normally only found close to the border with Tanzania – but has been recent isolated in central Zambia (Chisamba). In Pakistan, a new serotype O antigenic variant has been observed. This lineage appears to have very poor antigenic match with commercial vaccines from MSD and Boehringer-Ingelheim (new antigenic

variant); however, only two isolates have been detected to date in the Punjab. The spread of this lineage needs to be closely monitored.

Pool 1: South East Asia (RRLSEA, Thailand)

During 2018, samples have been received from Thailand (n=111) and Lao PDR (n=24). In Southeast Asia, the predominant serotype is serotype O, with the most common viral lineages being O/ME-SA/PanAsia, O/ME-SA/Ind2001e and O/SEA/Mya-98. Recent sero-surveillance undertaken in Thailand indicates that ~21% of the cattle population are positive for FMDV non-structural protein antibodies. VNT and LPBE vaccine matching against the locally produced O/189/87 vaccine shows that there is a good match for serotype O viruses. However, for serotype A, locally produced A118/87 and A/Sakolnakorn/97 appear not to be matched against all of the FMD virus isolates that have been tested (but the locally produced A/Lopburi/ 2012 vaccine is well matched against these viruses). Serotype Asia 1 has not been found in the region – except for the cases that occurred in Myanmar during 2017. A regional inter-laboratory PT scheme continues to be offered by the RRLSEA; where the latest exercise has involved 16 laboratories (9 outside of Thailand).

Pool 1: East Asia and China (LVRI, China)

Twenty four FMD outbreaks have been reported in China in 2018 affecting 12 different provinces. Samples collected show that the majority of these outbreaks are due to serotype O (with only one serotype A [A/ASIA/ASIA/SEA-97] detected in the year). The epidemiological picture for serotype O is complicated by the co-circulation of four different FMDV lineages in the country (O/CATHAY – 7 outbreaks, O/ME-SA/Ind-2001e – 8 outbreaks, O/SEA/Mya-98 – 3 outbreaks and O/ME-SA/PanAsia – 5 outbreaks). O/CATHAY is dominant in pigs and is poorly matched to vaccines used, while recent outbreaks of O/PanAsia appear to be due to a new introduction of the lineage into China during 2018. New risks are evident via an increase in illegal movements of animals from Southeast Asia. In addition, it is anticipated that recent outbreaks of ASF will have a dramatic impact on pig production that may influence the circulation of FMD in the country.

China has withdrawn the use of serotype Asia 1 from vaccines. During 2018, a cross challenge study in pigs has been performed using type O vaccine and O/Mya98 isolate O/17016 as the challenging virus, where monovalent and bivalent formulations both protected animals.

Pool 1: Korea and East Asia (APQA, Republic of Korea)

Outbreaks of serotype A/ASIA/SEA-97 were reported in two pig farms close to the North Korean border (12km distance between farms). This outbreak affected 1 province and lasted 7 days. The source of the outbreak is unknown. There have been changes to the vaccination protocol used in the country; fattening pigs are now vaccinated twice. Post vaccination is being carried out by SP(O) ELISA and the antibody levels recorded in fattening pigs have increased due to this change. Additional changes now mean that pigs receive multivalent vaccine (O-3039, O_1 Manisa and A_{22}), or O Primorksy and A Zabaikalsky vaccine strains. Across the country, sero-surveilance appears to highlight a decrease in the occurrence of NSP positive farms.

Pools 1 and 3: (FGBI-ARRIAH, Russia)

During 2018, samples have been tested from Russia (O/ME-SA/PanAsia), Mongolia (O/ME-SA/PanAsia, O/ME-SA/Ind-2001) and Pakistan (O/ME-SA/PanAsia-2, A/ASIA/Iran-05, Asia 1/Sindh-08). The FMDV outbreaks in Russia (Zabajkalkiy) occurred near the Mongolian border and were most genetically related to viruses collected in Mongolia during 2017/18. The results from vaccine-matching studies were presented describing results using representative viruses collected during the year (from Russia, Mongolia and Pakistan).

Pool 2: India (ICAR-DFMD, India) - Presented by Don King on behalf of the laboratory (NB: note change in the formal name of the laboratory).

Results for samples collected in India from suspect FMD cases (n=169) were presented. Serotype O (genetically highly related isolates within the O/ME-SA/Ind-2001e clade) continues to be the most dominant FMD viral strain

in the country; however, three viruses collected during 2017 were from the O/ME-SA/Ind-2001d sub-lineage. In addition to serotype O, there were also three cases due to serotype Asia 1, but none for serotype A.

Pool 3: Turkey (SAP Institute, Turkey) -Presented by Don King on behalf of the laboratory.

Samples received from Turkey (n=491) during 2018 are predominantly serotype O (O/ME-SA/PanAsia-2^{QOM-15}). Only a single serotype A FMD virus (A/ASIA/G-VII^{BAN-12}) has been detected this year (in January 2018). No cases due to A/ASIA/Iran-05 were reported, and the last case of due to serotype Asia 1 was in 2015. From a wider perspective, it is interesting to note that the A/ASIA/G-VII lineage appears not to have spread into all countries in the region, nor replaced the A/ASIA/Iran-05 lineage in countries such as Iran. Looking forward, it is possible that the A/ASIA/Iran-05 lineage will re-emerge into Turkey, and vaccine selection needs to consider this in view of the antigenic differences between A/ASIA/Iran-05 and A/ASIA/G-VII.

Pool 4: Kenya and East Africa (Embakasi, Kenya)

The FMD Reference laboratory has recently received samples from Kenya (n=77), South Sudan (n=38) and Tanzania (n=150, as part of an on-going project). FMD virus lineages detected in the Kenyan samples were O/EA-2, A/AFRICA/G-1, SAT 1/I and SAT 2/IV, where O/EA-2 appears to account for 85% of FMD outbreaks. Samples from South Sudan have also been sent to WRLFMD, where O/EA-3 was detected by real-time RT-PCR (see above). Vaccine matching testing has been performed using VNT showing that only 1/4 FMD viruses collected in Kenya during 2017 were matched against O K77/78.

Pool 4: Ethiopia and East Africa (NAHDIC, Ethiopia)

Samples (n=105) from Ethiopia have been received for testing during 2018. Serotypes reported were serotype O (most common, O/EA-3), A (A/AFRICA/G-IV and A/AFRICA/G-I) and SAT 2 (V-II^{ALX-12}). For the first time SAT 2 has been recorded in the far north of the country. The reports of A/AFRICA/G-I represent a new viral introduction into Ethiopia, since this lineage has not recently been detected in the country. NSP sero-surveillance indicates that 67% of cattle (n=2151) were antibody positive while less than 1% of small ruminants (n=1232) were seropositive.

Pool 5: West Africa (Sciensano, Belgium - including presentation on behalf of NVRI, Nigeria)

During 2017, there were FMD outbreaks due to serotype O (EA-3), A (G-VI) and SAT 2 (VII); however, in 2018 only serotype O (in three states) and SAT 2 (in one state) have been detected. During this period, O/WA and SAT 1 X have not been detected which was unexpected. NVRI also received four samples from Sierra Leone, where serum samples were positive for NSP; and the swabs were all negative by rRT-PCR. Importation of animals into Nigeria (particularly from Niger and Chad) appears to be an important risk-factor for FMD in the country. The trans-Saharan highway now links Algeria, Mali, Niger and Nigeria, and traffic on this new road may increase opportunities for the spread of FMD in the region (and beyond).

Pool 5: West Africa (ANSES, France)

Samples (n=53) have been collected (from FMD cases that occurred in 2017 and 2018) from Guinea (O/EA-3), Mauritania (O/EA-3 and A/G-VI) and Tunisia (A/AFRICA/G-IV). In addition, a small number of serum samples from Guinea (n=13 – 30.8% positive) and Mauritania (n=47 – 27.7% positive) have been tested. Sequences shared with WRLFMD indicate that the O/EA-3 topotype is spreading at a rapid pace (as described above in the headline summary). One point raised during the presentation is that recent FMD cases in West Africa may be associated with higher mortality in small ruminants which may be the reason why samples have been collected for these cases. Training carried out by ANSES includes Madagascar, Senegal, Mauritania, Guinea, Tunisia and Cameroon.

North Africa: (IZSLER, Italy)

No clinical samples have been received during 2018 for laboratory confirmation or characterisation. However, sero-surveillance studies in cattle and sheep have been performed for the Maghreb (Algeria, Morocco and

Tunisia) in support of the vaccination campaigns that are underway. To date, work has been completed for sera received from Morocco testing SP responses (by VNT and ELISA) to vaccination in naïve and previously vaccinated animals. Training has also been provided to Botswana and Libya and there is an increasing demand for ELISA kits where 2002 kits have been sent to 48 countries during 2018.

Pools 4-6: Sub Saharan Africa (OVI, South Africa)

Virology tests have detected the presence of SAT 2 (topotype I) and SAT 3 in samples from South Africa and Mozambique, respectively. The SAT 2 FMDV was detected in the vaccination zone (Gyiani, Halahala, Khakala and Matiyane) and is considered to have been circulating for some time (most likely a number of years). Most outbreaks can be traced back to contact with buffalo as a source (based on sequence analyses), but more recently the potential role of small ruminants (such as goats) is receiving more attention. OVI-ARC has developed 5 new vaccine strains and are preparing for commercial release within 2 years. The presentation also summarised work that has been undertaken in Uganda (2014-18) where the FMD viruses detected were: A (AFRICA/G-I), SAT 1 (I, IV topotypes), SAT 2 (VII, IV and X topotypes) and O (EA-1 and EA-2). There is also evidence for SAT 3 circulation but only using serological approaches and work is currently underway to assess whether this might be due to the cross-reactivity of the ELISAs.

Pools: 4-6: Sub Saharan Africa (BVI, Botswana)

Five countries have submitted samples (n=55): Mozambique (no virus detection), Zambia (SAT 3 and O), Botswana (SAT 2), Malawi (SAT 2), Zimbabwe (SAT 2). Across the region the circulating FMDV lineages are: SAT 3/I, O/EA-2, SAT 2/III and SAT 2/II. BVI are planning to initiate training on collecting samples to decrease the number of negative samples that are submitted. A small number of sera for surveillance purposes were also received from Botswana, Malawi, Mozambique and Zambia. In addition, Botswana and Zimbabwe are carrying out post-vaccination studies with LPBE, which highlighted that vaccine coverage was low.

Pool 7: South America (PANAFTOSA, Brazil)

PANAFTOSA has received outbreak samples from Colombia for field outbreaks (n=5) that occurred between August and October 2018. Sequence analyses place these viruses within the O/EURO-SA/cluster 6 (described in 2011) and are 90% identical to outbreaks in Andean Region of South America. The affected species appear to be cattle and swine; evidence indicates that partially immunized cattle (mainly 1-2 years old) have been infected and moved into the affected region via illegal trade from Venezuela. EPP for the Colombia strain is 79.03% (with O1 Campos Br/58); however, further vaccine matching is still being undertaken. The vaccine strain C_3 Indaial will be withdrawn from the vaccines in Brazil, Paraguay and Bolivia in 2019. Brazil is currently in a transitional period with all vaccination stopping by 2023. Suriname is free without vaccination from 2018. Samples were also received from Trinidad and Tobago which were negative for FMDV, but positive for Orfvirus (contagious ecthyma).

Pool 7: South America (SENASA, Argentina)

Since 2006, there have been no FMD outbreaks in Argentina and no clinical samples have been received for FMDV testing. Samples have been received for differential diagnosis including bovine herpesvirus 1, contagious ecthyma, and BVD. During 2018, 14,000 sera have been received for epidemiological surveillance purposes to demonstrate absence of FMD virus circulation. Training in laboratory diagnostic methods has been provided to Paraguay.

Update from Winnipeg, Canada

Twenty-one samples from Canada were received; of which fifteen were positive for Seneca Valley Virus (SVV). Vesicular cases due to SVV now appear to be decreasing in Canada. Samples (23 clinical samples and 603 sera) were also received from Ghana. Testing is still ongoing; however, initial results from sero-surveillance support the circulation of serotypes A, O and SAT 2 (testing done by VNT).

Update from FADDL, USA

NBAF in Kansas is currently being constructed to replace the facility at Plum Island. The USA is still reporting a large number of SVV outbreaks, which clinical signs that are very similar to FMD; however, the number of outbreaks appears to be stabilising. Since 2014, SVV has increased from 2% to 98% of all vesicular diagnostic cases. National laboratories are carrying out rRT-PCR for SVV; therefore only inconclusive or suspect FMD cases are now being sent to Plum Island. Complete FMDV genome sequencing have been undertaken for samples from Colombia (2017), Uganda and from the FADDL repository. Additional samples are tested from FMD endemic countries as part of on-going research project undertaken by ARS, providing data that would be helpful to include in reports from the global laboratory network (point discussed at recent GFRA meeting in Argentina).

Action O1-18 – FADDL to investigate whether a summary of ARS data can be included in reports

Update from CSIRO, Australia

One of the roles of CSIRO is to ensure that vaccine in the Australian bank continue to be efficacious. Recent vaccine matching carried (by LPBE) suggest that O-3039 and A/MAY/97 may protect against the majority of circulating FMDV field isolates in Southeast Asia. No vaccine efficacy studies have been performed during 2018, but future studies may consider the extent to which the new A/G-VII vaccines provide protection for A/ASIA/Iran-05 viruses, and whether the A/G-VII can replace A/Iran-05 in vaccine banks. Research at CSIRO is focussing on the role of goats in the epidemiology of FMD, testing new vaccine adjuvants, intradermal vaccination in pigs (using IDAL from MSD), and inactivation of FMDV using lysis buffers (RNAShield and RNAlater). A collaborative project with (Alejandra Capozzo, INTA, Argentina) has evaluated new approaches that might be used for vaccine matching.

8th November 2018

Review FMD status in endemic pools and significant epidemiological events (and gaps) and risks during 2018

Updates (with annotated maps) were provided from Pool 1, Pool 3, Pool 4, Pool 5 and Pool 6. Perhaps the most significant risk identified is the possibility that serotype SAT 2 (topotype VII) will enter North Africa in a pattern similar to A/AFRICA/G-IV and O/EA-3.

Discussion – How do we better link the phylogenetic trees to the field reports to show the viral pools are connected? In order to help visualise this links, the WRLFMD has a draft image that could be used (and improved).

Action O2-18 – WRLFMD to send around a draft figure for comment

Review of vaccine-matching work currently undertaken by Network partners – Anna Ludi

A summary of the vaccine matching that is currently being undertaken by the Network partners was described including the limitations of the currently used tests. Vaccine matching results generated by FMD reference laboratories typically only includes vaccines from one or two commercial vaccine suppliers (for instance WRLFMD data only evaluates MSD and Boehringer-Ingelheim vaccines). Clearly there is more work for the Network to do to (i) harmonise existing vaccine matching methods, (ii) expand the range of FMDV vaccine sera available that can be provided to FMD Reference Laboratories and (iii) continue to evaluate new methods to assess vaccine homologous potency and cross-protection.

Summary of topics that were discussed:

- Is there a better way to share data throughout the year? New WRLFMD website now includes vaccine matching reports.
- In addition to r_1-values, should reports also include heterologous titres?
- Reference sera: partners were reminded of previous discussions where we agreed to standardise the use of monovalent $6PD_{50}$ post vaccine sera collected from cattle at 21 or 28dpv.

- Gaps in serum panels and methods exist for pigs which are increasingly important in Asian countries (where there is sometimes uncertainty about the performance of an FMDV vaccine).

FMD vaccine matching: inter laboratory study for improved understanding of r_1 values - David Lefebvre

This presentations summarised a previous inter-laboratory exercise undertaken by the Network to assess the repeatability of r_1 values within and between laboratories as well as the comparability of r_1 values generated using VNT and LPBE methods. For all laboratories, individual and mean r_1-values by VNT were below 0.3 and this matched with experimental challenge data and field data. The LPBE gave a much more complicated picture and it appears that laboratories could/should adjust their cut-off to fit with the data.

A new model for independent FMDV vaccine QA/QC via an OIE twinning project with AU-PANVAC – David Paton

During 2019, a new project will start between WRLFMD and AU-PANVAC (in Ethiopia). This is a new opportunity to look at the way that QA/QC is undertaken for FMDV vaccines. The project will address two connected priorities for the use of FMDV vaccines in Africa: vaccine QA/QC (homologous protection) and vaccine performance in the field (heterologous responses). Considering the recommendations of the OIE, the project will produce new reference materials including panels of representative field viruses (involving work of the Network), BVS and recombinant antigens for use in ELISA formats (including new avidity and IgG1/IgG2 isotype ELISAs). The project will focus on approaches to evaluate homologous potency and heterologous match.

From our Industry partners: Industry perspective on vaccine QA/QC: who does what? And how can the Reference Laboratory Network contribute? – presented by Alasdair King

How does a country decide on whether a vaccine is "fit for purpose"? A lot of attention is placed on vaccine matching data, but vaccine performance is also dependent upon vaccine potency, vaccine quality, the adjuvant and vaccination regime used. The difficulty is that methods are complicated and there is no prospect of harmonisation across the Network laboratories (as well as those used by the different vaccine companies). Furthermore, most data generated by FMD reference laboratories only considers monovalent vaccines – and not the final formulated product that may contain complementary FMD virus strains to cover antigenic diversity. An important message from this talk was that vaccine matching data is often used incorrectly by customers, and that perhaps a priority for the Network should be education and standardisation of these methods. New reliable tests and harmonised reagents are certainly required, and also more work should be undertaken to better understand the relationship between antibodies and protection. The presentation also considered vaccine batch QA and minimum qualification of vaccines for use in different endemic settings (focussing on homologous responses). It was suggested that some products could be pre-qualified (subject to meeting GMP requirements); alternatively, each batch would need testing at national/pan-national level. Standardised sera could be provided by the manufacturers to assist the Network to define post-vaccination responses (using standardised viruses and methods to focus on heterologous responses), but if funding from the commercial sector is required for these activities, there must be a benefit to the producers.

Three level of fitness:

1. Quality reliable – each batch consistent
    a. External audits (manufacture w/ accredited source of documentation), GMP
2. Does the strain/adjuvant have good immunogenicity
    a. Homologous challenge studies (manufacturer through independent testing facilities)
3. Does the strain give field specific protection
    a. Heterologous data (laboratory network).

Discussion - Batch testing should not be complicated, but it may be difficult due to producing sera at the cut-off of protection. However, the network would benefit from having this cut-off sera for it would give laboratories an understanding of how the vaccine behaved before it left the factory. If there is a difference after vaccination

in the field, then the problem is with vaccination not the vaccine. Currently the batch cut-off is based on what potency they can expect.

Implementing PVM in endemic countries – Kees van Maanen

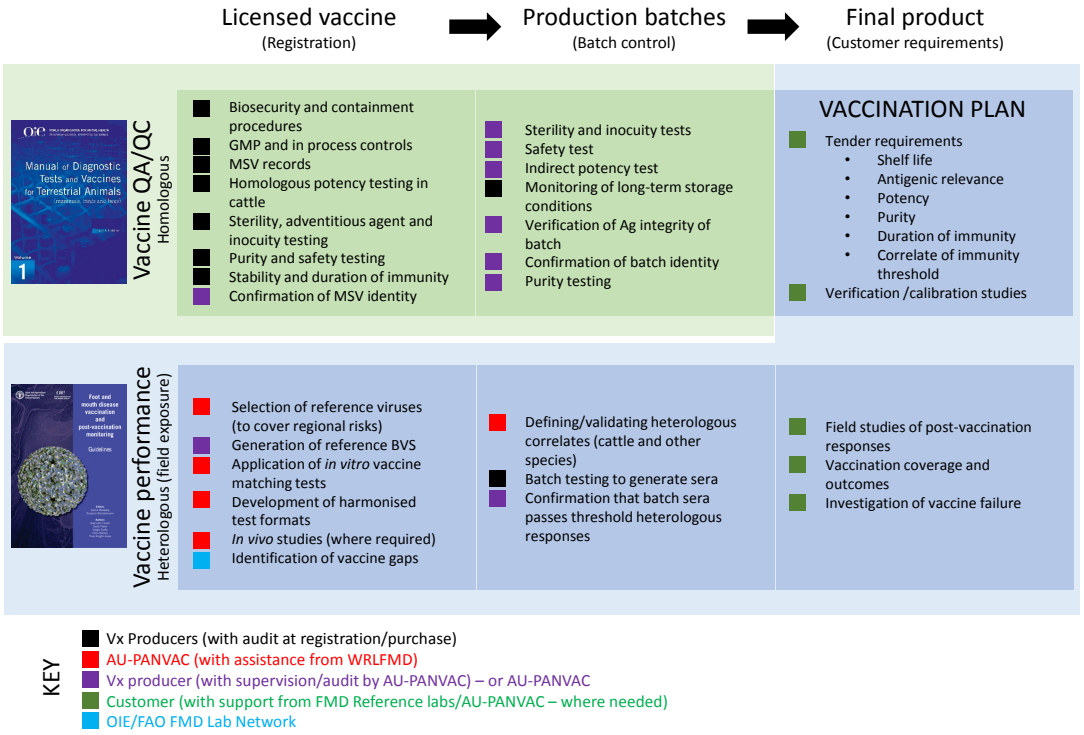
The relationship between probability of protection and serological results is sometimes not clear. There are different protective cut-offs for different serotypes and different assays. The talk discussed what the different options are for vaccine batch testing and a description of the various trials that can be done was presented.

Vaccine assessment: Actions and Recommendation to take forward:

1. For vaccine matching reports:
    a. Include how the r1-values are produced on each report (i.e. VNT, LBPE) and the reagents used including details of BVS.
    b. Make a note on each report with any limitations. This could include if the assay is based on a single test and whether the data should be interpreted by considering other isolates of the same lineage.
2. Limited data (including potency testing and *in-vitro* vaccine matching) is available for swine. This is particular a problem for Pool 1 and delegates may want to consider writing to the OIE for assistance.
3. How do we make reference sera available for post-vaccination study? Could there be a link between industry and reference laboratories?

    Action O3-18 – WRLFMD to draft a document containing the BVS currently available at The Pirbright Institute. Other institute including industry could then add to this list (large quantities would only be included). This could include a reference panel.

4. Action O4-18 - Invite vaccine manufacturer from China to next year's meeting
5. Action O5-18 – Delegates to provide feedback on the figure (see below) developed from ideas raised at last year's Network meeting regarding who takes responsibility for Vaccine QA/QC



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