Food and Agriculture
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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 | March

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

March 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.

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Please note that the report contains hyperlinks

I. HIGHLIGHTS

Summary comments:

I am very pleased to write a few words to summarise the current FMD situation. From January to March 2019, the WRLFMD has been particularly busy with >300 sample submissions. We have reported test results for sample submitted from Algeria, Burkina Faso, Egypt, Ethiopia, Hong Kong SAR, Israel, Korea (Republic of South Korea), Laos, Mongolia, Palestinian Autonomous Territories, Saudi Arabia, Sierra Leone, South Sudan, Thailand, Uganda, Vietnam, and Zambia. New sequence data submitted from Ghana, Russia (from ARRIAH, Vladimir) and a number of West/North African countries (from ANSES, France and IZSLER, Italy) were also analysed. Reports for these samples can be retrieved from the WRLFMD website (http://www.wrlfmd.org/country-reports).

During this quarter, FMD outbreaks due to the O/EA-3 topotype have continued to be recognised in North African (Maghreb) countries. In addition to the cases reported last year in Algeria and Mauritania, confirmed outbreaks due to this viral lineage have now been reported in Tunisia and Morocco. All sequences from North African countries (generated by VDRL, or provided by ANSES, France and IZSLER, Italy) show a close genetic relationship (~99% nt identity) to viruses recovered during 2018 from a number of West Africa countries, and are distinct to FMD viruses from the same O/EA-3 topotype recently circulating in Egypt and the Eastern Mediterranean. These outbreaks raise questions about trans-Saharan connectivity between countries and the precise routes by which FMDV is being spread from West to North Africa (the trans-Saharan Highway runs from Lagos in Nigeria directly north to Algiers in Algeria). Samples have also been tested from Egypt; where in addition to serotypes O and A, a new introduction of SAT 2 (topotype VII) into the country has been detected which is most closely related to samples collected from Ethiopia (2018). Elsewhere in Africa, samples recently sent to WRLFMD have detected A/AFRICA/G-I and O/EA-2 in Uganda consistent with the FMDV lineages that are known to circulate in this part of East Africa, while serotype SAT 2 cases in the surveillance zone have led to the suspension of the OIE-free status in Limpopo, South Africa. In East Asia, new FMD cases have been detected in the Republic of (South) Korea and Zabaikalskiy in the eastern part of Russia due to the O/ME-SA/Ind-2001e lineage. The rapid spread of this lineage across many countries in the region has been widely discussed in previous reports and sequences from both of these cases are most closely related to viruses detected in China (2018). The complexity of FMD epidemiology in East Asia is further demonstrated by the detection of additional new cases in eastern Russia which are due to the O/SEA/Mya-98 (in Primorskiy) and O/ME-SA/PanAsia (in Zabaikalskiy) lineages and share a closer relationship to viruses from Vietnam and Mongolia, respectively.

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)
23rd April 2019

STOP PRESS: On 17th April 2019, FMD was reported for the first time in Comoros (Indian Ocean). Sequence data for representative cases on the Island of Mwali (provided by ANSES, France) characterises these FMD virus as belonging to the O/EA-2 topotype most closely related to FMD viruses found recently in Tanzania (unpublished sequence data kindly provided by Prof. Christopher Kasanga, Sokoine University of Agriculture, Tanzania).

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] **–** A FMD outbreak due to serotype O was notified in cattle at Xinjiang on March 17th 2019.

Mongolia [2] – Field samples belonging to two of the three genetic lineages of FMDV serotype O detected in the bovine samples collected between February 2017 and 2018 were subjected to FMD Vaccine Matching Strain Differentiation (VMSD) tests obtaining good matching results with nearly all the vaccine strains employed.

Republic of Korea [2] **–** Two field isolates belonging to the O/ME-SA/Ind2001e lineage, detected in cattle samples collected during January 2019, obtained good matching results with the vaccine strains used in the VMSD tests.

Russian Federation [2, 3] – The All-Russian Research Institute for Animal Health (ARRIAH) reported the detection of FMDV serotype O in the outbreak that occurred on March 8th 2019, in cattle at Zabajkal`Skij Kray.
The VP1 sequences, forwarded by ARRIAH to the WRLFMD, of viruses isolated during FMD episodes that respectively occurred in February 2018, January and March 2019 belong to three different lineages of FMDv serotype O.

Viet Nam [2] **–** Three lineages belonging to FMDv serotype O were detected in a batch of bovine and porcine samples collected between January 2018 and 2019.

POOL 2 - SOUTH ASIA

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

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan [5] – For the reporting month, the Central Veterinary Research and Development Laboratory (CVDRL), Afghanistan detected FMDv serotypes ASIA 1 and O among the samples analysed.

Israel [2] – Three field isolates, belonging to O/ME-SA/PanAsia2^{Qom15} lineage, detected in a set of samples collected from different species, between April and December 2018 obtained good matching results with the vaccine strains employed in the VMSD tests.

Pakistan [6] **–** For the reporting month, 345 outbreaks due to FMDV serotypes A, ASIA 1 and O were reported in the provinces of Baluchistan, Khyber Pakhtunkhwa, Punjab and Sindh.

Palestine [1, 19] – A FMDv serotype O outbreak, occurred on a goat and sheep farm at Bani Naeem, West Bank on March 26th 2019.

Saudi Arabia [2] **–** FMDV O was detected in samples collected from Oryx, gazelle, cattle and sheep collected between January and December 2018.

POOL 3 – NORTH AFRICA

Egypt [2] **–** FMDv serotypes A, O and SAT 2 were detected among the 36 buffalo and bovine samples collected between January 2017 and November 2018.

Morocco [1, 2, 12] – Another eight new outbreaks, already reported as resolved, due to FMDv serotype O were notified during February and March 2019 on multispecies ruminant farms.
The six VP1 sequences of FMDVs collected during January 2019 and forwarded by the European Union Reference Laboratory (EURL), FAO Reference Centre & OIE Reference Laboratory for Foot-and-Mouth Disease chez Agence nationale de sécurité sanitaire – ANSES, Maisons-Alfort, Île-de- France, France were genotyped as O/EA-3.

Tunisia [2] **–** FMD due to serotype O was reported during February 2019 on two small farms at Jendouba and Sidi Bouzid.

POOL 4 - EASTERN AFRICA

Ethiopia [2, 14] – FMDV serotypes O and A were detected in the batch of 55 bovine samples collected in the country between August and December 2019.

Kenya [7] **–** The FMD National Reference Laboratory (FMDNRL), Embakasi, Kenya, reported the detection of FMDV serotype A.

Uganda [2] – A FMD outbreak due to serotype A was notified on January 25th 2019 on a cattle farm at Nakaseke.
A/AFRICA/G-I and O/EA-2 were the lineages detected in the outbreak samples collected in the country during January and February 2019.

POOL 5 - WEST/CENTRAL AFRICA

[8, 9, 10, 11] No events FMD events and activities were notified in this Pool during the reporting month.

POOL 6 - SOUTHERN AFRICA

Malawi [1] **–** A FMD outbreak for which serotyping is pending was reported on February 21st 2019 in cattle at Mzimba.

Mozambique [1] **–** FMD events are continuing in Nampula and in an area located close to Gonorezoe National Park.

Zambia [1] **–** A FMD outbreak due to serotype O was reported in cattle on February 11th 2019 in cattle at Southern.

Zimbabwe [1] **–** The country reported eight FMD outbreaks due to serotype SAT 2, in cattle at Mashonaland East during March 2019.

POOL 7 - SOUTH AMERICA [1, 13]

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 in Venezuela in 2013.

COUNTER

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

IV. DETAILED POOL ANALYSIS

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

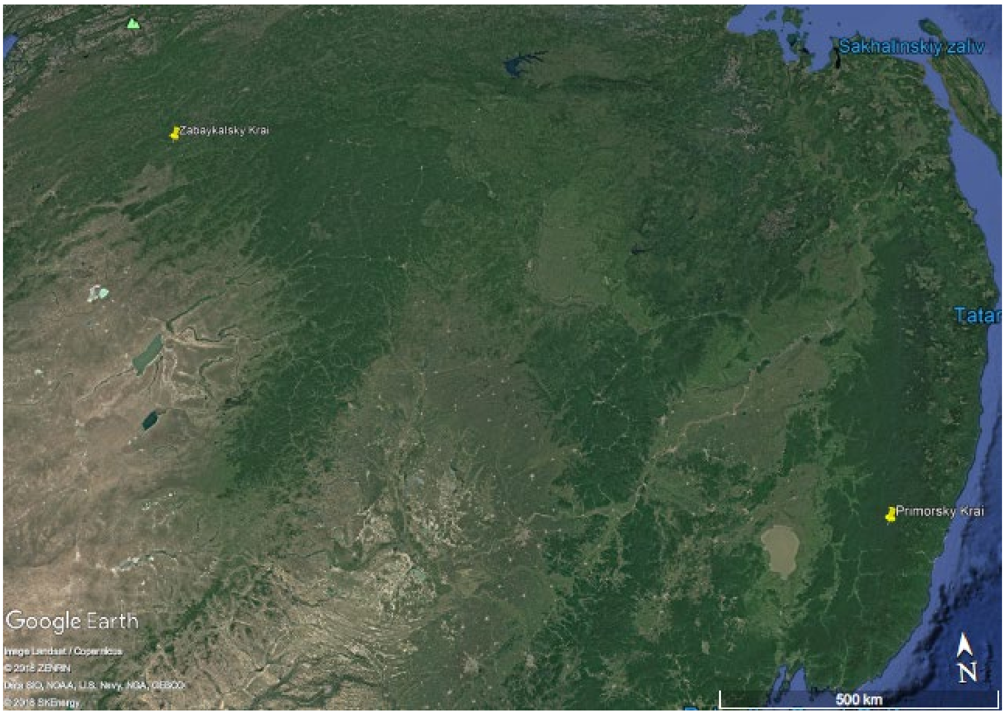
OUTBREAKS	
Country	*Description*
Serotype O in China [1]	FMD due to serotype O was notified at Xinjiang on March 17th 2019, on a cattle farm with a morbidity rate of 22.58% in the 31 animals present. The Lanzhou National Reference Laboratory for Foot and Mouth Disease (OIE Reference Laboratory) confirmed the diagnosis on March 22nd 2019 using reverse transcription - polymerase chain reaction (RT-PCR) and gene sequencing. The source of the outbreaks is unknown and general control measures were adopted including stamping out while no vaccination will be carried out. The current outbreak is a continuation of the series of events, which commenced in August 2018. Location of outbreak is reported at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29968. The latest lineages reported in the country for serotype O by the WRLFMD are O/SEA/Mya-98, O/CATHAY, O/ME-SA/PanAsia and O/ME-SA/Ind-2001, detected in samples collected in the country during 2018. *Interpretation* FMD occurs sporadically in China. This is a continuation of the event that started in August 2018.
Serotype O in Russian Federation [1]	A FMD outbreak due to FMDV serotype O was reported on a backyard farm of cattle, sheep and goats on March 8th 2019, at Zabajkal`Skij Kray where all species were clinically affected.. Apparent morbidity rates were respectively 15.94% in cattle (33 animals out of 207) and 0.55% in the small ruminants (6 animals out of 1100). The Regional Reference Laboratory for FMD (ARRIAH, Russia) confirmed the diagnosis on March 11th 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, elimination of animals and vaccination of 4.522 cattle and 4.433 small ruminants. Details on the type of vaccine employed were not provided. *Interpretation* FMD occurs sporadically in Russia. This is a continuation of an event that started reported in January 2019.

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
Mongolia [2]	Vacc.	Field isolates detected during 2018 and belonging to O/ME-SA/Ind-2001e and O/SEA/Mya-98 lineages were submitted to VMSD tests that provided good matching results with O 3039, O Manisa and O Tur 5/09, with exception of an isolate belonging to O/SEA/Mya-98 lineage with the O Manisa vaccine strain.
Republic of Korea [2]	Vacc.	The two field isolates detected during January 2019 and belonging to the O/ME-SA/Ind-2001e lineage were submitted to VMSD tests providing good matching results with O 3039, O Manisa, O Skr 7/10 and O Tur 5/09.
Russian Federation [1, 2, 3]	Surv. and Vacc.	For the reporting month, the ARRIAH, Russia identified the FMDV serotype O detected in the outbreaks that occurred at Zabaikalskiy Krai as O/ME-SA/Ind-2001 lineage that was submitted to VMSD tests with good matching results with vaccine strains O/SEA/Mya-98, O/PanAsia and O/PanAsia 2. Serological analysis was conducted on 3,554 serum samples collected from non-vaccinated animals. A summary of the results of the VP1 sequences forwarded by the laboratory to the WRLFMD are reported in Table 2 and Map 3. Three different lineages of FMDV serotype O were detected.

Table 2: summary of the genotyping results of the FMDV positive samples collected in Russia between February 2018 and March 2019 (source – WRLFMD).

Sample Identification	Location of origin of sample	Host species	Date of collection	Genotype	Most Closely Related Viruses not belonging to the country - Seq id %	Host species
Zabaikalskiy/1/RUS/2018	Chindantskoe, Borzinskiy raion, Zabaikalskiy krai	cattle	07/02/2018	O/ME-SA/PanAsia	MOG/8/2018 (>99.5)	cattle
Zabaikalskiy/2/RUS/2018	Novoborzinskoe, Borzinskiy raion, Zabaikalskiy krai		09/02/2018			
Zabaikalskiy/3/RUS/2018	Solovfevskoe, Borzinskiy raion, Zabaikalskiy krai					
Primorskiy/RUS/1/2019	RusAgro, Grigorfevka, Mihailovskiy raion, Primorskiy krai	porcine	09/01/2019	O/SEA/Mya-98	VN 18-27160 (>95.1%)	porcine
Primorskiy/RUS/2/2019	Merci-Treid, Prohory, Spasskiy raion, Primorskiy krai		16/01/2019			
Primorskiy/RUS/3/2019	Primorskiy Becon, Prohory, Spasskiy raion, Primorskiy krai		22/01/2019			
Zabaikalskiy/RUS/2019	Kailastuiskoe, Krasnokamenskiy raion, Zabaikalskiy kray	cattle	09/03/2019	O/ME-SA/Ind-2001e	GZZY/CHA/2018-B (99.2%)	cattle

Map 1: yellow icons indicate location of FMDV genotyped samples collected in Russia between February 2018 and March 2019 (source – WRLFMD, Google Earth Pro).

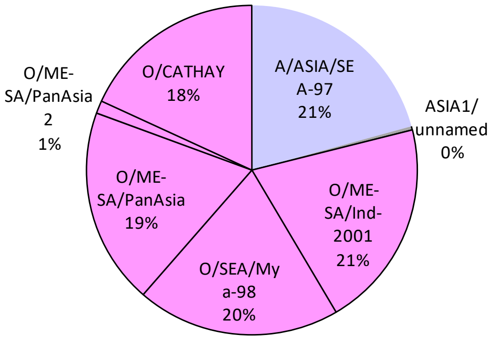


The country also reported vaccination activities that are summarized in Table 3. Details on the type of vaccination were not provided.

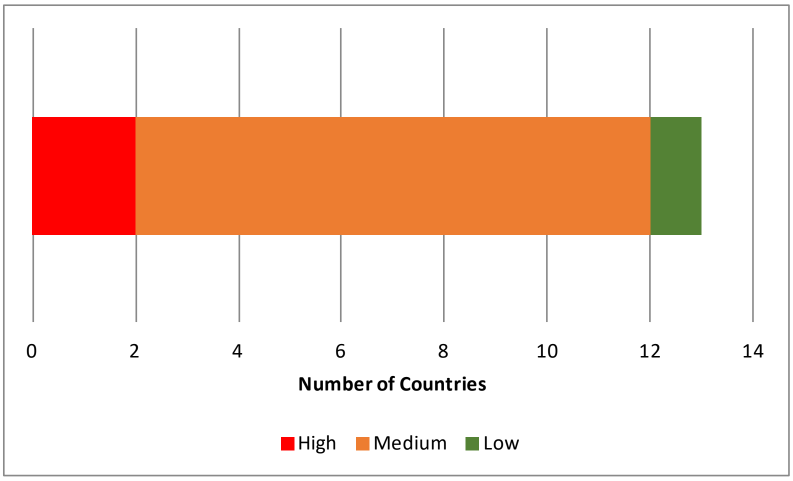
<table>
<tr><td></td><td></td><td>Table 3: vaccination activities carried out in the Russian Federation for the reporting month.
<table>
<tr><th>Administrative division</th><th>Species</th><th>Total Vaccinated</th></tr>
<tr><td>Khabarovskiy Kray</td><td>Cattle</td><td>6,241</td></tr>
<tr><td></td><td>Sheep / goats</td><td>3,075</td></tr>
<tr><td></td><td>Swine</td><td>7,473</td></tr>
<tr><td>Primorskiy Kray</td><td>Cattle</td><td>31,054</td></tr>
<tr><td></td><td>Sheep / goats</td><td>19,563</td></tr>
<tr><td></td><td>Swine</td><td>58,813</td></tr>
</table>
</td></tr>
<tr><td>Viet Nam 2</td><td>Surv.</td><td>Fifty-three of the 55 samples collected between January 2018 and 2019 from pigs (N° 43 samples), cattle (N° 7 samples), water buffaloes (N° 4 samples) and goats (N° 1 samples) were positive for only FMDV serotype O. The positive samples were genotyped with the following results:
O/ SEA/Mya-98 lineage was isolated in 28 pigs, with the isolates all closely related to those circulating in the country during 2018;
O/ME-SA/PanAsia lineage was isolated from two water buffaloes, seven cattle and one goat, with some of the field isolates not pertaining to the country, closely related to those isolated in Thailand during 2017 with a sequence identity (seq id) > 97.9% :
O/CATHAY lineage was isolated from three pigs, that were closely related to field isolates not pertaining to the country, detected in China in 2013, 2016 and 2018 (seq id > 92.9%).</td></tr>
</table>

Table 4 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 FMD epidemiological situation defined for each country of Pool 1 – see Annex for explanation).



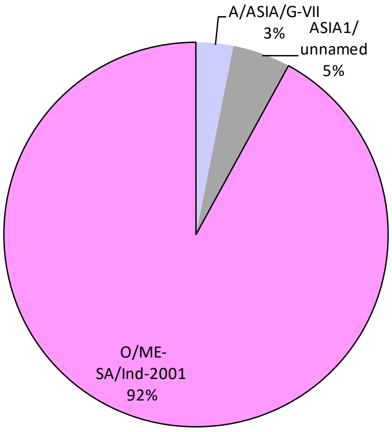
B. POOL 2 – South Asia

OUTBREAKS	
Country	*Description*
Serotype O in India [4]	ICAR-DFMD, Mukteswar, India detected FMDV serotype O among six bovine samples examined using FMDV antigen and/or RNA detection methods. *Interpretation* The information provided is consistent with that of previous reports. The causative serotype is the only reported 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 changing.

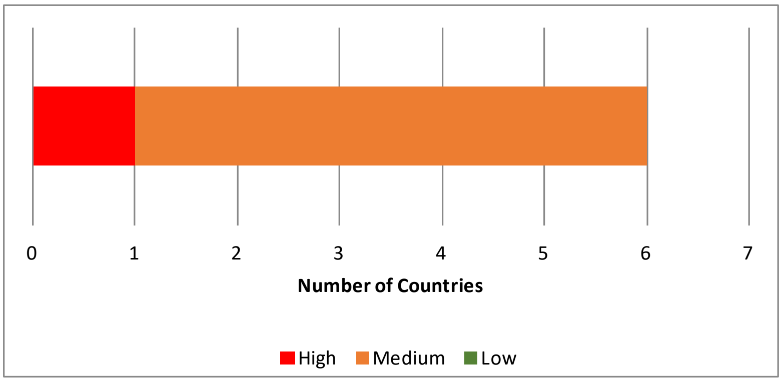
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
India [4]	Surv. and PVM	The laboratory analysed 423 sera collected in the course of epidemiological studies for the detection of FMD antibodies. The FMD diagnostics kits employed are those 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 issue of the ICAR-DFMD Annual Report of 2017-18.

Table 5 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

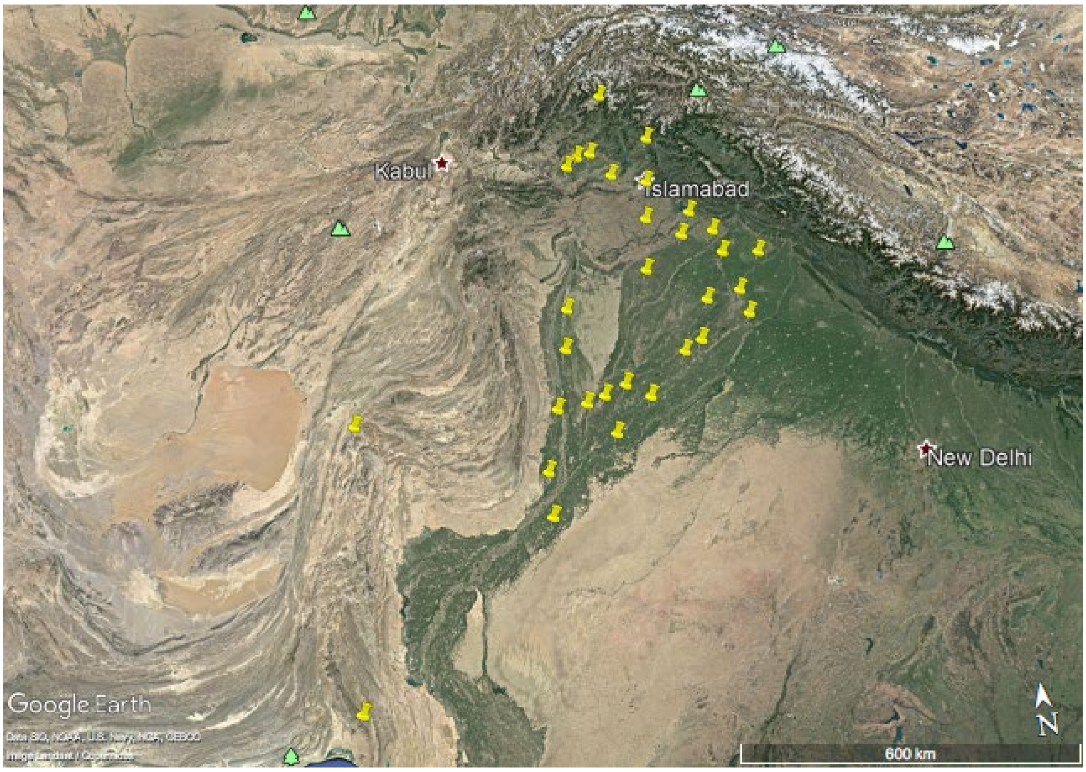


Graph 4: Categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 2 (see Annex for explanation).



C. POOL 3 – West Eurasia & Middle East

OUTBREAKS	
Country	***Description***
Serotypes ASIA 1 and O in Afghanistan [5]	The CVDRL, Afghanistan detected FMDV serotypes ASIA 1, in eight samples, and O, in five samples, of the 13 serotyped samples. Another seven FMDV positive samples are undergoing serotyping while nine of the total 29 samples examined during the reporting month were negative. 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 partially consistent with previous reports as ASIA 1 was last detected in July of 2018. The causative serotypes are believed to respectively circulate from sporadically to endemically in the country.
Serotypes A, ASIA 1 and O in Pakistan [6]	For the reporting country, 345 outbreaks were notified in the provinces of Balochistan, Khyber Pakhtunkhwa, Punjab and Sindh caused by FMDV serotypes A, ASIA 1 and O. A summary of the outbreaks is reported in Table 6 and their location in Map 4. 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 to circulate endemically in the country.

OUTBREAKS	
	Map 2: yellow icon indicates location of outbreaks reported in Pakistan during March 2019 (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator, Google Earth Pro). 

OUTBREAKS

Table 6: number of outbreaks reported per serotype and per district in Pakistan during March 2019 (Source –Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator).

Province	District	Number Outbreaks	Number of Outbreaks due to FMD Virus Serotypes					
			O	A	Asia-1	Mixed	Not Typed	Negative
Punjab	Multan	12	5	1	-	-	1	5
	Khanewal	3	-	2	-	-	-	1
	Lodhran	4	3	-	1	-	-	-
	Vehari	1	1	-	-	-	-	-
	Rajanpur	1	-	-	-	-	1	-
	Layyah	9	-	-	-	-	9	-
	Muzaffar Grahh	20	-	-	-	-	20	-
	DG Khan	7	-	-	-	-	7	-
	Sargodha	1	-	-	1	-	-	-
	Mandi Baha ud Din	2	-	-	2	-	-	-
	Khushab	2	-	-	1	-	-	1
	Bhakkar	7	-	-	7	-	-	-
	Attock	2	1	-	1	-	-	-
	Rawalpindi	12	-	-	10	-	-	2
	Chakwal	9	3	-	1	02 (O+A)	-	3
	Okara	2	1	-	-	-	1	-
	Rahimyar khan	1	1	-	-	-	-	--
	Lahore	27	6	-	1	-	11	9
	Jehlum	8	-	-	7	-	-	1
	Kasur	8	1				6	1
	Gujranwala	1	1	-	-	-	-	-
	Narowal	1	-	-	-	-	-	1
	Sahiwal	3	-	-	-	-	3	-
	Gujrat	3	-	-	-	-	-	3
	Nankana	2	-	-	-	-	-	2
Sindh	Karachi	157	24	5	57	-	27(3 Rejected)	44
	Thatta	4	-	-	-	-	4	-
Baluchistan	Quetta	20	-	-	4	-	5	11
	Lasbella	1	-	-	1	-	-	-
KPK	Peshawar	2	1	-	1	-	-	-
	Mansehra	2	1	-	1	-	-	-
	Swat	9	2	-	4	-	-	3
	Charsadda	1	-	-	1	-	-	-
	Mardan	1	-	-	1	-	-	-
Total		**345**	**51 (14.8)**	**8 (2.3)**	**102 (29.6)**	**2 (0.6)**	**95 (27.5)**	**87 (25.2)**

OUTBREAKS	
Serotype O in Palestine [1, 19]	A FMD outbreak was notified on March 26th 2019 at Hebron, Bani Naeem, West Bank on a goat and sheep farm and diagnosed by the Central Veterinary Laboratory Al-Arub (National laboratory) by RRT-PCR on April 1st 2019. Samples analysed the Kimron Veterinary institute using antigen ELISA and serotype specific PCR were positive for FMDv serotype O. Molecular typing is ongoing by the same Laboratory. Apparent morbidity and mortality were respectively 18.48% and 2.31% in the 433 animals present. The source of the outbreak is unknown with the farm vaccinated last in December 2017, as the country is experiencing a shortage of vaccines supplies. General control measures were applied, including control of wildlife reservoirs and the vaccination of the herd with a vaccine against FMDV serotypes A and O. Location of the outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=30019. *Interpretation* clinical FMD is detected sporadically in the country and further surveillance activities would better define the level of circulation of the infection. The latest lineage reported by the WRLFMD is in 2017 and 2018 is O/EA-3.

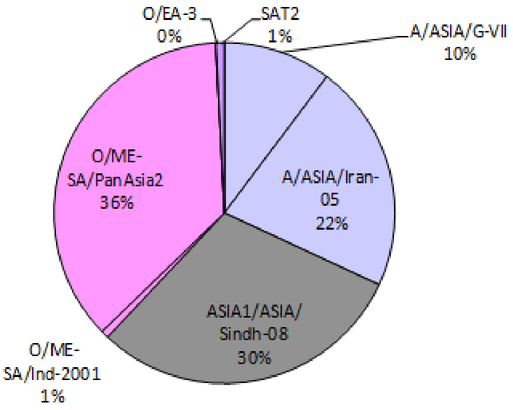
<table>
<tr><th colspan="3">SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)</th></tr>
<tr><td><i>Country</i></td><td><i>Activity</i></td><td><i>Description</i></td></tr>
<tr><td>Israel [2]</td><td>Vacc.</td><td>Three field isolates, belonging to the O/ME-SA/PanAsia2^{Qom15} lineage detected in 70 of the 85 diagnostic specimens collected between April and December 2018, from different cattle, sheep, gazelle, deer and wild boar, that were subjected to VMSD tests obtained good matching results with the following vaccine strains: O 3039, O Manisa and O TUR 5/09.</td></tr>
<tr><td>Pakistan [6]</td><td>Vacc.</td><td>
<table>
<tr><th>Province</th><th>Ring Vaccination (Doses)</th></tr>
<tr><td>Punjab</td><td>37,075</td></tr>
<tr><td>Sindh</td><td>25,000</td></tr>
<tr><td>KP</td><td>150</td></tr>
<tr><td>ICT</td><td>75</td></tr>
<tr><td>Total</td><td>62,300</td></tr>
</table>
During the reporting month, a ring vaccination campaign was carried out in some of the Provinces of the country as reported in Table 7.

Table 7: summary of the ring vaccination campaign carried out in some of the Provinces of the country during March 2019 (Source – Progressive Control of Foot and Mouth Disease in Pakistan, <i>Dr. Muhammad Afzal</i>, Project Coordinator).

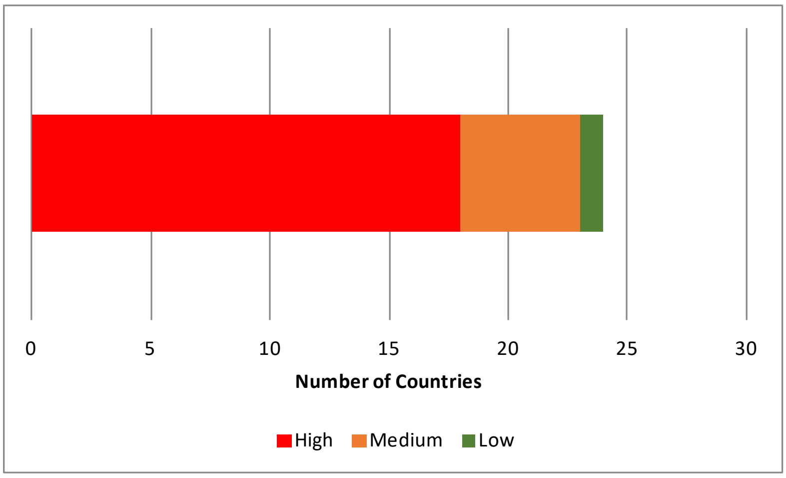
Veterinary capacity building training courses were conducted in the provinces of Khyber Pakhtunkhwa, Islamabad Capital Territory and Punjab with the attendance of 5 female and 28 male Veterinary Officers.</td></tr>
<tr><td>Saudi Arabia [2]</td><td>Surv.</td><td>FMDV O was detected among the eleven samples collected from Oryx (N° 1), gazelle (N° 1), cattle (N° 8) and sheep (N° 1) collected between January and December 2018 in Alhassa (where the sample from the Oryx was collected) and Riyadh. All the species analysed tested positive and the genotyping results identified all the six isolates as O/ME-SA/Ind-2001e, most closely related to the field isolate not pertaining to the country, represented by UAE/1/2015 isolated in a gazelle with a seq id >98.1%.</td></tr>
</table>

Table 8 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*
Serotype O in Morocco[1]	Another eight new outbreaks, already reported as resolved, due to FMDV serotype O were notified in the country during February and March 2019 on multispecies ruminant farms. The outbreaks occurred at Souss-Massa, Tanger-Tétouan-Al Hoceïma and Fès-Meknès. The source of the outbreaks was unknown and the general control measures that were adopted are movement control, quarantine vaccination as reported in Table 10, official destruction of animals and animal products. Screening and surveillance is being carried out within and outside the containment and/or protection zones. A summary of the animals involved and location of outbreaks are reported in Table 9 and location of the outbreaks is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29996.

Table 9: summary of the animals involved in the eight outbreaks that occurred in Algeria between February and March 2019 (Source – WAHIS).

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate
Cattle	35	18	1	34	0	51.42%	2.86%
Goats	63	0	0	63	0	0%	0%
Sheep	116	0	0	116	0	0%	0%
Total	**214**	**18**	**1**	**213**	**0**	**8.41%**	**0.47%**

Table 10: details of the vaccination activities carried out in Morocco following the outbreaks that occurred between January and February 2019 (Source – WAHIS).

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

Interpretation This is a continuation of events that started in December 2018 caused by the same serotype, which is also reported in neighbouring countries of the same virus pool.

Serotype O in Tunisia [1]

FMDV serotype O was responsible for two outbreaks that occurred during February 2019 on small farms at Jendouba and Sidi Bouzid as a continuation of the events that had started in December 2018. The events are already resolved.
A summary of the animals involved is reported in Table 11 and location of the events in Map 7.
The source of the outbreaks was unknown and the general control measures that were adopted are surveillance within and outside the containment and/or protection zones and vaccination will be adopted in response to outbreaks.

Table 11: summary of the animals involved in the two outbreaks that occurred in Tunisia between February 2019 (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	14	5	0	0	0	35.71%	0.00%	0.00%	0.00%
Sheep	40	0	0	0	0	0.00%	0.00%	-	0.00%

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

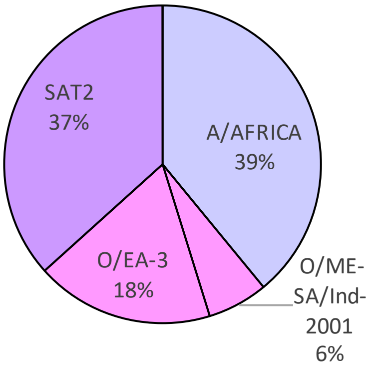
Interpretation This is a continuation of events that started in December 2018 caused by the same serotype ,which is also reported in neighbouring countries in the same virus pool.

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

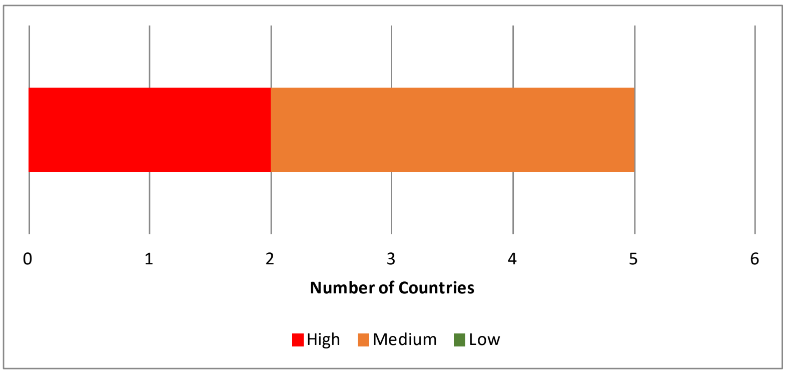
Country	*Activity*	*Description*
Egypt [2]	Surv.	Among the 36 buffalo (N° 7) and cattle (N° 29) samples collected between January 2017 and November 2018, one sample was positive for serotype A, one for serotype O and six samples for serotype SAT 2. All positive samples were from cattle.
Morocco [2, 12]	Surv.	The six VP1 sequences of FMDVs collected during January 2019 the EUR), FAO Reference Centre & OIE Reference Laboratory for Foot-and-Mouth Disease ANSES, France were genotyped as O/EA-3 with the most closely related field virus, not pertaining to the country, represented by different isolates detected in Algeria during 2018 with a seq id of >98.7%. Location of sample collection is represented in Map 3. **Map 3**: Yellow icons indicate location of the genotyped samples collected in Morocco during January 2019 (Source – WRLFMD, Google Earth Pro). 

Table 12 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/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).



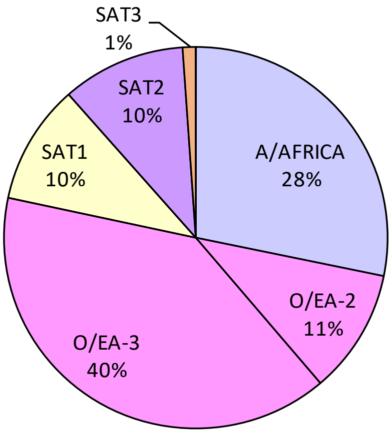
E. *POOL 4 – Eastern Africa*

OUTBREAKS	
Country	*Description*
Serotype A in Uganda [1], [2]	A FMD outbreak due to serotype A was notified on January 25th 2019 in cattle at Nakaseke. The diagnosis was confirmed by the WRLFMD on March 8th 2019, as described in more detail in the following section dedicated to surveillance. The affected animals are cattle belonging to local and cross breeds of different sex and age groups that are in a pastoral system. The affected farms are clustered in close contact during grazing and watering at River Kafu that separates three districts of Nakaseke, Masindi and Nakasongola. The area is characterised by numerous animal movements due to pastures, water points and cattle markets. The source of the outbreak was attributed to legal and illegal movement of animals. General control measures were adopted including surveillance within and outside the protection zone and vaccination of 20,000 cattle using a trivalent vaccine, but information on the serotypes included is not provided. Apparent morbidity rate was very low, 0.1% with no mortality in a susceptible population of 150,000. Location of outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29882. *Interpretation* – This report is consistent with previous reports. The causative serotype is believed to be present in the country further surveillance activities would better define the level of circulation of the infection.

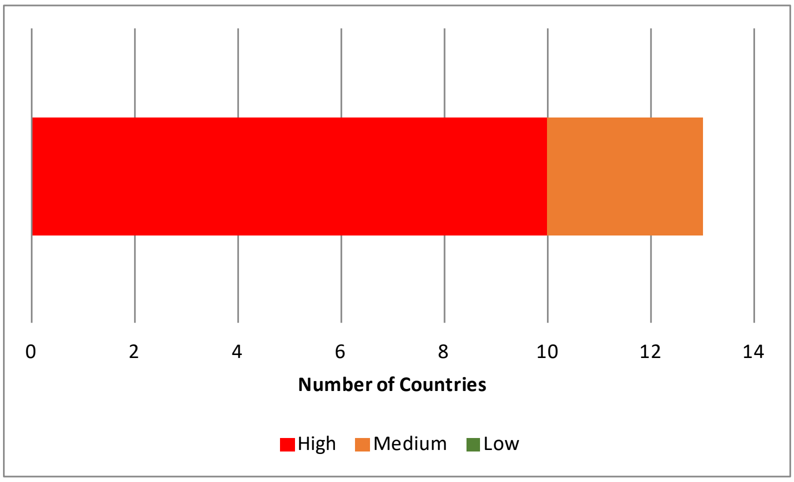
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Ethiopia [2, 14]	Surv.	A/AFRICAG-IV (72.22%) and O/EA-3 (27.78%) were the lineages detected in 36 of the 54 cattle samples collected between August and December 2018. The samples positive for the first lineage were collected in the Amhara Region and the Oromia Region, while those positive for the second lineage were collected in the Tigray Region and the Oromia Region. All the samples were closely correlated to other strains circulating in the country.
Kenya [7]	Surv. And Vacc.	The FMDNRL, Embakasi, Kenya, reported the detection of FMDV serotype A in one sample among the two bovine specimens analysed. The virus isolate was submitted to VMSD test with good matching results. Vaccine strains used are not reported. 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.
Uganda [2]	Surv.	Four and eight samples resulted respectively positive for A/AFRICA/G-1 and O/EA-2 out of a set of 52 samples collected from cattle during January and February 2019. Most closely related to field isolates not pertaining to the country for A/AFRICA/G-1 were those detected in Kenya in 2017 a with a seq id >94.9%, while for O/EA-2, the most closely related isolates are also field viruses not pertaining to the country were again those detected in Kenya in 2017 with a seq id > 96.5%.

Table 13 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

[8, 9, 10, 11] No events FMD events and activities were notified in this Pool during the reporting month.

Table 14 and Graph 11: Conjectured circulating FMD viral lineages in Pool 5 (further detail (country-level) in Annex).

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]	A FMD outbreak for which serotyping is pending was reported on February 21st 2019 in cattle at Mzimba. Laboratory diagnosis was based on the detection of antibodies to non-structural proteins of the FMDV. Outbreaks are occurring as the population at risk is in a communal grazing system. Illegal animal movement is the main source suspected for the introduction of infected animals is the area. Movement control, quarantine and surveillance are the measures adopted for containing the spread of infection. Vaccination will be adopted in response to the outbreaks if a suitable vaccine is available. No mortality was notified in the affected animals while apparent morbidity rate was 0.36% in the 80,000 susceptible cattle. Location of the outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29808. *Interpretation* – Further information is required to assess if this represents a new incursion or if the serotype responsible of the outbreak has been circulating subclinically/unreported. Timely serotyping of

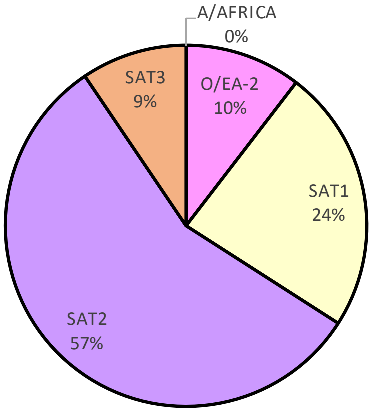
	the FMD viruses causing the outbreaks would aid the country in choosing the appropriate vaccine.
Serotyping pending Mozambique [1]	Two separate FMD events are reported in the country as following: The first event refers to an outbreak, which occurred on May 17th 2018. Cattle of all ages and sexes were affected. Diagnosis was confirmed on serological basis by the Central Veterinary Laboratory, Directorate of Animal Science (DCA), Institute for Agrarian Research of Mozambique (IIAM) (National laboratory) on May 24th 2018, using a non-structural protein ELISA. The outbreak involved cattle of a village of Nampula that registered only a low apparent morbidity of 3.27% in a population of 2,200 animals. The source of the outbreak is due to the illegal movement of animals and for this movement control was set up for the containment of the spread of infection. Other control measures were set up including the vaccination of 49,529 cattle using a trivalent vaccine containing SAT 1, SAT 2 and SAT 3. From the beginning of the event in May 2018, up to 30 of October 2018, 493 clinical cases of FMD were observed after which no other clinical cases of FMD were reported and for this considered as resolved. Location of the outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=26959. The second event affected the area that is located close to Gonorezoe National Park in Zimbabwe. The investigation conducted in the surrounding crush pens and the routine clinical inspection on site and vicinity areas indicate that no cases of FMD were detected and the disease affected cattle of one village. Even in this case, the source of the outbreak is due to the illegal movement of animals. The Veterinary Authority instituted as disease control measures, the ban of livestock movement, vaccination in the whole district and branding. Vaccination was administered to 116,150 cattle in Gaza using a trivalent aqueous vaccine containing FMDV serotypes SAT 1, SAT 2 and SAT. The clinical inspection of cattle in the affected area and neighbouring areas showed no new cases of FMD since April 2018 up to present. *Interpretation* – Further information is required to assess if these events represent a new incursion or if the serotypes responsible of the outbreaks were circulating subclinically/unreported. Timely serotyping of the FMD viruses causing the outbreaks would aid the country in choosing the appropriate vaccine.
Serotype O Zambia [1]	The FMD outbreak due to serotype O that was reported on February 11th 2019 in cattle at Southern was diagnosed by Central Veterinary Research Institute and the Botswana Vaccine Institute (FMD Regional Reference Laboratory) on March 13th 2019, using antigen detection ELISA and NSP ELSIA. Only an apparent morbidity of 6.82% was observed in the 8,214 affected cattle. The outbreak is due to the illegal movement of animals and the affected cattle are mainly on commercial farms in Chisamba District of Central Province, while in Southern Province, the affected animals are on the traditional sector. General control measures set up include vaccination of 13,643 cattle (ring vaccination) in Central Province and 99,855 cattle in Southern province. Location of outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=30035. *Interpretation* - This serotype was not previously reported in this province although it has been previously reported in the north of country. This report suggests that there has been spread within the country.
Serotype SAT 2 in Zimbabwe [1]	The country reported other eight FMD outbreaks of the episodes that started during June 2018 due to serotype SAT 2. The new outbreaks diagnosed on clinical basis are on different cattle farms at Mashonaland East during March 2019 with an apparent morbidity of 8.03% in the 2,652 affected cattle. As reported for the other countries of the same pool, the notified events are due illegal movement of animals, as well as, contact with infected animals at grazing/watering. Location of the outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=30030. A total of 5,796 cattle were vaccinated in the containment zone marked around the infected farms in

	Seke district. While in Mashonaland Central and East, 127,265 and 120,000 were respectively vaccinated. No details on the vaccine type were provided. Intensive surveillance and implementation of control measures remain in force in the affected districts. Veterinary checkpoints complimented by police are in place in strategic points in the infected areas and all illegally moved cattle are being destroyed. *Interpretation* - This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country. Trivalent (SAT1, SAT2, SAT3) vaccine supplied by Botswana Vaccine Institute is in use.

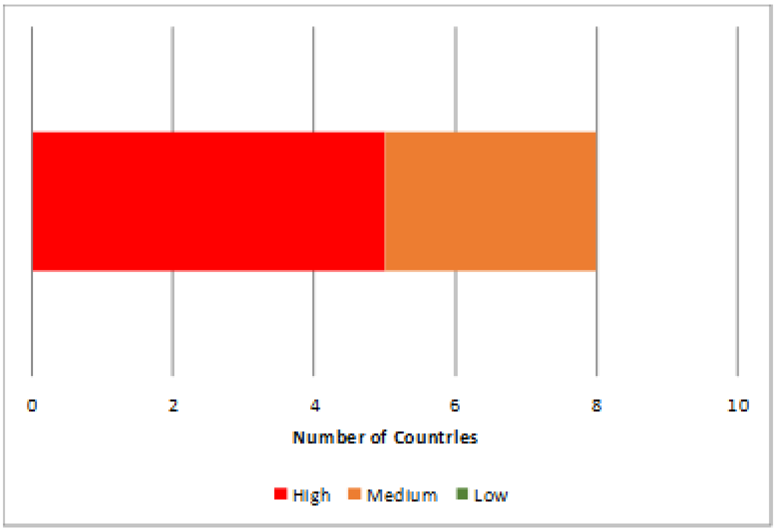
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
South Africa [15]	Surv.	The ARC-Onderstepoort Veterinary Institute analysed 7,659 sera using liquid-phase blocking ELISA and 1,313 sera in solid phase competition ELISA for the detection of antibodies against SAT 1, SAT 2 and SAT while 61 serum samples were tested using a non–structural protein antibody ELISA.

Table 15 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).

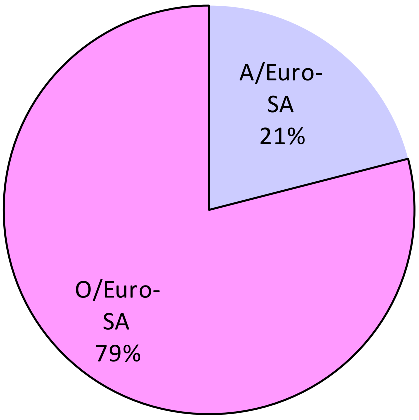


H. POOL 7 – South America

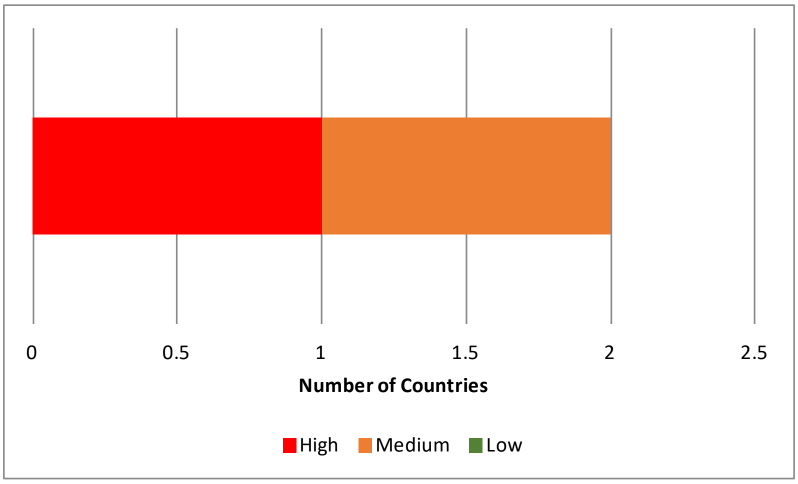
SURVEILLANCE (Surv), VACCINATION (Vacc) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
Colombia [1]	Surv	Following the outbreaks that occurred in the country due to FMDV serotype O, last notified in October 2018, the veterinary services have completed on February 18th 2019 the verification of absence of the circulation of FMDV through the use of sentinels in the primary and secondary outbreaks. This was conducted through the clinical examination for absence of FMD signs and the serial serological control confirming the absence of viral activity because negative for FMD antibodies. At the end of these controls the animals were removed by slaughter and burial.

Table 16 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).



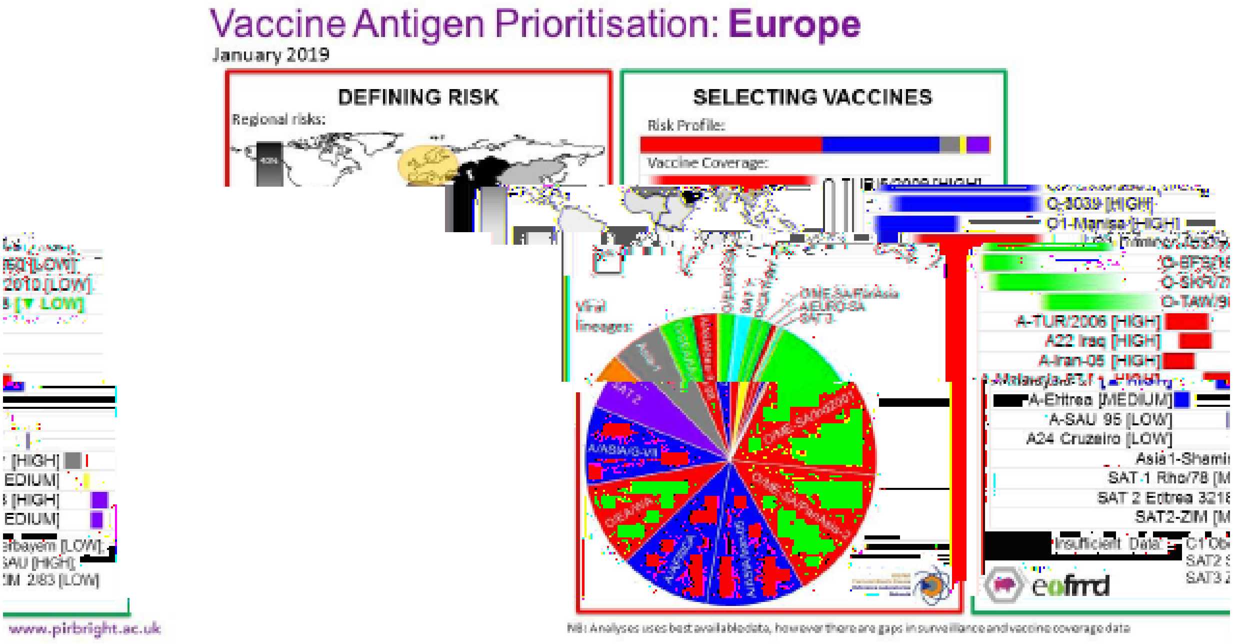
V. OTHER NEWS

[2]The 4th WRLFMD Quarterly Report for the period Octoer – December 2018 contains a new format for recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of Table 17 is contained within the report.

Table 17: 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	-	-	-	-	-	-	-	-



NB: Analyses uses best available data, however there are gaps in surveillance and vaccine coverage data

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 f
these outputs to other geographical regions. NB: Vaccine-coverage da
on available data and may under-represent the true performance of ind

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

VI. REFERENCES – Superscripts

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6. Progressive Control of Foot and Mouth Disease in Pakistan - *Dr. Muhammad Afzal*, Project Coordinator.
7. National FMD Reference Laboratory, Embakasi, Kenya – *Dr. Kenneth Ketter.*
8. Laboratoire National Vétérinaire (LANAVET) - Garoua, Cameroon - *Dr. Simon Dickmu Jumbo*.
9. ghana
10. FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria - *Dr. Ularamu Hussaini*
11. *senegal*
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13. OIE/FAO FMD Reference Laboratory Network, Annual Report 2016
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19. Acting Chief Veterinary Officer of the Israeli Veterinary Services and Animal Health - Dr. Tamir Goshen

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. **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 18: Conjectured circulating FMD viral lineages in each country of Pool 1 (current to March 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	March 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, 16
REPUBLIC OF KOREA (SOUTH KOREA)	Jan 2019/O, April 2018/A	low/sporadic	◑		◕	◑		◕					low	2
RUSSIAN FEDERATION	March 2019/O, Oct 2016/Asia 1, Jan 2016/ A	low/sporadic			●			◑	◑	◑			medium	2
TAIWAN PROVINCE OF CHINA	Jun 2015/A	low/sporadic			●							●	high	as per HONG KONG
THAILAND	Oct 2018 /A & O	high	◔		◕	◔		◔	◔	◔			medium	2
VIETNAM	Jan 2019/O, November 2017/A and not typed	high	◑		◕	◑		◔	◑	◔		◔	medium	2

Table 19: Conjectured circulating FMD viral lineages in each country of Pool 2 (current to March 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	17
BHUTAN	Apr 2018/O, Sep 2017/A	high	◔		◕	◔		◕	medium	2
INDIA	Mar 2019/O, Apr 2015/A, ASIA 1	high		○	●		○	●	medium	2
NEPAL	Feb 2018/O, Mar 2018/Asia 1, April 2017/A	high	◔	◑	◕	◔	◑	◕	medium	2
SRI LANKA	May 2018/O	high			●			●	medium	2

Table 20: Conjectured circulating FMD viral lineages in each country of Pool 3 –West Eurasia (current to March 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	Mar 2019/O & Asia 1, Dec 2018/A	high	◑	◔	◑			◑	◔		◑			medium	4
ARMENIA	Dec 2015/A	low/sporadic	◔		◕		◔				◕			high	13
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	Mar 2019/ A, O & Asia 1	high	◔	◕	◔			◔	◕		◔			medium	2
PALESTINE	Mar 2019/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	Dec 2018/O & Oct 2016/A	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 21: Conjectured circulating FMD viral lineages in each country of Pool 3 - North Africa (current to March 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	Nov 2018/Sat 2, Feb 2018/A & April 2017/O	high	◔	◔	◕	◔		◔	◕	medium	2
LIBYA	Oct 2013/O	high	◑	◑		◑	◔	◔		high	18
MOROCCO	Mar 2019/O	low/sporadic		●				●		high	2
TUNISIA	Feb 2019/O, April 2017/A	medium	◑	◑		◑		◑		medium	2

Table 22: Conjectured circulating FMD viral lineages in each country of Pool 4 (current to March 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**	**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
KENYA	Mar 2019/A & SAT 2, Nov 2018/O, May 2018/ SAT 1	high	◔	◕	◔	◔		◔	◕		◔	◔		medium	2
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 23: Conjectured circulating FMD viral lineages in each country of Pool 5 (current to March 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 24: Conjectured circulating FMD viral lineages in each country of Pool 6 (current to March 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
ZAMBIA	Feb 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 25: Conjectured circulating FMD viral lineages in each country of Pool 7 (current to March 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

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