Food and Agriculture Organization of the United Nations

eufmd
european commission for the control of foot-and-mouth disease

GLOBAL Monthly Report

Foot-and-Mouth Disease

Foot-and-Mouth Disease Situation | 2019 | February

Foot-and-Mouth Disease Situation
Food and Agriculture Organization of the United Nations
Monthly Report

February 2019

MAIN INFORMATION SOURCES USED:

Databases:

OIE WAHID World Animal Health Information Database
FAO World Reference Laboratory for FMD (WRLFMD)
FAO Global Animal Disease Information System (EMPRES-i)

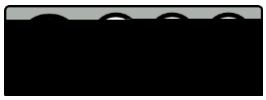
Other sources:

FAO/EuFMD supported FMD networks
FAO/EuFMD projects and field officers

The sources for information are referenced by using superscripts.
The key to the superscripts is on the last page.

Please note that the use of information and boundaries of territories should not be considered to be the view of the U.N. Please, always refer to the OIE for official information on reported outbreaks and country status.

Required citation:
FAO/EuFMD. 2019. *Global Monthly Report. Foot-and-Mouth Disease Situation February 2019*. Rome, FAO.



CONTENTS

Please note that the report contains hyperlinks

I. HIGHLIGHTS

Dear Readers,
Which vaccines do you recommend for use in my country, and how will they perform?
These are questions frequently asked to anyone working with or within countries that are endemic for FMDV, and answering is not usually a simple matter, even if in reality few vaccines are available.
The work of the OIE/FAO Reference Laboratory network, led by the World Reference Laboratory at Pirbright, is extremely important in providing data on circulating FMDV, and no effort is spared to provide vaccine matching results in as quick a time frame as possible after submission.
Inevitably, the data they can provide is limited by the numbers of submissions in relation to the numbers of countries where virus circulates and the frequency with which the balance of serotype and viral lineages changes within virus pools, as epidemics emerge and succeed each other.
It has been of concern for some time to provide more quantitative estimates of virus prevalence within countries and pools, in order to populate tools to assist decision making by those that buy vaccines and antigens. The PRAGMATIST tool, developed by EuFMD and the WRL, aims to assist decision makers by providing a means to quantitate the risks posed by virus lineages for entry into the region or country at risk, and the utility of antigens available to protect against these risks. The tool is dependent on estimates of virus lineage prevalence in source regions, and on laboratory results on vaccine matching. The outputs of PRAGMATIST are now used in every EuFMD Session to provide a clear summary of the risks and the relative value of the antigens available for use in European emergency reserves (antigen banks).
In this GMR, we provide estimates of the relative prevalence of FMDV lineages in each virus pool, on the basis of the results of the previous months of laboratory findings and the relative contribution of each country in the region to the burden of FMDV in circulation.
Pool 1 (South East and East Asia) makes an interesting example. Around 80% of the virus circulation is considered to be from 4 lineages of serotype O, and of these, 3 of the 4 lineages have caused recent incursions into countries at the margin of the endemic pool (Russian Federation, Republic of Korea and Mongolia). Serotype A, lineage Asia/SEA-97 is estimated to make up about 20% of the circulating FMDV, yet it has not been reported to cause outbreaks in the past month.
FMD epidemics often follow a pattern in which there may be waves of infection with peaks of cases every 3-4 years associated with single serotypes. During inter-epidemic periods, few samples reach laboratories to confirm infections remain in circulation. Now would make a good time to understand where the A /Asia/SEA-97 linage remains circulating in this region and consider if from these locations new epidemic waves may emerge and spread. This situation, of epidemics emerging and affecting vast numbers of animals in a short time and affecting multiple countries in a pool, has recently been well observed in West Africa, where the O EA-3 lineage undertook a spectacular expansion in 2018, affecting most of the sahelian countries of West Africa and many of the coastal countries in a short period between June and November 2018. The incursion into North Africa and the continued spread into 2019 indicates the epidemic has not yet run its course, and risks becoming endemic in the vast small ruminant population in North Africa.
Our ability to predict the next wave of FMDV within a pool, and its temporal and spatial likely spread, is an area of intense interest and importance.
The data in the charts provided may assist to develop PRAGMATIST outputs for each pool or country at risk, to improve selection of vaccines. This is the next stage for the use of this tool, but we must also develop a way to project forward the changes in prevalence within a pool. This is an area EuFMD hopes to progress in 2019 with greater involvement of the OIE/FAO network and by expert opinion from within each region.
We hope to start providing projections within a few months, as our system for making projections is developed. Keep watching this space! And keep alert for further changes in FMD risk!

Keith Sumption
Executive Secretary
EUFMD

II. GENERAL OVERVIEW

Pools represent independently circulating and evolving foot-and-mouth disease virus (FMDV) *genotypes; within the pools, cycles of emergence and spread occur that usually affect multiple countries in the region. In the absence of specific reports, it should be assumed that the serotypes indicated below are continuously circulating in parts of the pool area and would be detected if sufficient surveillance was in place (Table 1).*

Table 1: List of countries representing each virus pool for the period 2014 – 2018 (source EuFMD)

POOL	REGION/COUNTRIES – colour pools as in Map	SEROTYPES
1	**SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA** Cambodia, China, China (Hong Kong, SAR), Taiwan Province of China, Democratic People's Republic of Korea, Republic of Korea, Lao People's Democratic Republic, Malaysia, Mongolia, Myanmar, Russian Federation, Thailand, Viet Nam	**A, Asia 1 and O**
2	**SOUTH ASIA** Bangladesh, Bhutan, India, Mauritius, Nepal, Sri Lanka	**A, Asia 1 and O**
3	**WEST EURASIA & MIDDLE EAST** Afghanistan, Armenia, Azerbaijan, Bahrain, Georgia, Iran (Islamic Republic of), Iraq, Israel, Jordan, Kazakhstan, Kuwait, Kyrgyzstan, Lebanon, Oman, Pakistan, Palestine, Qatar, Saudi Arabia, Syrian Arab Republic, Tajikistan, Turkey, Turkmenistan, United Arab Emirates, Uzbekistan	**A, Asia 1 and O (SAT 2)***
	NORTH AFRICA Algeria, Egypt, Libya, Morocco, Tunisia	**A and O**
4	**EASTERN AFRICA** Burundi, Comoros, Djibouti, Eritrea, Ethiopia, Kenya, Rwanda, Somalia, Sudan, South Sudan, United Republic of Tanzania, Uganda, Yemen	**O, A, SAT 1, SAT 2 and SAT 3**
5	**WEST/CENTRAL AFRICA** Benin, Burkina Faso, Cameroon, Cabo Verde, Central Afr. Rep., Chad, Democratic Republic of Congo, Congo, Côte d'Ivoire, Equatorial Guinea, Gabon, Gambia, Ghana, Guinea-Bissau, Guinea, Liberia, Mali, Mauritania, Niger, Nigeria, Sao Tome Principe, Senegal, Sierra Leone, Togo	**O, A, SAT 1 and SAT 2**
6	**SOUTHERN AFRICA** Angola, Botswana, Malawi, Mozambique, Namibia, South Africa, Zambia*, Zimbabwe	**{O, A}**, SAT 1, SAT 2 and SAT 3**
7	**SOUTH AMERICA** Colombia, Venezuela (Bolivarian Republic of)	**O and A**

*REPORTED ONLY IN OMAN IN 2017

** ONLY IN NORTH ZAMBIA AS SPILL-OVER FROM POOL 4

III. IN THIS REPORT

POOL 1- SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA

China [1] – FMD due to serotype O was notified on a cattle farm at Chifeng, Inner Mongolia on February 13th 2019.

China (Hong Kong, SAR) [2] – Field isolates detected in pig samples collected between September and December 2018 and belonging to the O CATHAY lineage obtained poor matching results with vaccine strains used in the vaccine matching strain differentiation (VMSD) tests.

Lao People's Democratic Republic [2] – Field isolate detected in cattle in January 2018 and belonging to the O/ME-SA/PanAsia lineage obtained very good matching results with vaccine strains used in the VMSD tests.

Mongolia [1] – Three genetic lineages of FMDV serotype O were detected in the bovine samples collected between February 2017 and 2018.

Republic of Korea [2] – O/ME-SA/Ind2001e was detected in cattle samples collected during January 2019.

Russian Federation [1, 3] – Six outbreaks due to FMDV serotype O occurred principally on pig farms between January and February 2019 at Primorskiy Kray. The Regional Reference Laboratory for FMD (ARRIAH, Russia) reported the detection of O/SEA/Mya-98.

POOL 2 - SOUTH ASIA

India [4] - ICAR-Directorate of Foot and Mouth Disease (ICAR-DFMD), Mukteswar, India, continues to report the detection of FMDV serotype O.

Nepal [5] - The National Foot and Mouth Disease and TADS Laboratory reported the circulation of FMDV serotype O in the country.

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan [6] - The Central Veterinary Research and Development Laboratory (CVDRL), Afghanistan detected FMDV serotype O among the samples examined during February 2019.

Israel [1, 2] – Three outbreaks due to O/ME-SA/PanAsia2 were notified on cattle holdings in different areas of Hazafon during January and February 2019.
O/ME-SA/PanAsia2^{Qom15} was detected in a batch of samples collected from different species between April and December 2018.

Pakistan [15] – For February, 327 outbreaks due to FMDV serotypes A, ASIA 1 and O were reported in the provinces of Balochistan, Khyber Pakhtunkhwa, Punjab and Sindh.

POOL 3 – NORTH AFRICA

Algeria [1, 2] – Fifty nine FMD outbreaks due to serotype O, were reported between November and December 2018, mainly occurring in the northern part of the country.
The VMSD tests conducted on field isolates collected between 2018 and 2019 and belonging to the O/EA-3 lineage produced good matching results with the vaccine strains used.
The detection of FMDV serotype A in a bovine sample collected during December 2018 as described in the January 2019 issue of this report was not confirmed by genotyping.

Morocco [1] – Eleven outbreaks due to FMDV serotype O were notified during January and February 2019 on multispecies farms with the same outbreaks already resolved.

POOL 4 - EASTERN AFRICA

Ethiopia [7] – The National Animal Health Diagnostic and Investigation Center (NAHDIC) reported the detection of FMDV serotypes A and O.

Kenya [8] **–** The FMD National Reference Laboratory (FMDNRL), Embakasi, Kenya, reported the detection of FMDV serotypes A and SAT 2.

South Sudan [2] **–** The field virus detected in a sample collected in 2017 and genotyped as O/EA-3 obtained good matching results in the VMSD tests.

Uganda [2] - FMDV serotypes O and A were detected in outbreak samples collected in January and February 2019.

POOL 5 - WEST/CENTRAL AFRICA

Burkina Faso [2] **–** The O/EA-3 lineage detected in seven of the 18 cattle samples collected in the country between June and August 2018 obtained good matching results in the VMSD tests.

Cameroon [9] **-** The Laboratoire National Vétérinaire (LANAVET), Garoua, Cameroon detected FMDV in the samples analysed during the reporting month.

Sierra Leone [2] **–** The FMDV serotype O detected in August 2018 obtained partially good matching results in the VMSD tests**.**

POOL 6 - SOUTHERN AFRICA

Malawi [1] **–** FMD cases as reported on February 2nd 2019, for which serotyping is pending, are continuing in the country with new cases notified in Ipenza.

South Africa [1, 10] **–** Another FMD outbreak due to serotype SAT 2 was reported on January 31st 2019 in cattle of a village of Limpopo. This outbreak has occurred in South Africa's FMD High Surveillance Area, which is part of South Africa's suspended FMD Free Zone.

POOL 7 - SOUTH AMERICA [1, 11]

No outbreaks are reported for this Pool. FMD in Latin America was last detected in Colombia in October 2018 with outbreaks due to FMDV serotype O, while PANAFTOSA reported historical outbreaks due to serotype A that occurred in Venezuela in 2013.

COUNTER

****** 175 MONTHS SINCE THE LAST SEROTYPE C OUTBREAK WAS REPORTED***

IV. DETAILED POOL ANALYSIS

A. *POOL 1 – SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA*

<table>
<tr><th colspan="2">OUTBREAKS</th></tr>
<tr><td>Country</td><td>Description</td></tr>
<tr><td>Serotype O in China [1]</td><td>FMD due to serotype O was notified at Chifeng, Inner Mongolia on February 13th 2019, on a cattle farm where a relatively high mortality rate of 41.2% (35 animals out of 85) was registered. The Lanzhou National Reference Laboratory for Foot and Mouth Disease (OIE Reference Laboratory) confirmed the diagnosis on February 20th 2019 using reverse transcription - polymerase chain reaction (RT-PCR) and gene sequencing. The source of the outbreaks is inconclusive and general control measures were put in place, including vaccination of the local bovine and pig populations. This outbreak is a continuation of the event that started in July 2018. Location of outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29636.

The lineages reported last by the WRLFMD in the country for serotype O are O/SEA/Mya-98, O/CATHAY, O/PanAsia and O/ME-SA/Ind-2001 that were detected in samples collected in the country during 2018.

Interpretation FMD occurs sporadically in China. This is a continuation of an event that was first reported on July 30th 2018.</td></tr>
<tr><td>Serotype O in Russian Federation [1]</td><td>
<table>
<tr><th>Administrative division</th><th>Species</th><th>Total Vaccinated</th></tr>
<tr><td rowspan="3">Khabarovskiy Kray</td><td>Cattle</td><td>5,994</td></tr>
<tr><td>Sheep / goats</td><td>2,740</td></tr>
<tr><td>Swine</td><td>7,019</td></tr>
<tr><td rowspan="3">Primorskiy Kray</td><td>Cattle</td><td>29,196</td></tr>
<tr><td>Sheep / goats</td><td>17,928</td></tr>
<tr><td>Swine</td><td>55,789</td></tr>
<tr><td colspan="2">Total</td><td>118,666</td></tr>
</table>
Six outbreaks due to FMDV serotype O were reported during January and February 2019 in different areas of Primorskiy Kray, clinically affecting pigs. The Regional Reference Laboratory for FMD (ARRIAH, Russia) confirmed the diagnosis of the first outbreaks on February 1st 2019 for the outbreaks of January 30th 2019 using real-time reverse transcriptase/polymerase chain reaction (RRT-PCR). The source of the outbreaks is unknown and general control measures were adopted including vaccination of which a summary is reported in the present table. Details on the type of vaccination were not provided.

Location of outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29549.

The lineage reported last in the country by the WRLFMD for FMDV serotype O is O/ME-SA/Ind-2001d that was detected in samples collected in the country during 2017.

Interpretation FMD occurs sporadically in Russia. This is a continuation of an event that was first reported on January 11th 2019.</td></tr>
</table>

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
China (Hong Kong, SAR) [2]	Surv. and Vacc.	O CATHAY lineage was detected in three of the six pig samples collected at the Sheung Shui Slaughterhouse, Sheung Shui, New Territories between September and December 2018. The most closely related sequences belonged to field viruses were those detected in the same country during 2018. Two of the three field viruses were subjected to the VMSD tests in which they obtained poor matching results with vaccine strains O 3039, O Manisa and O TUR 5/09.
Lao People's Democratic Republic [1]	Vacc.	Field isolate O/ME-SA/PanAsia detected in January 2018 obtained very good matching results with vaccine strains O 3039, O Manisa and O TUR 5/09 used in the VMSD tests.
Mongolia [1]	Surv.	O/ME-SA/PanAsia, O/ME-SA/Ind-2001e and O/SEA/Mya-98 were the lineages detected in the bovine samples collected between February 2017 and 2018. A summary of the genotyping results are presented in Table 2 and location of the positive samples collected in Map 1. **Table 2**: genotyping results of the FMDV positive bovine samples collected in Mongolia between collected between February 2017 and 2018 (source – WRLFMD).

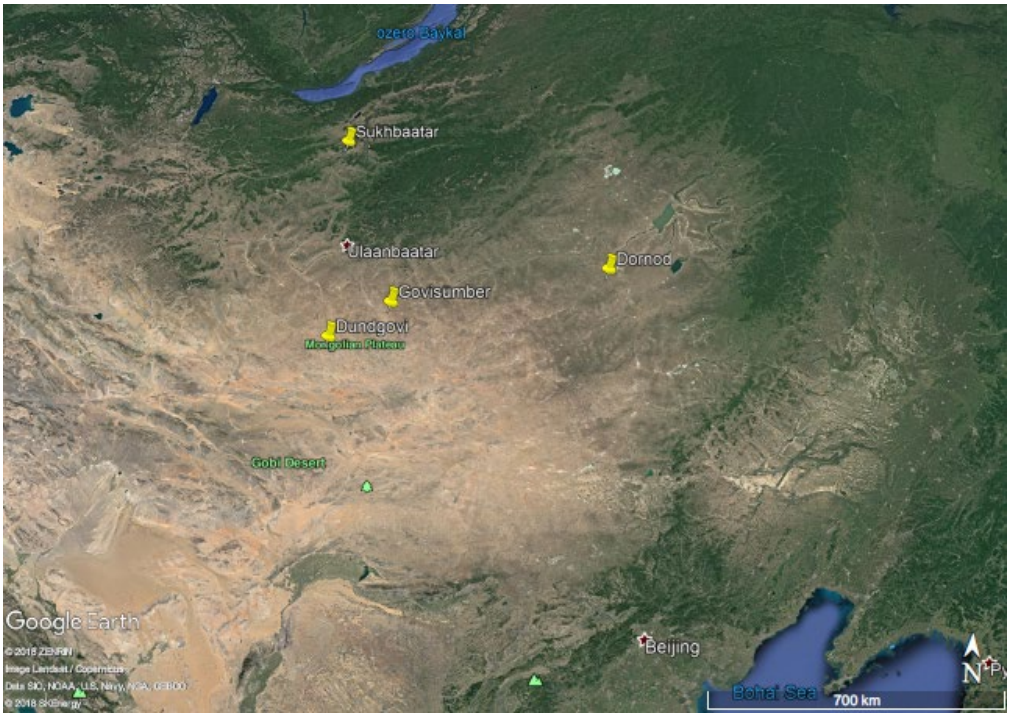
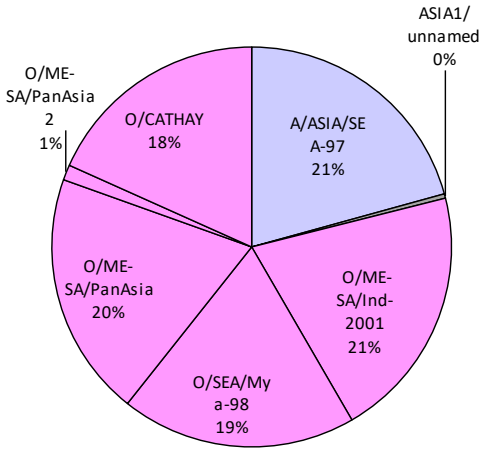
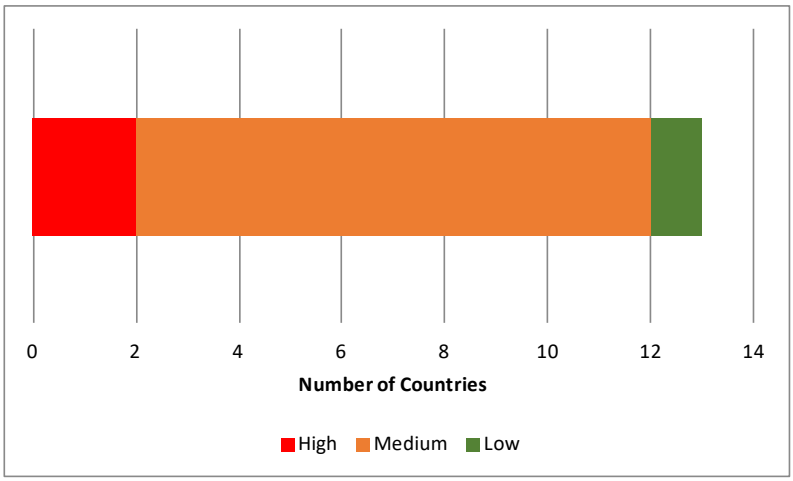
		<table><tr><th>Sample Identification</th><th>Location origin of sample</th><th>Date of collection</th><th>Genotype</th><th>Most Closely Related Viruses not belonging to the country - Seq id %</th><th>Host species</th></tr><tr><td>MOG/16/2017</td><td>Sukhbaatar</td><td>03/02/2017</td><td>O/ME-SA/PanAsia</td><td>VIT/5/2011 (99.4)</td><td>cattle</td></tr><tr><td>MOG/21/2018</td><td>Govisumber</td><td>02/01/2018</td><td rowspan="3">O/ME-SA/Ind-2001e</td><td colspan="2">/</td></tr><tr><td>MOG/22/2018</td><td rowspan="2">Dornod</td><td rowspan="2">21/02/2018</td><td>MAY/4/2018 (>98.3)</td><td>cattle</td></tr><tr><td>MOG/23/2018</td><td colspan="2">/</td></tr><tr><td>MOG/24/2018</td><td>Dundgovi</td><td rowspan="2">26/02/2018</td><td rowspan="2">O/SEA/Mya-98</td><td>NXYCh/CHA/2018-B</td><td>cattle</td></tr><tr><td>MOG/25/2018</td><td>Sukhbaatar</td></tr></table> **Map 1**: yellow icons indicate location of FMDV positive bovine samples collected in Mongolia between collected between February 2017 and 2018 (Source – WRLFMD, Google Earth Pro). 
[Republic of Korea](#) [2]	Surv.	O/ME-SA/Ind-2001e was detected in the five cattle samples collected at Osan-ri, Geumgwang-myeon, Anseong-si, Gyeonggi-Do during January 2019. The most closely related sequences not of field viruses pertaining to the country was GZZY/CHA/2018-B isolated in cattle in China with a sequence identity (seq id) of 99.4%.
Russian Federation [3]	Surv.	For the reporting month, the ARRIAH, Russia detected FMDV serotype O in 19 samples and the genotyped viruses belong to the O/SEA/Mya-98 lineage. However, the Laboratory did not report when this lineage was detected. The laboratory also conducted vaccine matching tests on the field viruses using O/SEA/Mya-98, O/Russia/2000 and O/PanAsia-2 vaccine strains with matching found only with the first vaccine strain. Serological analysis was conducted on 461 and 3,178 serum samples respectively for vaccine monitoring purposes and testing of non-vaccinated animals.

Table 3 and Graph 1: Conjectured circulating FMD viral lineages in Pool 1 (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 13 countries of Pool 1
A	A/ASIA/SEA-97	8
ASIA 1	ASIA1/ unnamed	1
O	O/ME-SA/Ind-2001	7
	O/SEA/Mya-98	5
	O/ME-SA/PanAsia	8
	O/ME-SA/PanAsia2	1
	O/CATHAY	4



Graph 2 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 1 – see Annex for explanation).



B. POOL 2 – South Asia

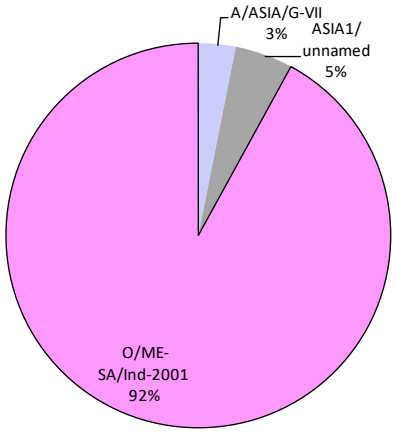
OUTBREAKS	
Country	*Description*
Serotype O in India [4]	ICAR-DFMD, Mukteswar, India detected FMDV serotype O among 9 bovine samples examined using FMDV antigen and/or RNA detection methods. *Interpretation* This report is consistent with previous reports. The causative serotype is the only serotype to circulate endemically in the country since 2016. Data on genotyping of the current circulating strains is required to confirm that the epidemiological situation is not modifying.
Serotype O in Nepal [5]	The National Foot and Mouth Disease and TADS Laboratory reported the circulation of FMDV serotype O in the country. The last lineage reported by the WRLFMD of FMDV serotype responsible for the current outbreaks was O/ME-SA/Ind-2001d detected in 2017. *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country however more information is required to define if this is the only serotype present in the country and if the lineage is that reported in 2017.

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*

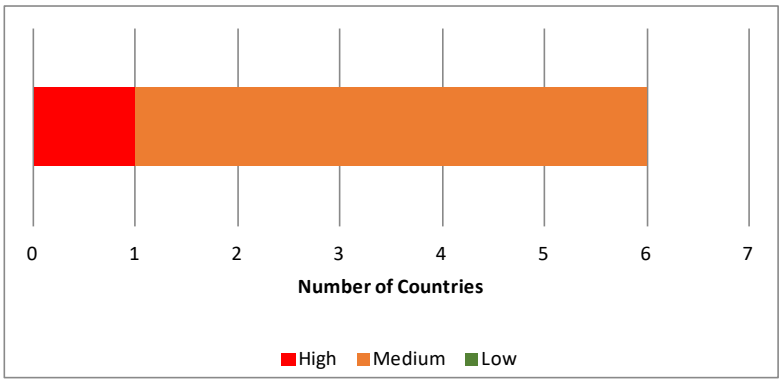
India [4]	Surv. and PVM	The laboratory subjected one FMDV serotype O field isolate for vaccine matching tests. The laboratory analysed 242 sera collected in the course of epidemiological studies for the detection of FMD antibodies. The FMD diagnostics kits employed are those developed at ICAR-PDFMD. The sublineages currently circulating in the country are represented by O/ME-SA/2001d and O/ME-SA/2001e as described in the latest ICAR-DFMD Annual Report of 2017-18.

Table 4 and Graph 3: Conjectured circulating FMD viral lineages in Pool 2 (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 5 countries of Pool 2
A	A/ASIA/G-VII	3
Asia 1	ASIA1/ unnamed	3
O	O/ME-SA/Ind-2001	5

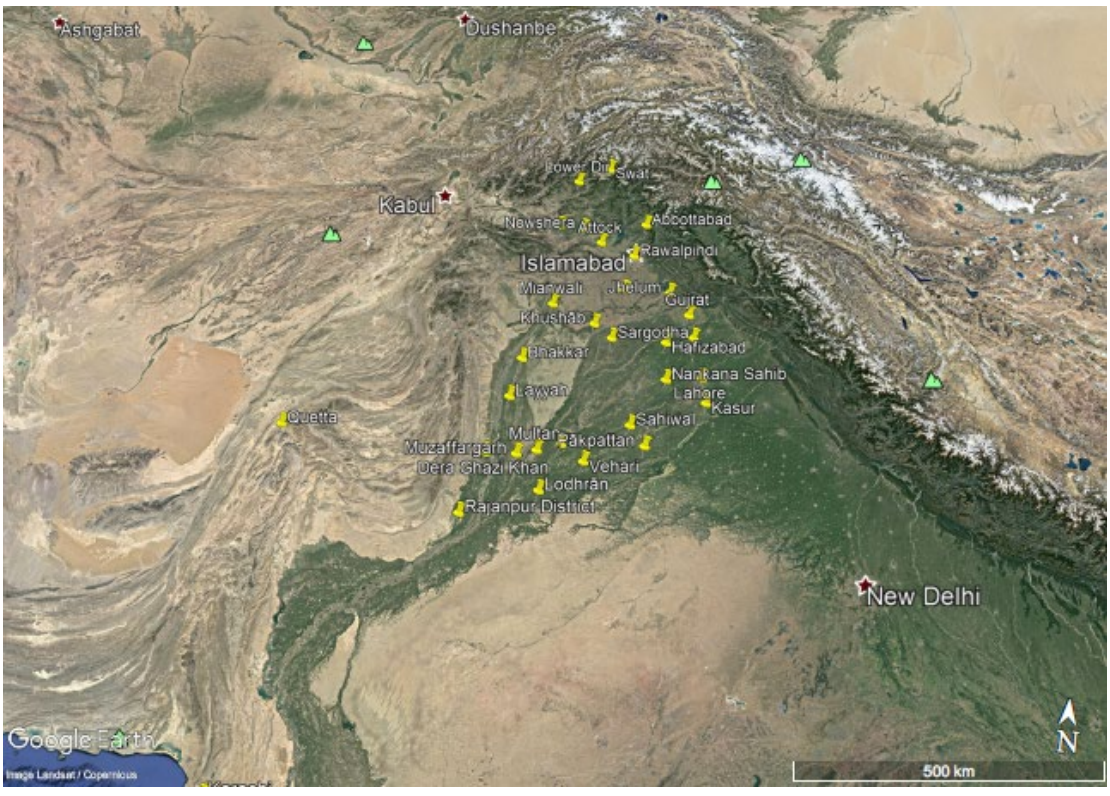


Graph 4 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 2 (see Annex for explanation).



C. POOL 3 – West Eurasia & Middle East

OUTBREAKS	
Country	***Description***
Serotype O in Afghanistan [6]	The CVDRL, Afghanistan detected FMDV serotype O in five of the eight samples examined. A/ASIA/Iran-05 and O/ME-SA/PanAsia-2 are the most recent lineages detected by the WRLFMD in samples collected in the country during 2018. *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country.
Serotype O in Israel [2]	Three outbreaks due to O/ME-SA/PanAsia2 were notified between January 25th and February 1st 2019 of which one was reported as resolved. The outbreaks occurred on cattle holdings at Tsefat, Acco and Golan, Hazafon as reported in Map 4. The affected farms are free ranging beef cattle herds with two o them vaccinated in December 2018 and the third farm, two years ago. FMD typical clinical signs were mainly observed in calves, presenting lesions on the tongue and limping. The source of the outbreaks is

OUTBREAKS	
	unknown and general control measures put in force were movement control, quarantine and zoning. Surveillance is being carried out within and outside the containment and/or protection zones. Location of outbreaks is available at the following links: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29414 https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29524 *Interpretation* This report is consistent with previous reports. The causative strain is believed to circulate sporadically in the country due to incursions from neighbouring regions with the potential of endemic circulation of the virus, especially in small ruminants and wild species.
Serotypes A, ASIA 1 and O in Pakistan [15]	For the reporting country, 327 outbreaks were notified in the provinces of Balochistan, Khyber Pakhtunkhwa, Punjab and Sindh due to FMDV serotypes A, ASIA 1 and O. A summary of the outbreaks is reported in Table 5 and their location in Map 5. The FMD control project is currently operated only Punjab and information relative to other areas of the country are provided on voluntarily basis. Last reported lineages in the country by the WRLFMD were A/ASIA/Iran-05, ASIA 1/Sindh-08/ and O/ME-SA/PanAsia2 detected in 2017. *Interpretation* This report is consistent with previous reports; The causative serotypes are believed circulate endemically in the country. **Map 2**: yellow icons indicate location of outbreaks reported in Pakistan during February 2019 (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator, Google Earth Pro).  **Table 5:** number of outbreaks reported per serotype and per district in Pakistan during February 2019 (Source –Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project

OUTBREAKS

Coordinator).

Province	District	Number Outbreaks	Number (%) of Outbreaks due to FMDV Serotype						
			O	A	Asia-1	Mixed	Un-Typed	Negative	NYT
Punjab	Multan	14	8	-	3	1	-	2	-
	Khanewal	4	1		-	2	-	1	-
	Lodhran	11	3	-	-	--	-	8	-
	Vehari	5	2	-	1	-	-	2	-
	Rajanpur	5	-	-	-	-	5	-	-
	Layyah	9	-	-	-	-	9	-	-
	Muzaffargarh	63	-	-	-	-	63	-	-
	DG Khan	26	-	-	-	-	26	-	-
	Sargodha	3	1	1	-	-	-	1	-
	Mianwali	2	-	-	-	-	-	2	-
	Khushab	3	-	-	1	-	-	2	-
	Bhakkar	19	4	1	-	-	-	14	-
	Attock	6	4	-	1	1	-	-	-
	Rawalpindi	11	5	-	2	-	3	1	-
	Chakwal	5	1	1	-	-	3	-	-
	Pakpatan	1	1	-	-	-	-	-	-
	Gujrat	5	-	-	-	-	-	5	-
	Lahore	12	4	-	1	-	-	7	-
	Kasur	3	1	-	-	-	-	2	-
	Hafizabad	3	1	-	-	-	-	2	-
	Jhelum	3	2	-	-	-	-	1	-
	Nankana	1	-	-	-	-	-	1	-
	Sahiwal	2	1	-	1	-	-	-	-
	Gujranwala	3	-	-	2	-	-	1	-
Sindh	Karachi	95	18	6	14	1	14	42	-
KPK	Peshawar	2	-	-	-	-	1	1	-
	Noshehra	1	-	-	1	-	-	-	-
	Swat	2	-	-	1	-	1	-	-
	Abottabad	1	1	-	-	-	-	-	-
	Lower Dir	1	-	-	-	-	-	1	-
Baluchistan	Quetta	6	-	-	-	-	-	-	6
Total		**327**	**58**	**9 (2.8)**	**28 (8.6)**	**5 (1.5)**	**125 (38.2)**	**96 (29.4)**	**6 (1.8)**

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING(PVM)

Country	*Activity*	*Description*
Israel [2]	Surv.	O/ME-SA/PanAsia2^{Qom15} was detected in 70 of the 85 diagnostic specimens collected between April and December 2018, from different cattle, sheep, gazelle, deer and wild boar. The detected lineage grouped into two principal clades. Location of were samples were collected is reported in Map 3. **Map 3**: yellow icons indicate location of the genotyped samples collected between April and December 2018 in Israel (Source –WRLFMD, Google Earth Pro).

Pakistan [15] — Vacc.

For the reporting month, a ring vaccination campaign was carried out in some of the Provinces of the country as reported in Table 6.

Province	Ring Vaccination (Doses)
Punjab	40,775
Sindh	22,500
KP	2,700
Baluchistan	1,950
Total	**67,925**

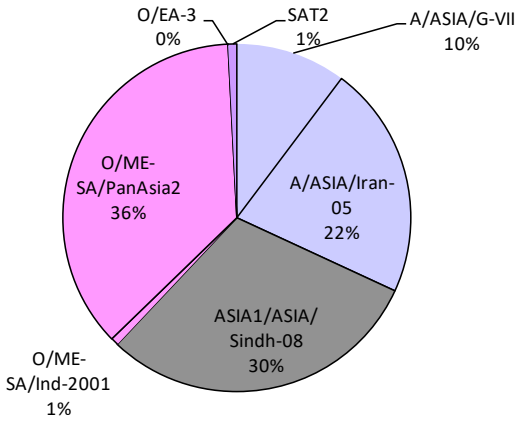
Table 6: summary of the ring vaccination campaign carried out in some of the Provinces of the country (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator).

Veterinary capacity building training courses were conducted in different provinces for Veterinary Officers and Assistants as reported in the table below.

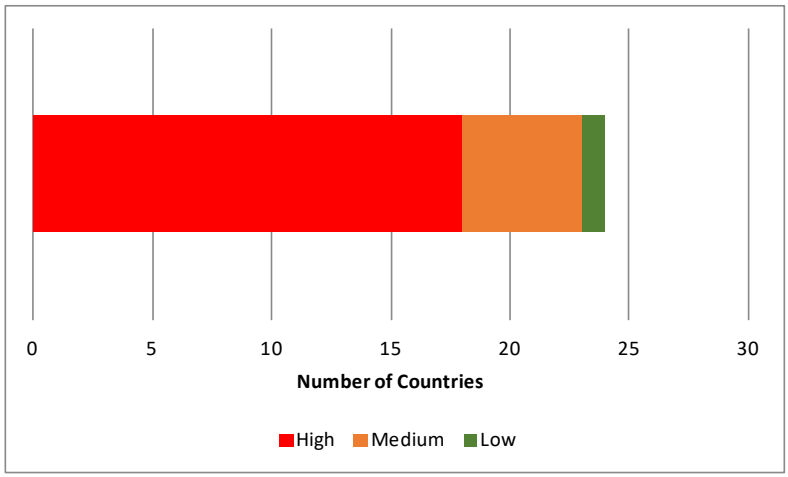
Province	Venue	No. of Workshops	Participants	
			Veterinary Officers	Veterinary Assistants
KPK	Swat	2	38	23
Sindh	Hyderabad	2	38	41
Sindh	MirpurKhas	2	34	37
Punjab	DG Khan	2	43	32
Total		**8**	**153**	**133**

Table 7 and Graph 5: Conjectured circulating FMD viral lineages in Pool 3 - West Eurasia & Middle East (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 24 countries of Pool 3 - West Eurasia
A	A/ASIA/G-VII	18
	A/ASIA/Iran-05	10
ASIA 1	ASIA1/ASIA/Sindh-08	10
O	O/ME-SA/Ind-2001	6
	O/ME-SA/PanAsia2	22
	O/EA-3	2
SAT2	SAT2	1



Graph 6 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 3 – West Eurasia & Middle East (see Annex for explanation).



D. POOL 3 – North Africa

OUTBREAKS	
Country	*Description*
Algeria [1]	Fifty nine FMD outbreaks due to serotype O, were reported mainly in the northern part of the country between November and December 2018, with the unusual reporting of cases and subsequent deaths, principally in sheep. The source of the outbreaks is unknown and the general control measures adopted are movement control, vaccination, selective killing and slaughter. Surveillance is being carried out within and outside the containment and/or protection zones. In addition, all livestock markets in the country were closed for 30 days starting from December 25th 2018. A summary of the species and number of animals involved is reported in Table 8 and location of outbreaks at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29717. *Interpretation* This is a continuation of the circulation of this serotype since 2018; the serotype was also reported in other countries in the same virus pool. **Table 8**: summary of the animals involved in the 59 outbreaks that occurred in Algeria between November and December 2018 (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Sheep	14,172	1,792	724	1	0	12.64%	5.11%	40.40%	5.12%
Cattle	197	44	1	0	2	22.34%	0.51%	2.27%	1.52%
Goats	959	51	20	5	0	5.32%	2.09%	39.22%	2.61%

*Removed from the susceptible population through death, destruction and/or slaughter

Morocco [1]

Eleven outbreaks due to FMDV serotype O were notified during January and February 2019 on multispecies farms with all outbreaks reported as already resolved.
The source of the outbreaks was unknown and the general control measures that were adopted are movement control, quarantine vaccination as reported in Table 9, official destruction of animal products. Screening and surveillance is being carried out within and outside the containment and/or protection zones.
A summary of the animals involved is reported Table 10 and location of outbreaks at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29494.

Administrative division	Species	Total Vaccinated	Details
BÉNI MELLAL-KHÉNIFRA	Cattle	6,278	886 farmers
CASABLANCA-SETTAT	Cattle	41,447	8758 farmers
FÈS-MEKNÈS	Cattle	951	180 farmers
MARRAKECH-SAFI	Cattle	644	129 farmers
SOUSS-MASSA	Cattle	1,271	163 farmers
TANGER-TÉTOUAN-AL HOCEÏMA	Cattle	269	21 farmers

Table 9: details of the vaccination activities carried out in Morocco following the outbreaks that occurred between January and February 2019

Table 10: summary of the animals involved in the 59 outbreaks that occurred in Algeria between November and December 2018 (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	104	29	1	103	0	27.88%	2.04%	6.25%	100.00%
Goat	84	0	0	84	0	0.00%	0.00%	**	100.00%
Sheep	385	0	0	385	0	0.00%	0.00%	**	100.00%

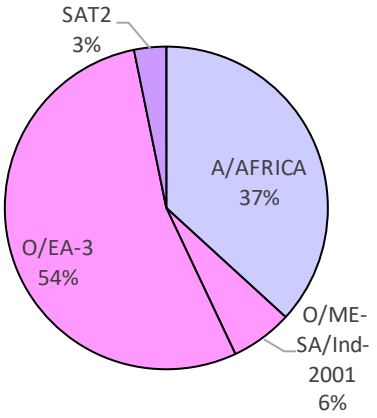
*Removed from the susceptible population through death, destruction and/or slaughter

Interpretation This is the first report of this serotype in the country in 4 years. The same serotype has also been reported in other countries in the same virus pool.

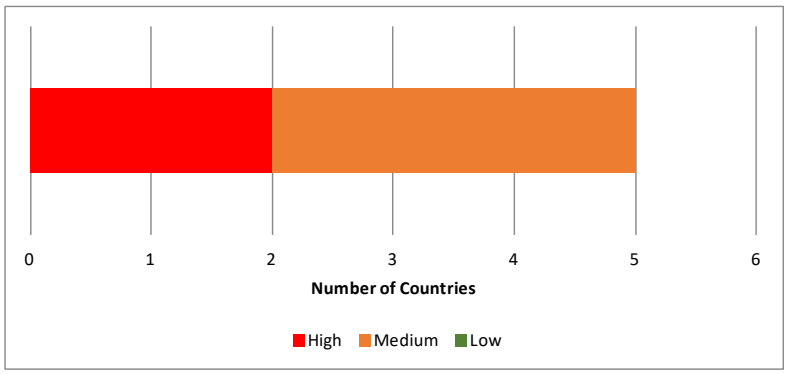
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING(PVM)		
Country	*Activity*	*Description*
Algeria [2]	Surv.	The VMSD tests conducted on two field isolates collected between 2018 and 2019 and belonging to the O/EA-3 lineage produced good matching results with the vaccine strains O 3039, O Manisa and O Tur 5/09.

Table 11 and Graph 7 Conjectured circulating FMD viral lineages in Pool 3 - North Africa (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 5 countries of Pool 3 - North Africa
A	A/AFRICA	5
O	O/ME-SA/Ind-2001	1
	O/EA-3	5
SAT 2	SAT 3	1



Graph 8 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 3 – North Africa (see Annex for explanation).



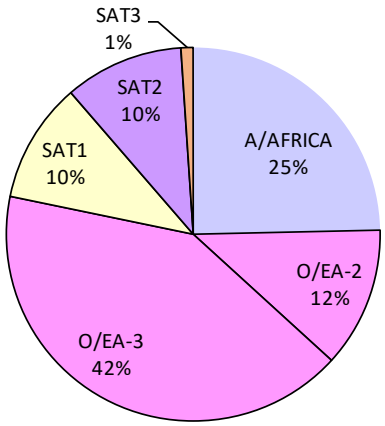
E. POOL 4 – Eastern Africa

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Ethiopia [7]	Surv.	The NAHDIC, Sebeta, Ethiopia reported the detection of FMDV serotypes A and O in probang, swab and tissue samples collected from cattle in an outbreak area. The most recent lineages detected in the country belonging to the above serotypes are A/AFRICA/G-I, A/AFRICA/G-IV and O/EA-3/unnamed in samples collected in 2018. The Laboratory has also participated to the FMD Proficiency Testing trials organised by the WRLFMD.
Kenya [8]	Surv.	The FMDNRL, Embakasi, Kenya, reported the detection of FMDV serotypes A in one sample and SAT 2 in three samples among the ten bovine specimens analysed. The most recent lineages detected in the country belonging to the above serotypes are A/AFRICA/G-I and SAT 2/IV/unnamed in samples collected in 2017. Vaccine matching tests were conducted on field samples but results of these are not available. The Laboratory also conducted the training of field staff on appropriate sampling procedures for FMD and shipment requirements for such samples.
South Sudan [2]	Surv.	The field virus detected in a sample collected in 2017 and genotyped as O/EA-3 obtained good matching results with vaccine strains O 3039, O Manisa and O TUR 5/09.

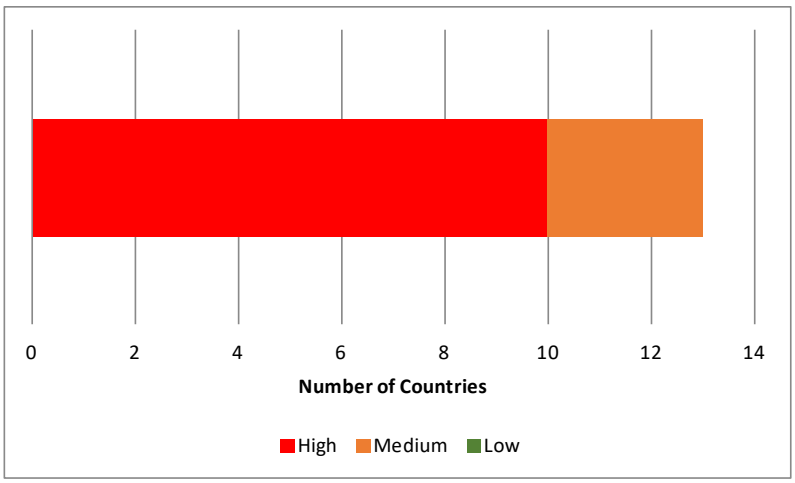
Uganda [2]	Surv.	The field viruses detected from samples collected in January and February 2019 confirmed the circulation of FMDV serotypes A and O. These outbreaks occurred in cattle farms with herds that had been vaccinated four months before in the districts of Nakaseke, with the spread of the infection to Masindi and Nakasongola. The source of these outbreaks was due to introduction of new live animals, illegal movements and contacts with infected animals at grazing and watering points along River Kafu in the dry months of the year.

Table 12 and Graph 9: Conjectured circulating FMD viral lineages in Pool 4 (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 13 countries of Pool 4 - East Africa
A	A/AFRICA	11
O	O-EA2	3
	O EA-3	9
SAT1	SAT1	10
SAT2	SAT2	6
SAT3	SAT3	5



Graph 10 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 4 (see Annex for explanation).



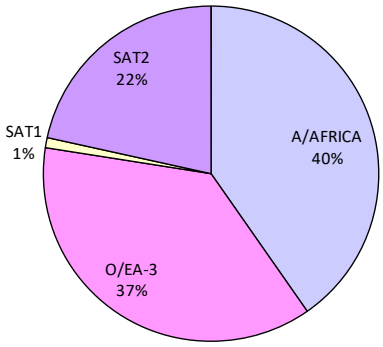
F. POOL 5 – West / Central Africa

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Burkina Faso [2]	Surv.	Two of the seven field isolates identified as O/EA-3 lineage that were detected in cattle samples collected in the country between June and August 2018, obtained good matching results in the VMSD tests using vaccine strains O 3039, O Manisa and O TUR 5/09.
Cameroon [9]	Surv.	The LANAVET, Garoua Cameroon detected FMDV in 17 (6.54%) of the 260 environmental (soil and air samples) analysed. Samples from this country were last submitted to the WRLFMD in 2013 with the detection of A/AFRICA/G-IV and SAT 2/VII/Lib-12 and SAT 2/VII/unnamed.

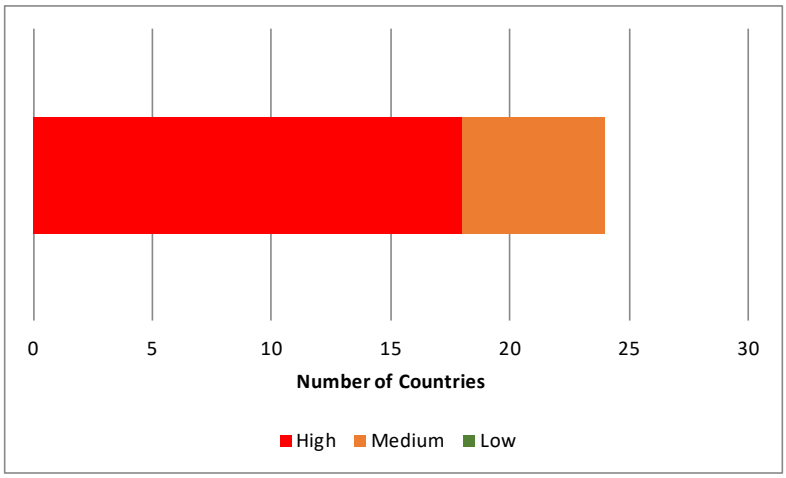
Sierra Leone [2]	Surv.	The FMDV detected in a sample collected from cattle in August 2018 that was identified as O/EA-3 obtained good matching results in the VMSD tests with vaccine strains O 3039 and O Manisa, but not with O TUR 5/09.

Table 13 and Graph 11: Conjectured circulating FMD viral lineages in Pool 5 (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 24 countries of Pool 5 -West Africa
A	A/AFRICA	14
O	O/EA-3	22
SAT1	SAT1	2
SAT2	SAT2	14



Graph 12 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 5 (see Annex for explanation).



G. POOL 6 – Southern Africa

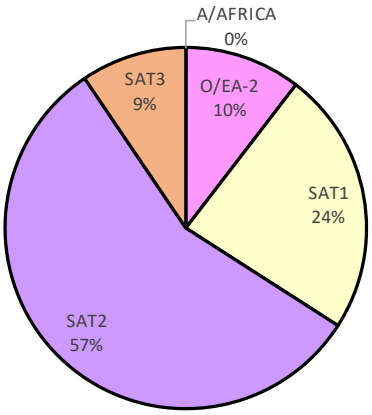
OUTBREAKS	
Country	*Description*
Serotyping pending in Malawi [1]	Clinical suspicions of seven cases of FMD outbreaks were notified in the country in a new dip tank close to Ipenza. The outbreaks are due to introduction of new live animals, illegal movement of animals, animals in transit and contact with infected animals at grazing and watering points. Movement control, quarantine and vaccination are the measures adopted for containing the spread of infection. *Interpretation* This report is consistent with previous reports. FMDV serotypes SAT 1 and SAT 2 are believed to circulate endemically in the country. Specific information is required on the field virus responsible for the notified outbreaks.
Serotype SAT 2 in	A FMD outbreak due to serotype SAT 2 was reported on January 31st 2019 in a cattle population of 8,000 animals at Makhado, Limpopo. This outbreak spilled over into South Africa's FMD High Surveillance Area,

South Africa [1, 10]	which is part of South Africa's suspended FMD Free Zone. The source of the outbreak is due to contact with wild species and the containment measures applied are movement control and quarantine, together with surveillance within containment and/or protection zone. Location of the outbreak is reported at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29442. *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country within the wildlife species in the Kruger National park. The affected areas surround the park and therefore the event is not unexpected.

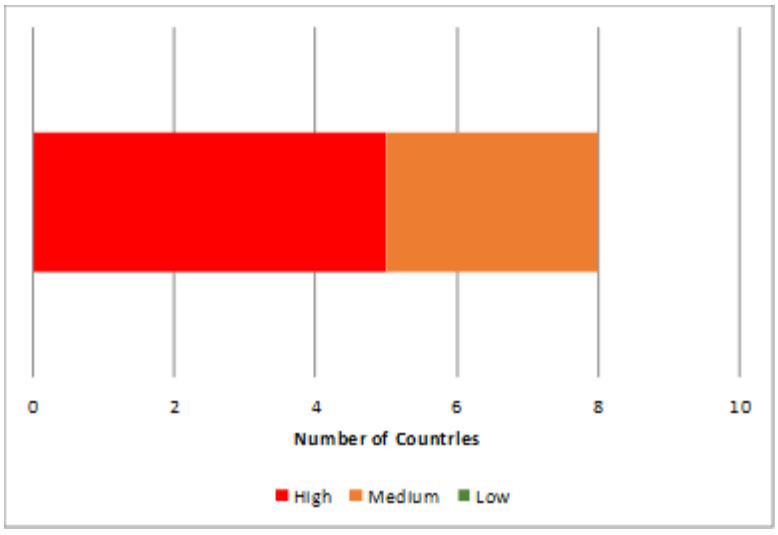
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
South Africa [11]	Surv.	The ARC-Onderstepoort Veterinary Institute reported the detection of FMDV in 2 of the 18 samples analysed. The Laboratory examined 3,480 sera using liquid-phase blocking ELISA and 3, 951 sera in solid phase competition ELISA for the detection of antibodies against SAT 1, SAT 2 and SAT while 61 serum samples were tested using a non–structural protein antibody ELISA.

Table 14 and Graph 13: Conjectured circulating FMD viral lineages in Pool 6 (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 8 countries of Pool 6 -Southern Africa
A	A/AFRICA	1
O	O-EA-2	2
SAT1	SAT1	6
SAT2	SAT2	8
SAT3	SAT3	3



Graph 14 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 6 (see Annex for explanation).

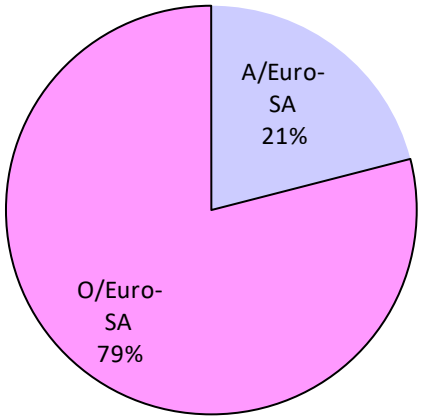


H. POOL 7 – South America

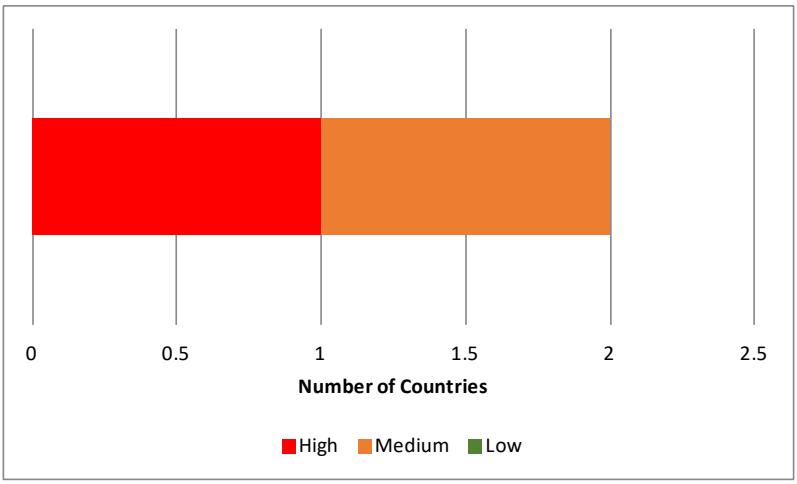
SURVEILLANCE (Surv), VACCINATION (Vacc) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
Colombia [1]	Surv	Following the outbreaks that occurred in the country due to FMDV serotype O, last notified in October 2018, the veterinary services introduced sentinels in the primary and secondary outbreaks. This process will be conducted with bovine and porcine animals free of antibodies, which were controlled for absence of contact with FMDV in the primary outbreaks of El Papayo and in the secondary outbreaks of Maravillas, El Cerrito, Tierra Prometida and Los Vila - Villa Castilla. These animals undergo individual clinical inspections and collection of serological samples on days 10, 20 and 30 that are carried out by the official services. The sentinel programme will end on February 18th 2019 and the animals used will be killed and buried.

Table 15 and Graph 15: Conjectured circulating FMD viral lineages in Pool 7 (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 2 countries of Pool 7 -South America
A	A/Euro SA	1
O	O/Euro SA	2



Graph 16 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 7 (see Annex for explanation).



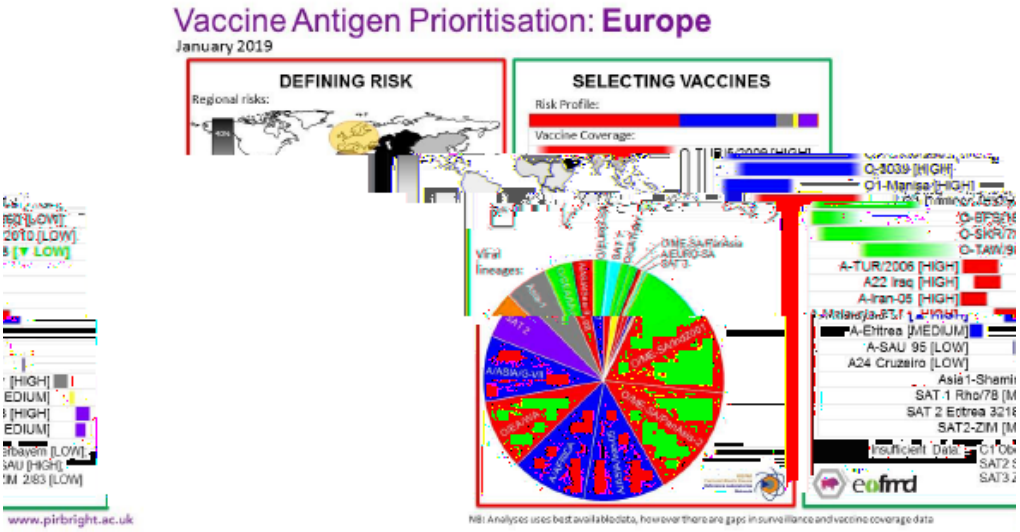
V. OTHER NEWS

[1]The 4th WRLFMD Quarterly Report for the period October – December 2018 contains a new format for recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of Table 16 is contained within the report.

Table 16: Recommendations from WRLFMD® on FMD virus strains to be included in FMDV antigen banks (for Europe).

This report provides recommendations of FMDV vaccines to be included in antigen banks. These outputs 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 OIE FAO FMD Laboratory Network regarding FMDV lineages that are present in different *source regions* (see Table below), as well as available *in vitro, in vivo* and field data to score the ability of vaccines to protect against these FMDV lineages.

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



e eight *source regions*, r Europe (using data for assistance to tailor ata presented is based ividual vaccines.

The table defines the relative distribution of FMDV lineages in each of th while the figure highlights the importance of these *source regions* fo collected at the EU-RL Workshop); please contact WRLFMD EuFMD these outputs to other geographical regions. NB: Vaccine-coverage da on available data and may under-represent the true performance of ind

VI. REFERENCES – Superscripts

1. http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home
2. World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD), www.wrlfmd.org.
3. Regional Reference Laboratory for FMD (ARRIAH, Russia) - *Dr. Svetlana. Fomina.*
4. Project Directorate on Foot and Mouth Disease (PD-FMD), Indian Council of Agricultural Research, Mukteswar, India - *Dr. S. Saravanan*.
5. National Foot and Mouth Disease and TADS Laboratory, Nepal - *Dr. Sharmila Chapagain.*
6. Central Veterinary Research and Development Laboratory (CVDRL), Aghanistan - *Dr. Wahid Bahir* Head of Laboratory
7. National Animal Health Diagnostic and Investigation Center (NAHDIC) – *Dr. Daniel Gizaw*.
8. National FMD Reference Laboratory, Embakasi, Kenya – *Dr. Kenneth Ketter.*
9. Laboratoire National Vétérinaire (LANAVET) - Garoua, Cameroon - Dr. Simon Dickmu Jumbo.
10. ARC -Onderstepoort Veterinary Institute, Republic of South Africa - Dr LE Heath/Ms E Kirkbride
11. OIE/FAO FMD Reference Laboratory Network, Annual Report 2016
12. FMD Situation in SEACFMD Countries 2015-2016; presentation at the The 23rd SEACFMD Sub-Commission Meeting 9-10 March 2017, Siem Reap, Cambodia, http://www.rr-asia.oie.int/fileadmin/sub_regional_representation/sub_regional_programme/seacfmd/SEACFMD_Activities/sub_com/23nd_Meeting__2017_/presentations/1.3_Regional_FMD_situation.pdfhttps://www.ncbi.nlm.nih.gov/pmc/articles/PMC5283054/
13. Islam, M. S., et al. "Distribution of foot and mouth disease virus serotypes in cattle of Bangladesh." SAARC Journal of Agriculture 15.1 (2017): 33-42. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5283054/ and neighbouring countries (A lineage).
14. Ibrahim Eldaghayes et al. Exploiting serological data to understand the epidemiology of foot-and-mouth disease virus serotypes circulating in Libya Open Vet J. 2017; 7(1): 1–11 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5283054/
15. Progressive Control of Foot and Mouth Disease in Pakistan - *Dr. Muhammad Afzal*, Project Coordinator.
16. http://www.fao.org/eufmd/meetings-and-events/detail/en/c/1151840/

VII. Annex

The estimates of the relative prevalence of serotypes and strains presented in the Tables below are based on the best data available to us and we are always trying to improve them. The accuracy of these estimates is only as good as the level of surveillance and reporting permits. Readers with relevant data or information are encouraged to contact EuFMD so that it can be included in the report.

In this report, the N. African countries of Morocco, Algeria, Tunisia and Libya considered together as a separate group, as the epidemiological situation is distinct and of interest to risk managers.

Description of methods

How to interpret the estimates of the relative prevalence of serotypes and strains:

If 100 animals that had been infected with FMD virus in the last 12 months were randomly selected from a country or virus pool:

1. How many animals would be infected with each serotype?
2. Within each serotype, how many would be infected with each virus strain?

Pool-level estimates and assumptions:

As the data required to calculate the relative prevalence of serotypes and strains are not directly available in most countries, they were estimated in 3 steps as follows:

1. First, each country in the pool is assigned a weight according to the number of animals infected with FMD each year:

$$weight_{country\ 1} = \frac{(FMD\ incidence * susceptible\ population)_{country1}}{\sum_{country\ 1}^{country\ n}(FMD\ incidence * susceptible\ population)}$$

   The expected FMD incidence was based on the paper by Sumption *et al* 2008 as follows: i) Low/Sporadic: 0.029 new infections per 1000 animals/year; ii) Medium: 0.458 new infections per 1000 animals/year; iii) High: 1.759 new infections per 1000 animals/year.

   The susceptible livestock population is the sum of sheep, goat, cattle, buffalo and pig populations from FAOStat.

2. For each country, the relative prevalence (RP) of each FMD serotype and strains within serotype is specified for all countries where FMD is believed to circulate endemically. First, the relative prevalence of each serotype is specified by dividing 100 points according to the serotypes that would be represented if 100 animals infected with FMDV in the previous year were randomly selected from the country. Subsequently, the relative prevalence of each serotype is broken down to reflect the distribution of circulating strains within each serotype.

   - If no information is available for a given country, then the circulating serotypes and strains are inferred from the neighbouring countries.
   - If there is only information about presence of serotypes and/or strains, but no data on the relative prevalence, then it is assumed that the serotypes/strains are circulating in equal prevalence.
   - When available, data from the last 24 months are considered, otherwise the most recent data available are used as well as the current situation in the region.
   - In the absence of reporting, a country is considered infected until it (re)gains recognition of freedom from the OIE

3. Data from steps 1 and 2 are combined at pool level according to the following formula:

$$relative\ prevalence_{serotype\ or\ strain} = \sum_{country\ 1}^{country\ n} \left(weight_{country} * RP_{serotype\ or\ strain}\right)$$

Similarly to what is described above are the criteria adopted for the categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country:

High: There has been little or no reporting of laboratory results (serotype and/or molecular characteristics) from this country within the last 24 months. The serotype/strain distribution is based on inferences from the situation in neighbouring countries;

Medium: There is some information available about the circulating serotypes and/or strains, but from a low number of samples and/or not representative of entire country or different sectors and/or not from the past 24 months;

Low: There is reliable information available about the circulating serotypes and/or strains, obtained from analysis of a large number of samples that represent the country's livestock population.

Legend of icons in the following tables

●	>=95%
◕	>=60%
◑	>=30%
◔	>=5%
○	<5%
	no strain circulating

Table 17: Conjectured circulating FMD viral lineages in each country of Pool 1 (current to February 2019)

			Presumed serotype distribution within country			Presumed viral lineage distribution within country								
Country	**Last Outbreak Repoted/Serotype**	**FMD incidence rate**	**A**	**Asia1**	**O**	**A/ASIA/SEA-97**	**ASIA1/ unnamed**	**O/ME-SA/Ind-2001**	**O/SEA/Mya-98**	**O/ME-SA/PanAsia**	**O/ME-SA/PanAsia2**	**O/CATHAY**	**Uncertainty**	**Reference**
CAMBODIA	Dec 2016/ A & O	high	◑		◑	◑				◑			medium	2
CHINA	Jan 2019/O, May 2017/A	high	◔		◕	◔		◔	◔	◔		◔	medium	2
CHINA (HONG KONG, SAR)	Dec 2018/O	high			●							●	medium	2
KOREA, DEMOCRATIC PEOPLE'S REPUBLIC OF	May 2014/not confirmed, July 2014/O	high	◑		◕	◑		◕					high	as per REPUBLIC OF KOREA (SOUTH KOREA)
LAO PEOPLE'S DEMOCRATIC REPUBLIC (LAOS)	Jan 2018/O Mar 2015/A	high	◔		◕	◔			◕	◔			medium	2
MALAYSIA	May 2018/O, August 2016/A	medium			●					●			medium	2
MONGOLIA	May 2018/O, Sept 2016/A	medium			●			◑		◕			medium	2
MYANMAR	May 2018/O, April 2017/Asia 1, July 2016/ not typed, Oct 2015/A	high	◔	◔	◕	◔	◔	◑			◑		medium	2, 12
REPUBLIC OF KOREA (SOUTH KOREA)	Jan 2019/O, April 2018/A	low/sporadic	◑		◕	◑		◕					low	2
RUSSIAN FEDERATION	Feb 2019/O, Oct 2016/Asia 1, Jan 2016/ A	low/sporadic			●				◑	◑			medium	2, 3
TAIWAN PROVINCE OF CHINA	Jun 2015/A	low/sporadic			●							●	high	as per HONG KONG
THAILAND	Oct 2018 /A & O	high	◔		◕	◔		◔	◔	◔			medium	2
VIETNAM	November 2017/A, Jan 2018/O and not typed	high	◑		◕	◑		◔	◔	◔		◔	medium	2

Table 18: Conjectured circulating FMD viral lineages in each country of Pool 2 (current to February 2019)

			Presumed serotype distribution within country			**Presumed viral lineage distribution within country**				
Country	**Last Outbreak Repoted/Serotype**	**FMD incidence rate**	A	Asia1	O	A/ASIA/G-VII	ASIA1/ unnamed	O/ME-SA/Ind-2001	**Uncertainty**	**Reference**
BANGLADESH	Dec 2016/A, ASIA 1 and O	high	◔	◔	◕	◔	◔	◕	high	13
BHUTAN	Apr 2018/O, Sep 2017/A	high	◔		◕	◔		◕	medium	2
INDIA	Feb 2019/O, Apr 2015/A, ASIA 1	high		○	●		○	●	medium	2, 4
NEPAL	Feb 2018/O, Mar 2018/Asia 1, April 2017/A	high	◔	◑	◕	◔	◑	◕	medium	2, 5
SRI LANKA	May 2018/O	high			●			●	medium	2

Table 19: Conjectured circulating FMD viral lineages in each country of Pool 3 –West Eurasia (current to February 2019)

			Presumed serotype distribution within country			Presumed viral lineage distribution within country									
Country	**Last Outbreak Repoted/Serotype**	**FMD incidence rate**	A	Asia1	O	sat2	A/ASIA/G-VII	A/ASIA/Iran-05	ASIA1/ASIA/Sindh-08	O/ME-SA/Ind-2001	O/ME-SA/PanAsia2	O/EA-3	SAT2	**Uncertainty**	**reference**
AFGHANISTAN	Feb 2018/O, Dec 2018/A, July 2018/ Asia 1	high	◑	◔	◑			◑	◔		◑			medium	6
ARMENIA	Dec 2015/A	low/sporadic	◔		◕		◔				◕			high	16, as per turkey
AZERBAIJAN	2007/0	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
BAHRAIN	Mar 2015/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
GEORGIA	2001/ASIA 1	low/sporadic	◔		◕		◔				◕			high	as per Turkey
IRAN, ISLAMIC REPUBLIC OF	Feb 2018/A, Asia 1& O,	high	◑	◔	◑		◔	◑	◔		◑			medium	2
IRAQ	Dec 2013/A, ASIA 1	high	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
ISRAEL	Feb 2019/O, June2017/A	low/sporadic	◔		◕		◔				◔	◑		low	2
JORDAN	Mar 2017/O	low/sporadic	◕		◑		◕			◔	◔			high	2, as per Saudi Arabia
KAZAKHSTAN	Jun 2013/ A & Aug 2012/O	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
KUWAIT	April 2016/O	high	◕		◑		◕			◔	◔			high	2, as per Saudi Arabia
KYRGYZSTAN	Aug 2014/not typed & Apr 2013 /O, A,	low/sporadic	◔	◕	◔			◔	◕		◔			high	as per Pakistan
LEBANON	2010/not typed	low/sporadic	◔		◕		◔				◕			high	as per Turkey
OMAN	May 2015/SAT 2	high				●							●	high	2
PAKISTAN	Feb 2019/ A, O & Asia 1	high	◔	◕	◔			◔	◕		◔			medium	2
PALESTINE	July 2018/Untyped, Dec 2017/O, Mar 2013/Sat 2	low/sporadic			●							●		medium	2
QATAR	Dec 2013/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
SAUDI ARABIA	Oct 2016/A & April 2016/O	high	◕		◑		◕			◔	◔			high	2
SYRIAN ARAB REPUBLIC (SYRIA)	2002/ A & O	high	◔		◕		◔				◕			high	as per Turkey
TAJIKISTAN	Nov 2012/ not typed & Nov 2011/Asia 1,	low/sporadic	◔	◕	◔			◔	◕		◔			high	as per Pakistan
TURKEY	Oct 2015/ A May, 2014-2015/ Asia 1 and O	high	◔		◕		◔				◕			medium	2
TURKMENISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
UNITED ARAB EMIRATES	Sep 2016/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
UZBEKISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran

Table 20: Conjectured circulating FMD viral lineages in each country of Pool 3 - North Africa (current to February 2019)

			Presumed serotype distribution within country			Presumed viral lineage distribution within country					
Country	**Last Outbreak Repoted/Serotype**	**FMD incidence rate**	**A**	**O**	**SAT 2**	**A/AFRICA**	**O/ME-SA/Ind-2001**	**O/EA-3**	**SAT 2**	**Uncertainty**	**Reference**
ALGERIA	Dec 2018/O, Nov 2016/A May-Jun 2016/Sat 2, Aug 2016/typing pending	medium	◕	◔		◕		◔		medium	2
EGYPT	April 2017/O, Nov 2016/A May-Jun 2016/Sat 2, Aug 2016/typing pending	high	○	◕	◔	○		◕	◔	medium	2
LIBYA	Oct 2013/O	high	◑	◑		◑	◔	◔		high	14
MOROCCO	Feb 2019/Not typed, Oct 2015/O	low/sporadic	◕	◔		◕		◔		high	as per Algeria
TUNISIA	Jan 2019/O, April 2017/A	medium	◑	◑		◑		◑		medium	2

Table 21: Conjectured circulating FMD viral lineages in each country of Pool 4 (current to February 2019)

			Presumed serotype distributio					Presumed viral lineage distribution							
Country	**Last Outbreak Repoted/Serotype**	**FMD incidence rate**	**A**	**O**	**sat1**	**sat2**	**sat3**	**A/AFRICA**	**O/EA-2**	**O/EA-3**	**SAT1**	**SAT2**	**SAT3**	**Uncertainty**	**Reference**
BURUNDI	Aug 2013 / not available	high	◑	◔	◔	◔		◑		◔	◔	◔		high	as per Tanzania
COMOROS	2010	high												high	no data available
DJIBOUTI	Not available	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
ERITREA	Nov 2016/not reported, Jan 2012/O	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
ETHIOPIA	Feb 2019/A& O, April 2018/ SAT 2, Feb 2018/SAT 1	high	◔	◕	◔		○	◔		◕	◔		○	medium	2, 7
KENYA	Feb 2019/A & SAT 2, Nov 2018/O, May 2018/ SAT 1	high	◔	◕	◔	◔		◔	◕		◔	◔		medium	2, 8
RWANDA	Nov 2012/not typed	high	◔	◕	◔	◔		◔	◕		◔	◔		high	as per Kenya
SOMALIA	June 2016/not reported	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
SOUTH SUDAN	June 2017/O & SAT 2, Mar 2018/A Dec 2016/ not sampled	high		●						●				high	2
SUDAN	May 2017/O	high	◑	◔		◔		◑		◔		◔		medium	2
TANZANIA, UNITED REPUBLIC OF	Oct 2016/SAT 1, Aug 2016/O & SAT 2, Jun 2016/ A	high	◑	◔	◔	◔		◑		◔	◔	◔		high	2
UGANDA	Feb 2019/A & O, Nov 2014/SAT1, Jan 2015/SAT 3, July 2015/ SAT 2 and untyped	high	◔	◕	◔	◔		◔	◕		◔	◔		high	2, as per Kenya
YEMEN	2009/O	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia

Table 22: Conjectured circulating FMD viral lineages in each country of Pool 5 (current to February 2019)

			Presumed serotype distribution within country				Presumed viral lineage distribution within country					
Country	**Last Outbreak Repoted/Serotype**	**FMD incidence rate**	**A**	**O**	**sat1**	**sat2**	**A/AFRICA**	**O/EA-3**	**SAT1**	**SAT2**	**Uncertainty**	**Reference**
BENIN	Jun 2014/O, A, SAT 1, SAT 2	high	◔	◔	◔	◔	◔	◔	◔	◔	high	1
BURKINA FASO	Aug2018/O	high	◑	◑		◑	◑	◑		◑	medium	1, as per Mali
CAMEROON	Dec 2019/untyped, Nov 2014/O, SAT 2, May 2014/SAT 1, Apr 2014/ A	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CAPE VERDE	Not available	low/sporadic		●				●			high	as per Senegal
CENTRAL AFRICAN REPUBLIC	Not available	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CHAD	Aug 2016/Not reported	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CONGO	Jun 2013/not typed	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CONGO, DEMOCRATIC REPUBLIC OF	Mar 2018/untyped	high	◑	◑	◑		◑	◑	◑		high	1
COTE D'IVOIRE	Jun 2018/O	high		●				●			high	1, as per Guinea
EQUATORIAL GUINEA	Not available	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
GABON	Not available	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
GAMBIA	July 2018/O	high		●				●			medium	1
GHANA	July 2018/untyped, June 2017/O, Dec 2016/ SAT 2,2014/not available	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
GUINEA	Sep 2018/O	high		●				●			medium	1
GUINEA-BISSAU	Aug 2018/O	high		●				●			high	as per Guinea
LIBERIA	Not available	high		●				●			high	as per Guinea
MALI	Oct 2016/not reported	high	◑	◑		◑	◑	◑		◑	high	1
MAURITANIA	July 2018/O, Dec 2014/SAT 2	high				●				●	medium	2
NIGER	2014/not sampled, May 2015/O	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
NIGERIA	Sep 2018/O &Sat 2, Sept 2016/ SAT 1, Nov 2015/A	high	◑	◑		◔	◑	◑		◔	high	2
SAO TOME AND PRINCIPE	Not available	0									high	no data available
SENEGAL	Sep 2018/O, Feb 2015/ A, 2014/ SAT 2	high		●				●			medium	2
SIERRA LEONE	Aug 2018/O	high		●				●			medium	as per Senegal
TOGO	2012/O	high	◑	◑		◔	◑	◑		◔	high	1, as per Nigeria

Table 23: Conjectured circulating FMD viral lineages in each country of Pool 6 (current to February 2019)

			Presumed serotype distribution within country					Presumed viral lineage distribution within country						
Country	**Last Outbreak Repoted/Serotype**	**FMD incidence rate**	**A**	O	SAT1	SAT2	SAT3	A/AFRICA	O/EA-2	SAT1	SAT2	SAT3	**Uncertainty**	**Reference**
ANGOLA	April 2016/SAT 2	high		◑	◔	◔	◑		◑	◔	◔	◑	high	as per Zambia
BOTSWANA	July 2018/SAT 2, June 2015/SAT 1	medium				●				○	●		medium	2
MALAWI	Feb 2019/untyed, Jan 2019/SAT 2, June 2016/SAT 1	medium			◑	◑				◑	◑		high	2
MOZAMBIQUE	June 2018/ Typing pending, Oct 2017/SAT 2, May 2015/ SAT 1	high				◕	◔				◕	◔	high	2
NAMIBIA	Sep 2017/SAT 2, Aug 2017/typing pending, May 2015/SAT 1	medium			◑	◑				◑	◑		high	2
SOUTH AFRICA	Jan 2019/SAT 2, Oct 2017/SAT 1, Dec 2015/SAT 3	medium			◔	◕				◔	◕		high	2, 10
ZAMBIA	Jan 2019/ A &O, May 2017/SAT 3, Mar 2017/SAT 2, Jan 2013/SAT 1	low/sporadic	◔	◑	◔	◔	◑	◔	◑	◔	◔	◑	medium	2
ZIMBABWE	Jan 2019/SAT 1 & SAT 2, Sep2018/typing pending, Jun 2013/SAT 3	high			◑	◑				◑	◑		medium	1, 2

Table 24: Conjectured circulating FMD viral lineages in each country of Pool 7 (current to February 2019)

			Presumed serotype distribution within country		Presumed viral lineage distribution within country			
Country	**Last Outbreak Repoted/Serotype**	**FMD incidence rate**	A	O	A/Euro SA	O/Euro-SA	**Uncertainty**	**Reference**
VENEZUELA	Oct 2018/O	medium	◑	◑	◑	◑	high	11
COLUMBIA	2011/O, 2013/A	medium		●		●	medium	1

This publication has been produced with the assistance of the European Union.
The contents of this publication are the sole responsibility of FAO and
can in no way be taken to reflect the views of the European Union.

European Commission for the Control of Foot-and-Mouth Disease | fao.eufmd.org

CA4024EN/1/10.19