Food and Agriculture Organization of the United Nations

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

GLOBAL Monthly Report

Foot-and-Mouth Disease

Foot-and-Mouth Disease Situation | 2019 | July

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

July 2019

MAIN INFORMATION SOURCES USED:

Databases:
OIE WAHIS 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 in references.

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.

CONTENTS

Please note that the report contains hyperlinks

I. HIGHLIGHTS

Summary comments:

I write this short editorial as the summer in the UK comes to an end. Since my last contribution (April 2019), the WRLFMD has reported test results for samples submitted from Algeria, Bhutan, Côte d'Ivoire, Ethiopia, Egypt, Guinea, Hong Kong SAR, Israel, Nepal, Myanmar, Pakistan, Palestine (State of), Saudi Arabia, Turkey, Uganda, Vietnam, Zambia. New sequence data submitted from Comoros and Tanzania (from ANSES, France and SUA, Tanzania), Libya (from IZSLER, Italy) and Malawi (from BVI) were also analysed. Reports for these samples can be retrieved from the WRLFMD website (http://www.wrlfmd.org/country-reports).

During July 2019, samples collected from FMD outbreaks in Punjab, Pakistan were tested by WRLFMD. These viruses were characterised as belonging to the O/ME-SA/Ind-2001e lineage. These new cases expand the geographical range of this pandemic lineage and represent the first time that O/ME-SA/Ind-2001 viruses have been recently detected in any of the three countries (Pakistan, Afghanistan and Iran) that play such an important epidemiological role in the maintenance of FMD in West Eurasia. Elsewhere, FMD cases (due to the O/EA-2 topotype) on the Islands of the Comoros (from the OIE Reference Laboratory at ANSES, Paris reported on the 17th April) were included at the end of the last report; where sequence data showed close genetic relationship to FMD viruses in Tanzania that are distinct to FMD viruses from the same topotype that are currently spreading into central Zambia. In North Africa, new outbreaks due to the O/EA-3 topotype continue to be detected. Most recent cases have led to samples being collected during May 2019 in Misrata and Tajoura, Libya which have been tested by the OIE/FAO Reference Laboratory in Brescia, Italy (IZSLER). Positive results were generated using a real-time RT-PCR specific for the O/EA-3 lineage, and sequence data has been recovered demonstrating close genetic relationship to FMD outbreaks that have been previously confirmed in other North African (Maghreb) countries, including Morocco, where cases have continued to be reported during this quarter.

The OIE/FAO FMD Laboratory Network (https://www.foot-and-mouth.org) encourages countries to submit appropriate clinical samples for laboratory analyses including sequencing and vaccine matching (testing is free-of-charge), for further information or assistance with shipments, please contact donald.king@pirbright.ac.uk.

Don King (WRLFMD, Pirbright)

September 2019

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	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, O and SAT 2**
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

Myanmar [1] **–** FMDV field isolate detected in 2013 and belonging to serotype A obtained partially good matching results when analysed in the vaccine matching strain differentiation (VMSD) tests.

POOL 2 - SOUTH ASIA

India [2] **-** ICAR-Directorate of Foot and Mouth Disease, Mukteswar, India detected FMDV serotype O for the reporting month.

Nepal [1] **–** FMDV field isolates detected in 2018 and 2019 and belonging to serotype O obtained good matching results when analysed in the VMSD tests.

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan [11] **-** The Central Veterinary Research and Development Laboratory (CVDRL) detected FMDV serotypes A, ASIA 1 and O among the samples analysed during July.

Israel [3] – A FMD outbreak due to serotype O was notified on August 1st 2019 at a cattle farm in Haifa.

Palestine [1] - FMDV field isolates detected in 2019 and belonging to FMDV serotype O obtained good matching results when analysed in the VMSD tests.

Turkey [1] – FMDV field isolates detected between 2017 and 2019, belonging to serotypes A and O obtained matching results of variable level when analysed in the VMSD tests.

Paksitan [13] **–** Sixty eight FMD outbreaks due to serotypes A, Asia 1 and O were reported during June in the provinces of Baluchistan, Khyber Pakhtunkhwa, Punjub, and Sindh.

POOL 3 – NORTH AFRICA

Morocco [1, 3] – An outbreak due to FMDV serotype O was notified in a multispecies ruminant farm at Souss-Massa on July 19th 2019.
A FMD field isolate detected in 2019 and belonging to serotype O obtained good matching results when analysed in the VMSD tests.

POOL 4 - EASTERN AFRICA

Kenya [4] - The FMD National Reference Laboratory (FMDNRL), Embakasi, Kenya detected during the current month, FMDV serotypes A, O and SAT 2.

Uganda [1] **–** Further to the results reported in the June edition of this report, other FMDV field isolates detected in 2019 belonging to serotype O obtained good matching results when analysed in the VMSD tests.

POOL 5 - WEST/CENTRAL AFRICA

Mauritania [1] – A FMDV field isolate belonging to serotype O was subjected to VMSD tests obtaining partially good matching results.

POOL 6 - SOUTHERN AFRICA

Malawi [3] – FMDV serotype SAT 2 was detected in April 2019 in cattle of a village of Central.

Zambia [3] – Four outbreaks due to FMDV serotype O were detected during June 2019 in cattle at Central, Copperbelt and Lusaka.

Zimbabwe [3] – FMDV serotype SAT 2 was responsible for the outbreak reported during July 2019 in a village of Matabeleland North.

POOL 7 - SOUTH AMERICA [3, 5]

No outbreaks were reported for this Pool. FMD was last reported in South America with outbreaks due to FMDV serotype O in Colombia during October 2018 and due to serotype A in Venezuela during 2013.

COUNTER

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

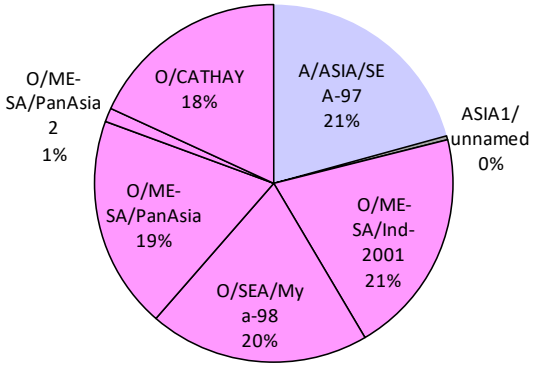
IV. DETAILED POOL ANALYSIS

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

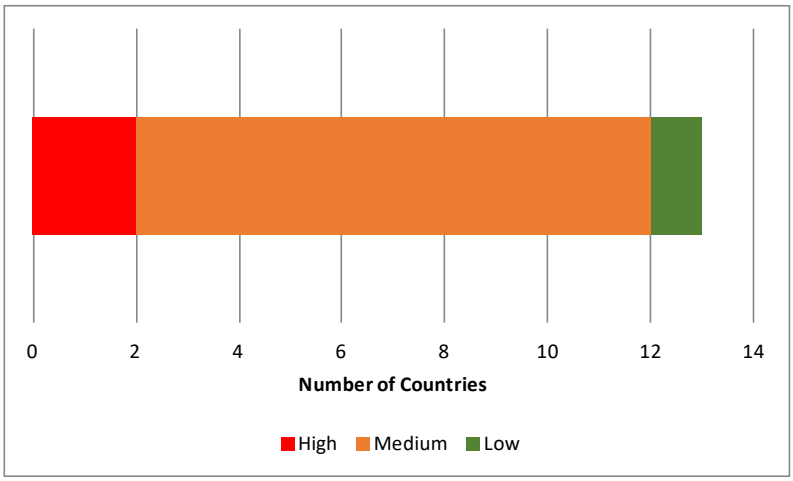
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Myanmar [1]	PVM	The field sample, O/MYA/2013, genotyped as O/SEA/Mya-98, obtained good matching results with O 3039, O Manisa (at the limit) and O Tur5 /09.

Table 1 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	8
	O/SEA/Mya-98	6
	O/ME-SA/PanAsia	8
	O/ME-SA/PanAsia2	1
	O/CATHAY	4



Graph 2: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 1 – see Annex for explanation).

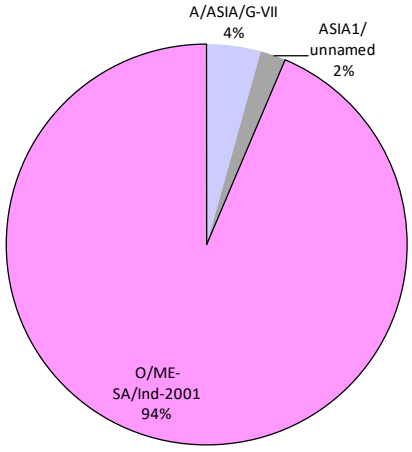


B. POOL 2 – South Asia

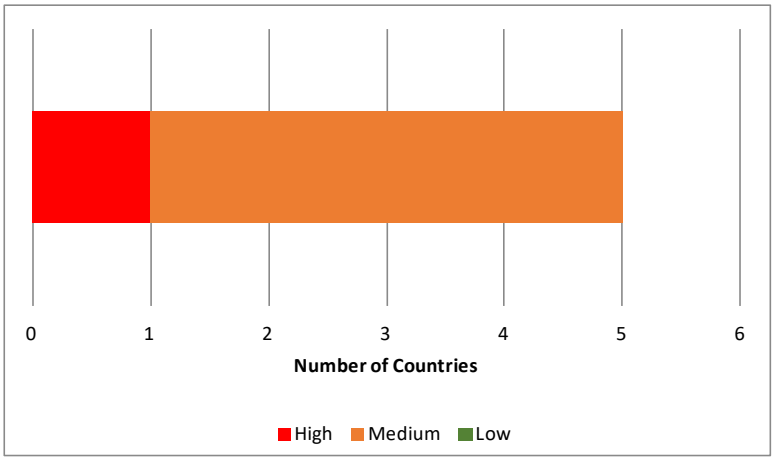
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
India [2]	Surv.	The ICAR-Directorate of Foot and Mouth Disease, Mukteswar, India detected FMDV serotype O in a cattle sample that was submitted to genotyping. The laboratory examined 1,654 serum samples collected within epidemiological studies and 17,682 serum samples collected within the FMD control programme. The sublineages currently circulating in the country are represented by O/ME-SA/2001d and O/ME-SA/2001e as described in the latest issue of the ICAR-DFMD Annual Report of 2017-18.
Nepal [1]	PVM	Two field samples, O/NEP/7/2018 and O/NEP/1/2019, detected in cattle samples and identified as O/ME-SA/2001e obtained good matching results with O 3039, O Manisa and O Tur5 /09.

Table 2 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	1
O	O/ME-SA/Ind-2001	5



Graph 4: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 2 (see Annex for explanation).



C. POOL 3 – West Eurasia & Middle East

OUTBREAKS	
Country	*Description*
Serotype O in Israel [3]	Following the outbreaks that were first reported in April 2019, a new episode still caused by O/ME-SA/PanAsia2 was detected on August 1st 2019 at cattle farm at Haifa (see Map 1). The apparent morbidity rate observed for the 700 animals present was 0.29% without any mortality. The Kimron Veterinary Institute, FMD Laboratory, confirmed the diagnosis on August 4th 2019 using real-time PCR and nucleotide sequencing. The origin of outbreak is unknown and general control measures were applied for the containment of the outbreak. Interpretation: This report is consistent with previous reports. The causative lineage is believed to circulate sporadically in the country. As various outbreaks occurred during the reporting year, surveillance of the current situation would aid to define the extent of the circulation of the virus in the country  Map 1: location of FMD outbreak (circled in violet), due to O/ME-SA/PanAsia 2 that occurred at En Ayyala, Hadera, Haifa on August 1st 2019 (Source - Wahis and UN Geospatial Information Section maps).
Serotypes A, Asia 1 and O in Pakistan [13]	Sixty eight FMD outbreaks due to serotypes A (1.62%), Asia 1 (3.22%) and O (11.29%) and not typed (83.87%) were reported during June in the provinces of Baluchistan, Khyber Pakhtunkhwa, Punjub, and Sindh. **Table 3**: number of outbreaks reported in different provinces of Pakistan during July 2019 (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator).

Province	District	Number Outbreaks	Number of Outbreaks per FMDV Serotype					
			O	A	Asia-1	Mixed	Not yet typed	Negative
Punjab	Rawalpindi	4	-	-	-	-	4	-
	Lahore	2	1	-	-	-	0	1
	Faisalabad	4	-	-	-	-	4	-
	Jhung	2	-	-	-	-	2	-
	Chiniot	1	-	-	-	-	1	-
Sindh	Karachi	29	-	-	-	-	29	-
Khyber Pakhtunkhwa	Swat	4	-	1	2	-	0	1
	Karak	5	4	-	-	-	0	1
	Mardan	1	-	-	-	-	0	1
	Charsadda	7	-	-	-	-	6	1
	Abbotabad	5	-	-	-	-	4	1
Baluchistan	Quetta	4	2	-	-	-	2	-
Total		68	7	1	2	-	52	6

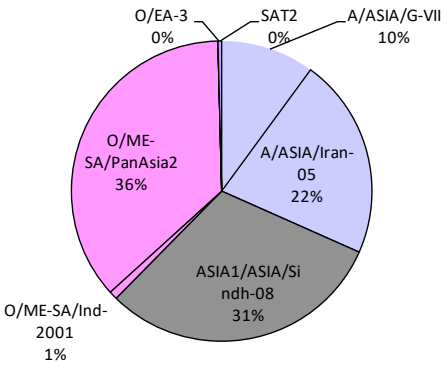
Interpretation This report is consistent with previous reports. Different serotypes of FMDV are believed to circulate endemically in the country. Details of the circulating serotypes and lineage that were genotyped by the WRLFMD will be provided in the next report.

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Afghanistan [11]	Surv.	The CVDRL, Afghanistan detected the following FMDV serotypes in the 47 samples analysed: A in one sample (2.64%), ASIA 1 in 22 samples (57.89%) and O in 11 samples (28.95%) while for 4 samples (10.52%), although positive for FMDV, serotyping was not achieved. A/ASIA/Iran-05, Asia 1/ASIA/Sindh-08 and O/ME-SA/PanAsia-2 are the most recent lineages detected by the WRLFMD in samples collected in the country during 2016 and 2017.
Pakistan [13]		Emergency vaccination was carried out in the country as reported in Table 4.
Palestine [1]	PVM	Two FMDV field isolates, O/PAT/3/2019 and O/PAT/3/2019, detected in cattle and genotyped as O/ME-SA/PanAsia2^{Qom15}, obtained good matching results in the VMSD tests conducted using vaccine strains O 3039, O Manisa and o Tur 5/09.
Turkey [1]	PVM	FMDV field isolates, A/TUR/1/2017 and A7TUR/13/2017 genotyped as A/ASIA/G-VII obtained good matching results with A/GVII but not with A Iran 2005, A TUR 20/06 and A22 IRQ/24/64. Field isolates, O/TUR/1172018 and O/TUR74/2019, genotyped O7ME-SA/PanaAsia-2^{QOM-15}, obtained good matching results with vaccine strains O 3039, O Manisa and o Tur 5/09.

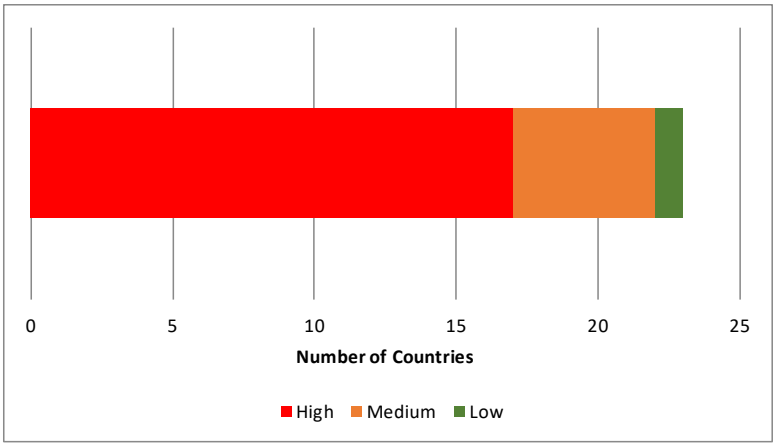
Province	Ring Vaccination (Doses)
Punjab	500
Sindh	725
Khyber Pakhtunkhwa	550
Baluchistan	0
Total	**1,775**

Table 5 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	17
	A/ASIA/Iran-05	9
ASIA 1	ASIA1/ASIA/Sindh-08	9
O	O/ME-SA/Ind-2001	7
	O/ME-SA/PanAsia2	22
	O/EA-3	2
SAT2	SAT2	1



Graph 6: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 3 – West Eurasia & Middle East (see Annex for explanation).



D. POOL 3 – North Africa

OUTBREAKS	
Country	*Description*
Serotype O in Morocco [3]	A FMD outbreak due to serotype O was detected on July 19th 2019 at El Mers, Belfaa, Chtouka Ait Baha, Souss-Massa on a multiple species (cattle, goat and sheep) ruminant farm. The episode was notified as resolved on July 25th 2019. Apparent morbidity and mortality rates were respectively 24% and 4% in the 25 cattle present and in the other species. Diagnosis was confirmed by the Regional Analysis and Research laboratory, Meknes on July 24th 2019 with the detection of FMDV in cattle, goat and sheep samples analysed using the real-time reverse transcriptase/polymerase chain reaction. The origin of the outbreak is unknown and among the control measures adopted was vaccination in response to the outbreak with the vaccination of cattle farms as reported in Table 0. Details on the type of vaccine used were not provided. Interpretation: This report is consistent with previous reports. The causative lineage is believed to circulate endemically in the country. More information through surveillance of the ongoing situation would aid to better interpret the significance of this report.

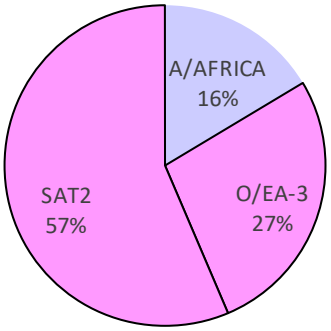
Administrative division	N° of animals vaccinated	N° of farms vaccinated
BÉNI MELLAL-KHÉNIFRA	6,278	886
CASABLANCA-SETTAT	41,447	8,758
FÈS-MEKNÈS	1,616	395
MARRAKECH-SAFI	644	129
RABAT-SALÉ-KÉNITRA	597	62
SOUSS-MASSA	4,227	477
TANGER-TÉTOUAN-AL HOCEÏMA	691	211
Totals	55,500	10,918

Table 6: summary of vaccination conducted in Morocco following the FMD outbreaks detected since the beginning of 2019.

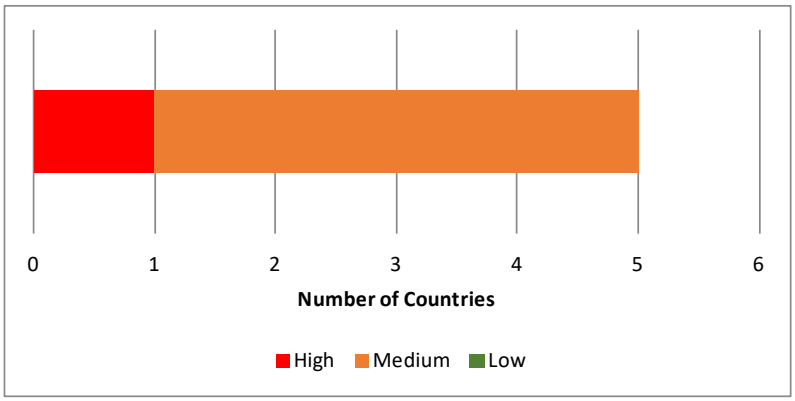
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Morocco [1]	PVM	The field isolate O/MOR/1/2019 genotyped as O/EA-3 obtained good matching results with vaccine strains O 3039, O Manisa and o Tur 5/09 employed in the VMSD tests.

Table 7 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	4
O	O/EA-3	5
SAT 2	SAT 2	2



Graph 8: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 3 – North Africa (see Annex for explanation).

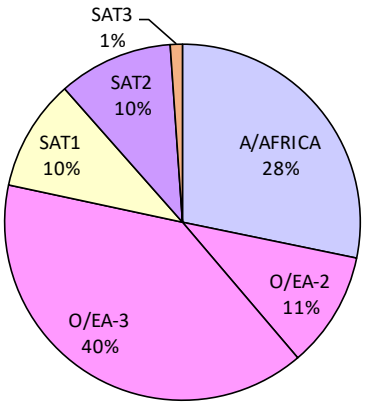


E. POOL 4 – Eastern Africa

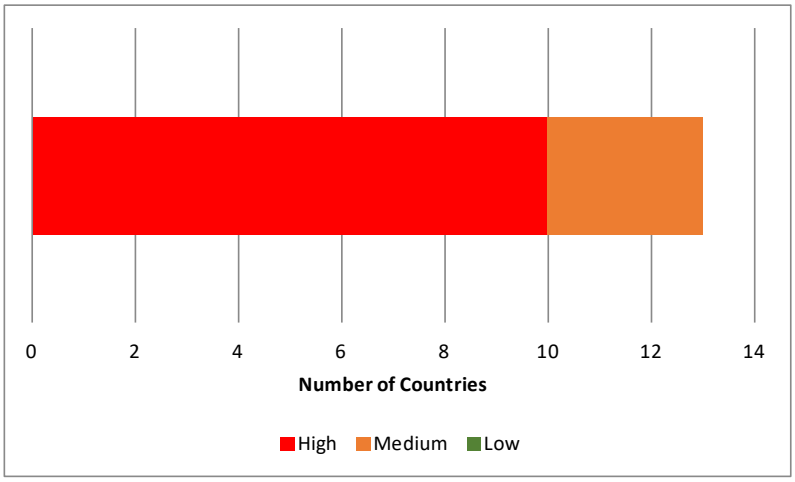
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Kenya [4]	Surv.	The FMD NRL, Embakasi, Kenya, reported the detection of FMDV serotypes A in two samples, O in three samples and SAT 2 in two samples, among the twenty-three bovine sample analysed. The most recent lineages detected in the country are A/AFRICA/G-I and SAT 2/IV/unnamed in samples collected in 2017.
Uganda [1]	Vacc.	Further to the results reported in the June edition of this report, field isolates belonging to lineage A/AFRICA/G-I (A/UGA/28/2019 and A/UGA/42/2019) did not obtain good matching results with another vaccine strain represented by A22 IRQ/24/64. In addition to field isolate O/UGA/10/2019, other field isolates, O/UGA/6/2019 and O/UGA/21/2019 were also analysed in the VMSD tests, obtaining good matching results with O 3039, O Manisa and O TUR5/09, contrary to what was obtained for the first field isolate.

Table 8and 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	4
	O EA-3	9
SAT1	SAT1	10
SAT2	SAT2	6
SAT3	SAT3	5



Graph 10: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 4 (see Annex for explanation).

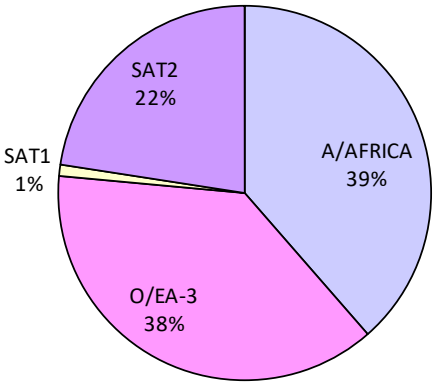


F. POOL 5 – West / Central Africa

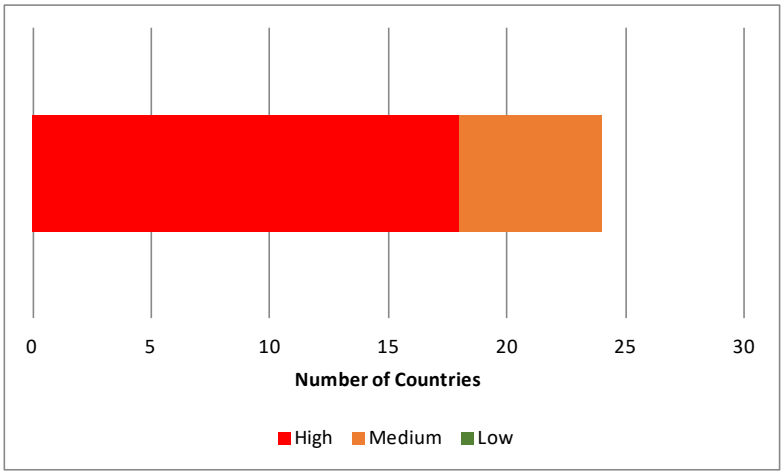
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Mauritania [1]	PVM	The field isolate O/MAU/1/2018, genotyped as O/EA-3, was analysed in VMSD tests and obtained good matching results with vaccine strains O 3039, and O TUR5/09 but not with O Manisa. Therefore, decision-makers should advice the utilization of vaccines containing the strains with good matching results for the genotyped O/EA-3. Further investigation needs to be undertaken to better understand the O Manisa vaccine activity.

Table 9 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	13
O	O/EA-3	22
SAT1	SAT1	2
SAT2	SAT2	14

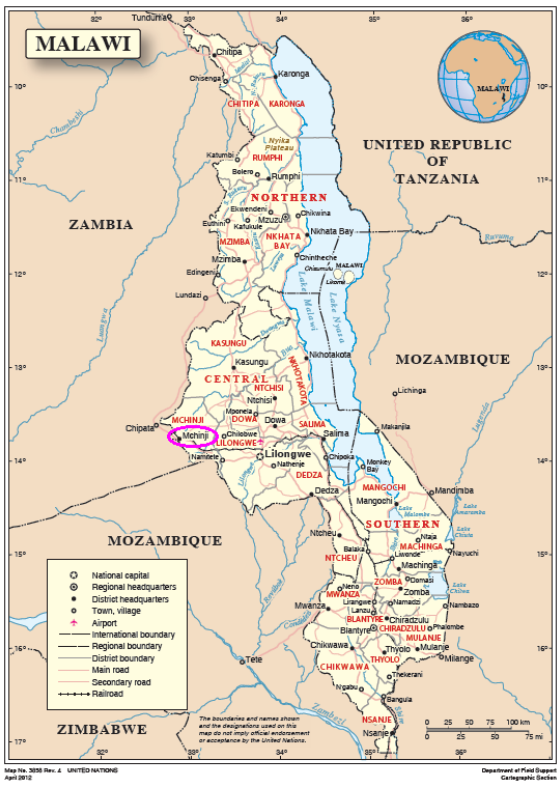


Graph 12: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 5 (see Annex for explanation).



G. POOL 6 – Southern Africa

OUTBREAKS	
Country	*Description*
Serotype SAT 2 in Malawi [3]	A FMD outbreak due to serotype SAT 2 was notified on 10th April 2019 in cattle at Mchinji, Central (see Map 2). The diagnosis was confirmed by the Botswana Veterinary Institute (OIE Reference Laboratory) on June 17th 2019 using virus isolation. The source of the infection is attributed to the introduction of new live animals, illegal movement of animals, animals in transit and contact with infected animals at grazing/watering points. Among other control measures adopted, primer vaccination was administered to 44,535 animals at Mzimba and to 13,746 animals at Kasungu and booster vaccinations was carried out in 40,893 animals at Mzimba and in 12,208 animals at Kasungu. As no cases were detected affected area, the containment measures were partially lifted on June 20th 2019. While no mortality was registered, apparent morbidity rate was 0.49% in the 20,000 exposed cattle. Interpretation: This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country.



Map 2: location of FMD outbreak (circled in violet), due to serotype SAT 2 that was detected on 10th April 2019 in cattle at Mchinji, Central (Source - Wahis and UN Geospatial Information Section maps).

Serotype O in Zambia [3]

Four FMD outbreaks due to O were detected during between June 12th and 28th 2019 in cattle at Central, Copperbelt and Lusaka (see Map 3), with two of the episodes located in the latter district. Diagnosis was carried out on July 1st 2019 by the Central Veterinary Research Institute using antigen detection ELISA and 3ABC ELISA.

The source of the outbreaks was attributed to the illegal movement of animals with the adoption of control measures, including the vaccination of 13, 643 cattle at Central (ring vaccination) and 99,855 cattle at Southern. Details of the type of vaccine used were not provided.

No mortality was observed, while apparent morbidity was 6.42% in the 1,728 exposed cattle.

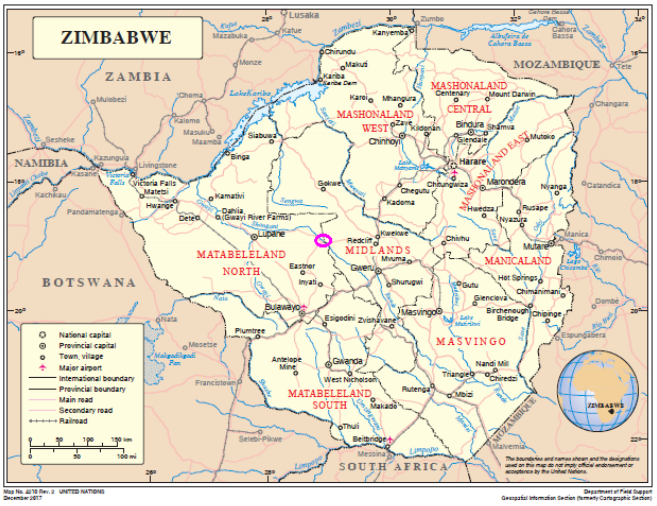
Interpretation: This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country.

Map 3: location (circled in purple) of the four FMD outbreaks due to O detected during between 12th and 28th June 2019 in cattle at Central, Copperbelt and Lusaka with two of the episodes located in the latter location (Source - Wahis and UN Geospatial Information Section maps).

Serotype SAT 2 in Zimbabwe [3]

A FMD outbreak due to serotype SAT 2 was detected on June 17th 2019 Tshugulu, Nkayi, Matabeleland North (see Map 4). The source of the outbreak was due to contact with infected wild and domestic animals at grazing and watering points.

The cases in the Nkayi district are in a area sharing a border with the previously infected Kwekwe district that is suspected to be due to illegal cattle movements in search of relief grazing. For this, Nkayi district was placed under quarantine with livestock inspections and farmer awareness campaigns.
Apparent morbidity was 0.19% in the 2133 exposed cattle, without any deaths.

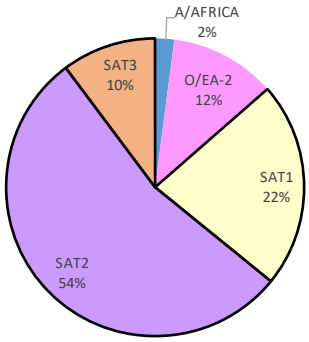


Map 4: location (circled in purple) of the FMD outbreak due to serotype SAT 2 was detected on June 17th 2019 Tshugulu, Nkayi, Matabeleland North (Source - Wahis and UN Geospatial Information Section maps).

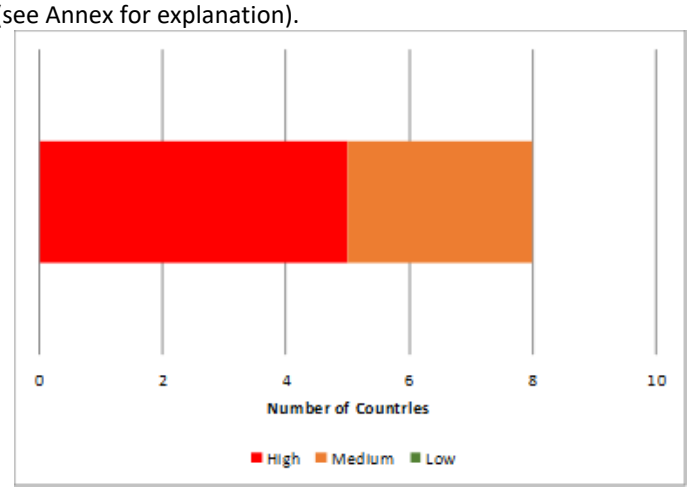
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
South Africa [6]	Surv.	The Agricultural Research Council, Onderstpoort Veterinary Institute, Transboundary Animal Diseases (OIE Reference Laboratory) analysed 6,024 sera in solid-phase competition ELISA for the detection antibodies against FMDV serotypes SAT 1, SAT 2 and SAT 3 and 123 in non-structural protein ELISA.

Table 10 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	2
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 prevalence of circulating serotypes/strains defined for each country of Pool 6 (see Annex for explanation).

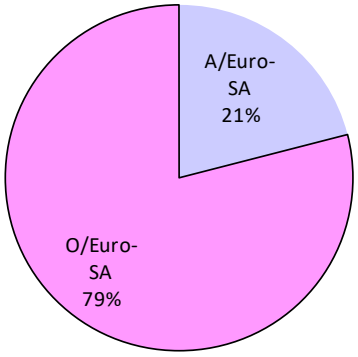


H. POOL 7 – South America

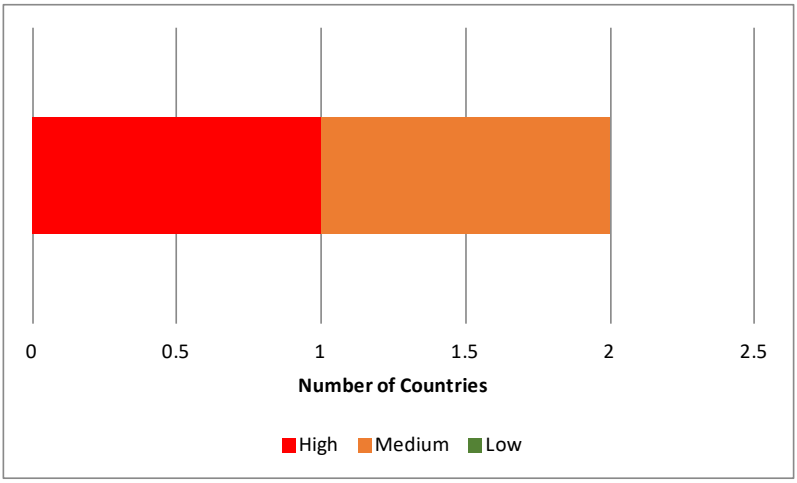
No outbreaks are reported for this Pool during the reporting month.

Table 11 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 prevalence of circulating serotypes/strains defined for each country of Pool 7 (see Annex for explanation).



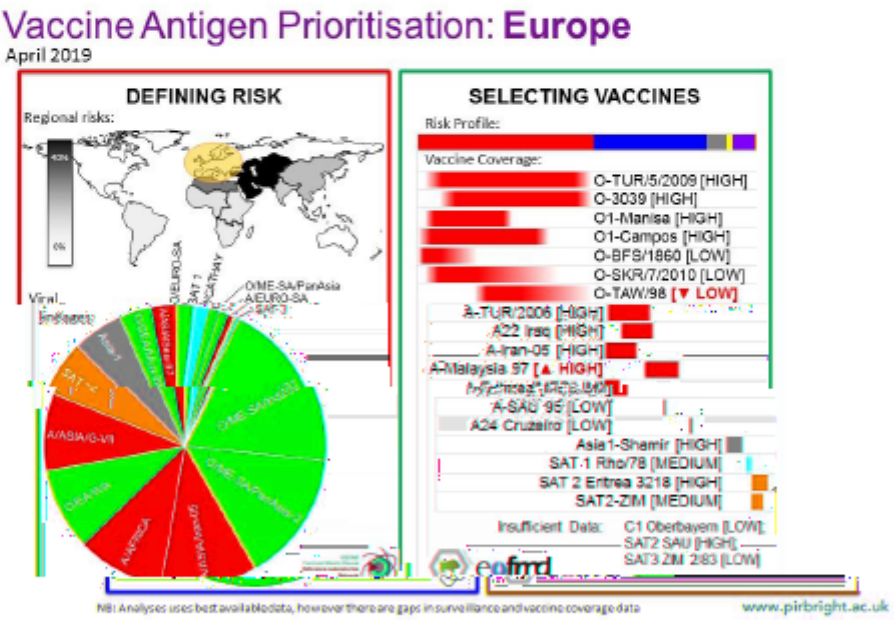
V. OTHER NEWS

[1]The 1st WRLFMD Quarterly Report for the period April-June 2019 contains the recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of Table 11 is contained within the report.

Table 12: 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	-	-	-	-	-	-	-	-



ions, The table defines the relative distribution of FMDV lineages in each of the eight *source reg*
data while the figure highlights the importance of these *source regions* for **Europe** (using
tailor collected at the EU-RL Workshop); please contact WRLFMD EuFMD for assistance to
ased these outputs to other geographical regions. NB: Vaccine-coverage data presented is b
on available data and may under-represent the true performance of individual vaccines.

VI. REFERENCES – Superscripts

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6. ARC -Onderstepoort Veterinary Institute, Republic of South Africa - *Dr LE Heath/Ms E Kirkbride*
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12. OIE/FAO FMD Reference Laboratory Network, Annual Report 2017
13. Progressive Control of Foot and Mouth Disease in Pakistan - *Dr. Muhammad Afzal*, Project Coordinator.

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 13: Conjectured circulating FMD viral lineages in each country of Pool 1 (current to July 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 on circulating serotypes**	**Reference**
CAMBODIA	Aug 2018/O, Aug 2016/ A	high	◑		◑	◑				◑			medium	1
CHINA	April 2019/O, May 2017/A	high	◔		◕	◔		◔	◔	◔		◔	medium	1
CHINA (HONG KONG, SAR)	Dec 2018/O	high			●							●	medium	1
KOREA, DEMOCRATIC PEOPLE'S REPUBLIC OF	Dec 2016/O	high	◑		◕	◑		◕					high	as per REPUBLIC OF KOREA (SOUTH KOREA)
LAO PEOPLE'S DEMOCRATIC REPUBLIC (LAOS)	Dec 2018/A & O	high	◔		◕	◔			◕	◔			medium	1
MALAYSIA	May 2018/O, August 2016/A	medium			●					●			medium	1
MONGOLIA	Jun 2018/O, Sept 2016/A	medium			●			◑	◑	◑			medium	1
MYANMAR	Dec 2018/O, April 2017/Asia 1, Oct 2015/A	high	◔	◔	◕	◔	◔	◑			◑		medium	1, 7
REPUBLIC OF KOREA (SOUTH KOREA)	Jan 2019/O, April 2018/A	low/sporadic	◑		◕	◑		◕					low	1
RUSSIAN FEDERATION	March 2019/O, Oct 2016/Asia 1, Jan 2016/ A	low/sporadic			●			◑	◑	◑			medium	1
TAIWAN PROVINCE OF CHINA	Jun 2015/A	low/sporadic			●							●	high	as per HONG KONG
THAILAND	Oct 2018 /A & O	high	◔		◕	◔		◔	◔	◔			medium	1
VIETNAM	Jan 2019/O, November 2017/A and not typed	high	◑		◕	◑		◔	◑	◔		◔	medium	1

Table 14: Conjectured circulating FMD viral lineages in each country of Pool 2 (current to July 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 on circulating serotypes**	**Reference**
BANGLADESH	Jun 2018/A, ASIA 1 and O	high	◔	◔	◕	◔	◔	◕	high	8
BHUTAN	Jan 2019/O, Dec 2017/A	high	◔		◕	◔		◕	medium	1
INDIA	July 2019/O, Apr 2015/A, ASIA 1	high	○		●	○		●	medium	1
NEPAL	June 2019/O, Mar 2018/Asia 1, April 2017/A	high			●			●	medium	1
SRI LANKA	Dec 2018/O	high			●			●	medium	1

Table 15: Conjectured circulating FMD viral lineages in each country of Pool 3 –West Eurasia (current to July 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 on circulating strains**	**reference**
AFGHANISTAN	June 2019/O & Asia 1, Dec 2018/A	high	◑	◔	◑			◑	◔		◑			medium	11
ARMENIA	Dec 2015/A	low/sporadic	◔		◕		◔				◕			high	12
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	Dec 2018/A, Asia 1& O,	high	◑	◔	◑		◔	◑	◔		◑			medium	1
IRAQ	Dec 2018/O, Dec 2016/A	high	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
ISRAEL	May 2019/O, June2017/A	low/sporadic	◔		◕		◔				◑	◔		low	1
JORDAN	Mar 2017/O	low/sporadic	◕		◑		◕			◔	◔			high	1, as per Saudi
KUWAIT	April 2016/O	high	◕		◑		◕			◔	◔			high	1, as per Saudi
KYRGYZSTAN	Sep 2014/A, O	low/sporadic	◔	◕	◔			◔	◕		◔			high	as per Pakistan
LEBANON	2010/not typed	low/sporadic	◔		◕		◔				◕			high	as per Turkey
OMAN	Dec 2018/O, May 2015/SAT 2	high			◑	◑				◔	◔		◑	high	1
PAKISTAN	July 2019/ A, Asia 1 & O	high	◔	◕	◔			◔	◕		◔			medium	1
PALESTINE	Mar 2019/Untyped, Dec 2017/O, Mar 2013/Sat 2	low/sporadic			●							●		medium	1
QATAR	Dec 2018/O, Oct 2017/A	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
SAUDI ARABIA	Dec 2018/O & Jun 2018/A	high	◕		◑		◕			◔	◔			high	1
SYRIAN ARAB REPUBLIC (SYRIA)	2002/ A & O	high	◔		◕		◔				◕			high	as per Turkey
TAJIKISTAN	Nov 2013/ not typed	low/sporadic	◔	◕	◔			◔	◕		◔			high	as per Pakistan
TURKEY	April 2019/O, Oct 2017/A, May 2015/ Asia 1	high	◔		◕		◔				◕			medium	1
TURKMENISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
UNITED ARAB EMIRATES	Jan 2018/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
UZBEKISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran

Table 16: Conjectured circulating FMD viral lineages in each country of Pool 3 - North Africa (current to July 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/EA-3**	**SAT 2**	**Uncertainty on circulating serotypes**	**Reference**
ALGERIA	Mar 2019/O, Nov 2016/A, Jun 2016/Sat 2	medium	◑	◕		◑	◕		medium	1
EGYPT	Nov 2018/Sat 2, Feb 2018/A April 2017/O	high	◔	◔	◕	◔	◔	◕	medium	1
LIBYA	June 2019/serotyping pending, Oct 2013/O	high	◔	◔	◕	◔	◔	◕	high	10, as per egypt
MOROCCO	July 2019/O	low/sporadic		●			●		medium	1
TUNISIA	Feb 2019/O, April 2017/A	low/sporadic	◔	◕		◑	◕		medium	1

Table 17: Conjectured circulating FMD viral lineages in each country of Pool 4 (current to July 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**	**O/EA-3**	**SAT1**	**SAT2**	**SAT3**	**Uncertainty on circulating serotypes**	**Reference**
BURUNDI	Dec 2017 / not available	high	◑	◔	◔	◔		◑		◔	◔	◔		high	as per Tanzania
COMOROS	March 2019/O	high		●					●					high	no data
DJIBOUTI	Not available	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
ERITREA	Oct 2018/not reported	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
ETHIOPIA	April 2019/A, O &SAT 2, Feb 2018/SAT 1	high	◔	◕	◔		○	◔		◕	◔		○	medium	1
KENYA	July 2019/A, O & SAT 2, May 2018/ SAT 1	high	◔	◕	◔	◔		◔	◕		◔	◔		medium	1
RWANDA	Oct 2018/ A, O , SAT 1 & Sat 2	high	◔	◕	◔	◔		◔	◕		◔	◔		high	as per Kenya
SOMALIA	June 2018/not reported	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
SOUTH SUDAN	June 2017/O & SAT 2, Mar 2018/A Dec 2018/ not sampled	high		●						●				high	1
SUDAN	Dec 2018/ not sampled, May 2017/O	high	◑	◔		◔		◑		◔		◔		medium	1
TANZANIA, UNITED REPUBLIC OF	Dec2018/O, Nov2018/ A & SAT 2, Sep 2018/SAT 1	high	◑	◔	◔	◔		◑		◔	◔	◔		high	1
UGANDA	Feb 2019/A & O, July 2017/SAT1, Jan 2015/SAT 3, July 2015/ SAT 2	high	◑	◑	◔	◔		◑	◑		◔	◔		high	1, as per Kenya
YEMEN	Dec 2016/not sampled	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia

Table 18: Conjectured circulating FMD viral lineages in each country of Pool 5 (current to July 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 on circulating serotypes**	**Reference**
BENIN	Dec 2017/O, SAT 1 &SAT 2, Apr 2017/A	high	◔	◔	◔	◔	◔	◔	◔	◔	high	3
BURKINA FASO	Dec 2018/not sampled, Aug2018/O	high	◑	◑		◑	◑	◑		◑	medium	3, 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	Dec 2018/Not sampled	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CONGO	Not available	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CONGO, DEMOCRATIC REPUBLIC OF	Jun 2018/A, O & Sat 1	high	◑	◑	◑		◑	◑	◑		high	3
COTE D'IVOIRE	Jun 2018/O	high		●				●			high	3, as per Guinea
EQUATORIAL GUINEA	Jun 2015/Disease suspected	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
GABON	Not available	high	◑	◑		◔	◑	◑		◔	high	
GAMBIA	Dec 2018/O	high		●				●			medium	3
GHANA	Dec 2018/SAT 2, Sep 2018/ O	high		◑		◑		◑		◑	high	1
GUINEA	Dec 2018/O	high		●				●			medium	3
GUINEA-BISSAU	Dec 2018/O	high		●				●			high	as per Guinea
LIBERIA	Not available	high		●				●			high	as per Guinea
MALI	Oct 2018/O, Jun 2018/A & SAT	high	◑	◑		◑	◑	◑		◑	high	3
MAURITANIA	Aug 2018/O, Dec 2014/SAT 2	high				●				●	medium	1
NIGER	Dec 2015/O	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
NIGERIA	June 2019/untyped/May 2019/A, Sep 2018/O &Sat 2, Sept 2016/ SAT 1	high	◑	◑		◔	◑	◑		◔	high	1, 12
SAO TOME AND PRINCIPE	Not available	0									high	no data available
SENEGAL	Nov 2018/A, O & Sat 2, Jun 2018/ Sat 1	high		●				●			medium	1
SIERRA LEONE	Aug 2018/O	high		●				●			medium	as per Senegal
TOGO	Dec 2017/ not sampled, Dec 2016/ O & Sat 1	high	◑	◑		◔	◑	◑		◔	high	3, as per Nigeria

Table 19: Conjectured circulating FMD viral lineages in each country of Pool 6 (current to July 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 on circulating serotypes**	**Reference**
ANGOLA	April 2016/SAT 2	high		◑	◔	○	◔		◑	◔	○	◔	high	as per Zambia
BOTSWANA	June 2018/SAT 2, Aug 2015/SAT 1	medium				●					●		medium	1
MALAWI	Apr 2019/A, SAT 2, June 2016/SAT 1	medium	◔		◔	◔		◔		◔	◔		high	1
MOZAMBIQUE	May 2019/ Typing pending, Oct 2017/SAT 2, May 2015/ SAT 1	high				◕	○				◕	○	high	1
NAMIBIA	Sep 2017/SAT 2, Aug 2017/typing pending, May 2015/SAT 1	medium			◑	◑				◑	◑		high	1
SOUTH AFRICA	Jan 2019/SAT 2, Oct 2017/SAT 1, Dec 2015/SAT 3	medium			○	◕				○	◕		high	1
ZAMBIA	Jun 2019/O, Apr 2019/SAT 2,Feb 2019/ A, May 2017/SAT 3, Jan 2013/SAT 1	medium	○	◑	○	○	◔	○	◑	○	○	◔	medium	1
ZIMBABWE	Jun 2019/SAT 2, April 2019/SAT 1, Jun 2013/SAT 3	high			◑	◑				◑	◑		medium	1, 3

Table 20: Conjectured circulating FMD viral lineages in each country of Pool 7 (current to July 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 on circulating serotypes**	**Reference**
VENEZUELA	Oct 2018/O	medium	◑	◑	◑	◑	high	5
COLUMBIA	2011/O, 2013/A	medium		●		●	medium	3

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