Food and Agriculture
Organization of the
United Nations

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

GLOBAL
Monthly
Report

Foot-and-Mouth Disease

Foot-and-Mouth Disease Situation | 2019 | January

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

January 2019

MAIN INFORMATION SOURCES USED:

Databases:

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

Other sources:

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

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

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

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Please note that the report contains hyperlinks

I. HIGHLIGHTS

Dear Readers,
This is the first release of the new design for our Global Monthly Report with changes to present the information in a format more useful to risk managers.

To do this, we have enlisted the assistance of three Global Intelligence Focal Points to monitor, review and (in future editions) even try to forecast the FMD situation in their "home Pools" (1, 4 and 6). You will meet them as Guest Editors in future editions of this report. The Focal Points will further assist us to include a brief '*Interpretation*' for each new outbreak reported, to provide some context for readers as to whether the outbreak is consistent with previous reports or if it appears to be an unusual event.

We are also including estimates of the relative prevalence of the FMD virus serotypes and strains circulating in endemic countries and viral pools. The estimates answer the questions:
If 100 animals that had been infected in the last 12 months were randomly selected from a country or virus pool:

- *How many animals would be infected with each serotype?*
- *Within each serotype, how many would be infected with each virus strain?*

Combined with information about vaccine matching, this should assist risk manager to make decisions regarding the most appropriate vaccines to use or maintain in vaccine banks. A description of the methodology by which we arrived at these estimates can be found in the Annex.

The estimates in the report are the best that we can provide given the information available. It is important to recognize that there is important uncertainty regarding the accuracy of the estimates, due to the dynamic nature of the FMD situation as well as limited resources available for surveillance.

It is our hope that by presenting these estimates, the readers of the report will be inspired to help us to continuously improve them by sharing more up-to-date or accurate surveillance results.

We plan to continuously improve and refine the report, and so please do send us your insights and comments! (eufmd@fao.org using as subject "Comments to the EuFMD GMR")

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, Laos 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

Russian Federation [1, 10] – Six outbreaks due to FMDV serotype O were reported between January 16th and 28th 2019 at Primorskiy Kray, affecting primarily pigs of large farms and backyard holdings.

South Korea [1,] – Three outbreaks due to FMDV serotype O were reported on cattle farms between January 26th and 31st 2019 at Gyeonggi-Do and at Chungcheongbuk-Do.

Thailand [2] – FMD vaccine matching strain differentiating (VMSD) tests conducted on field isolates belonging to A/ASIA/SEA-97 and O/ME-SA/PanAsia and O/ME-SA/Ind-2001 lineages and detected in 2017 and 2018 provided different levels of matching results with the vaccine strains employed.

POOL 2 - SOUTH ASIA

India [3] - For the reporting month, ICAR-Directorate of Foot and Mouth Disease (ICAR-DFMD), Mukteswar, India, reported the detection of FMDV serotype O.

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan [4] - The Central Veterinary Research and Development Laboratory (CVDRL), Afghanistan detected during January 2019 FMDV serotype O among the samples examined.

Israel [1, 2] – Seven outbreaks due to FMDV serotype O that occurred in different areas of Hazafon during November and December on cattle holdings were reported as resolved during January 2019.
FMD VMSD tests conducted on field isolates detected in early 2018 and belonging to O/ME-SA PanAsia2^{QOM-15} gave in general good matching results with the vaccine strains employed.

Pakistan [5] **–** For the reporting month, 137 outbreaks due to FMDV serotypes A, ASIA 1 and O were reported in the provinces of Balochistan, Khyber Pakhtunkhwa, Punjab and Sindh.

Palestine [2] **–** A sheep sample collected in July 2018 was genotyped as O/EA-3.

POOL 3 – NORTH AFRICA

Algeria [2] – FMDV serotypes A and O were detected in bovine samples collected during December 2018 and January 2019 for which genotyping is available only for serotype O which was identified as O/EA-3.

Morocco [1] **–** During January 2019, 16 outbreaks were notified on multispecies farms where only for some of the outbreaks serotyping was carried out with the detection of FMDV serotype O.

Tunisia [1] **–** Eight outbreaks due to FMDV serotype O were notified between December 27th 2018 and January 17th 2019.

POOL 4 - EASTERN AFRICA

Kenya [6] **–** The FMD National Reference Laboratory (FMDNRL), Embakasi, Kenya, reported the detection of FMDV serotype SAT 2 for the reporting month.

South Sudan [2] **–** The field virus detected in a sample collected in 2017 was genotyped as O/EA-3.

Uganda [16] – The National Animal Disease Diagnostic and Epidemiology Centre, Entebbe Uganda detected FMDV serotype O from samples received from three outbreaks, which occurred between December 2018 and January 2019. The samples will be forwarded to the WRLFMD for further characterization.

POOL 5 - WEST/CENTRAL AFRICA

Burkina Faso [2] **–** Lineage O/EA-3 was detected in seven of the 18 cattle samples collected in the country between June and August 2018.

Cameroon [7] **-** The Laboratoire National Vétérinaire (LANAVET), Garoua, Cameroon detected FMDV in the samples analysed during the reporting month.

Côte d'Ivoire [2, 8] **–** The VP1 sequences of FMDVs detected in June 2018 were genotyped as O/EA-3.

Gambia [2] **–** The VMSD tests conducted on a field isolate, collected during 2018 and genotyped as O/EA-3, provided good matching results.

Nigeria [9] **–** The National Veterinary Research Institute (NVRI) Vom, Nigeria notified a suspicion of a FMD outbreak.

Sierra Leone [2] **–** The FMDV detected in a sample collected from cattle in August 2018 was identified as O/EA-3**.**

POOL 6 - SOUTHERN AFRICA

Malawi [1] **–** Forty two FMD cases were notified on clinical basis during December 2018.

South Africa [1, 11] **–** Five FMD outbreaks due to serotype SAT 2 were reported in September 2018 and in January 2019 in cattle of the villages of Limpopo. The episodes have caused the suspension of the country's FMD Free Zone.

Zambia [1, 2] **–** Three FMD outbreaks were reported in cattle, one in January 2018, at Central caused by serotype O and the other two in September 2018 and January 2019, at Northern caused by serotype A.
The detection of FMDV serotype A was confirmed by the WRLFMD as belonging to lineage A/AFRICA/G-1 that produced variable matching results in the VMSD tests that were conducted on the isolate.

Zimbabwe [1] **–** Outbreaks due to FMDV serotype SAT 1 and SAT 2 were reported in cattle

POOL 7 - SOUTH AMERICA[1, 12]

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

COUNTER

****** 174 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 Russian Federation [1, 10]	Six outbreaks due to FMDV were reported between January 16th and 28th 2019 at Primorskiy Kray, affecting primarily pigs of farms and backyard holdings. The All-Russian Research Institute for Animal Health (ARRIAH) confirmed the origin on January 24th and provided personnel to conduct outbreak investigations. The source of the outbreaks is inconclusive and general control measures were put in place, including vaccination of the local bovine and pig populations. Notification of previous occurrence of FMD was in April 2018 and the last lineages reported by the WRLFMD as circulating in the country are O/ME-SA/Ind-2001d detected in 2016 and A/ASIA/SEA-97 detected in 2014. *Interpretation* FMD occurs sporadically in Russia. This is a continuation of an event that was first reported to the OIE on 11 Jan 2019.
Serotype O in South Korea [1]	Three outbreaks due to FMDV serotype O were reported between January 26th and 31st 2019, at Gyeonggi-Do and at Chungcheongbuk-Do on cattle farms diagnosed by the Animal and Plant Quarantine Agency (OIE Reference Laboratory). The source of the outbreaks is unknown and general control measures were adopted, including vaccination in response to the outbreaks. Notification of previous occurrence of FMD was in April 2018 and the last reported lineages by the WRLFMD for the country were A/ASIA/SEA-97 in 2018 and O/ME-SA/Ind-2001d in 2017. *Interpretation* FMD occurs sporadically in S. Korea. This is a continuation of an event that was first reported to the OIE on 29 Jan 2019.

SURVEILLANCE (Surv), VACCINATION (Vacc) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
Russian Federation [10]	Surv, PVM	ARRIAH reported the detection of FMDV serotype O in the 98 samples genotyped as O/SEA/Mya-98 on which the laboratory is conducting immunological studies. The laboratory serologically examined 508 sera for post vaccination monitoring purposes and 70 sera from non-vaccinated animals.
Thailand [2]	Surv	VMSD tests conducted on filed isolates detected during 2017 and 2018 belonging to: - A/ASIA/SEA-97 provided good matching results with A MAY 97 and A22 IRQ/24/64 for at least one of the two isolates examined, but not with A IRN/2005 and A/TUR/20/2006, - O/ME-SA/PanAsia and O/ME-SA/Ind-2001 lineages gave overall good matching results with all vaccines strains used i.e. O 3039, O Manisa and O Tur 5/09.

Map 1: Red icons indicate location of areas of the FMD events reported for Pool 1 during the reporting month. (Source - OIE WAHIS and Google Earth Pro).

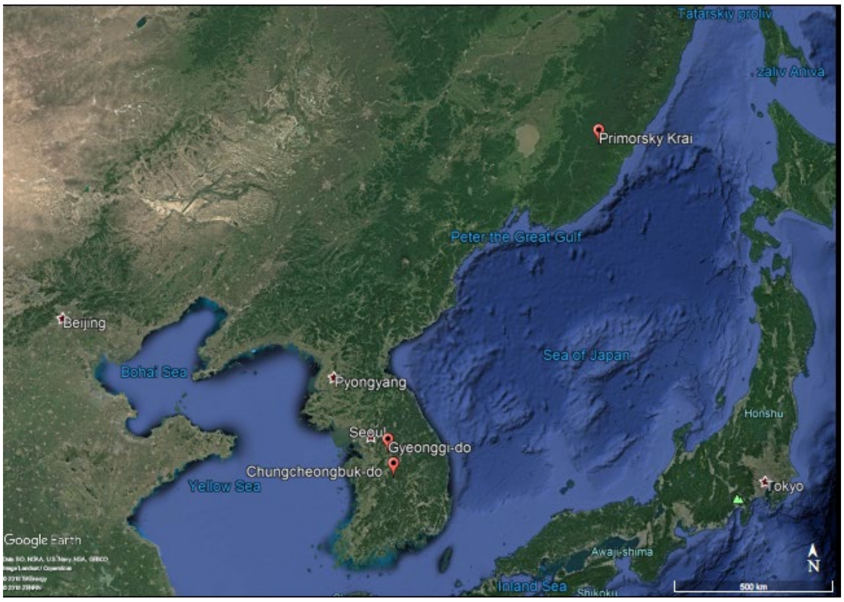
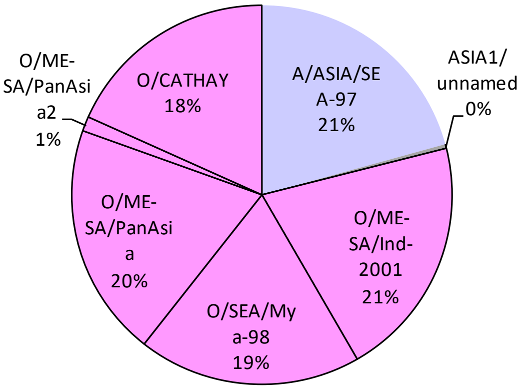
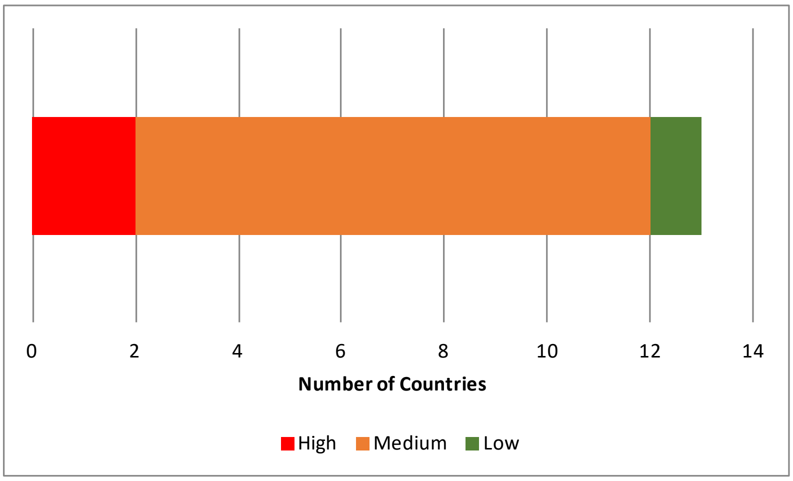


Table2 and Graph 1: Conjectured circulating FMD viral lineages in Pool 1 (further detail (country-level) in Annex).

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



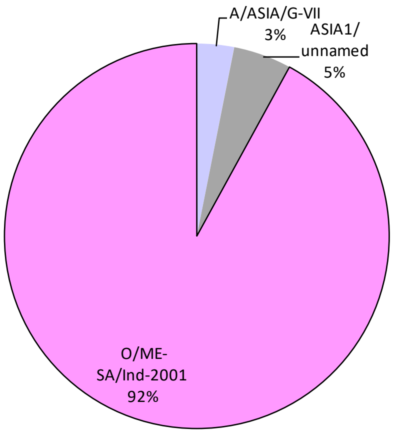
B. POOL 2 – South Asia

OUTBREAKS	
Country	*Description*
Serotype O in India[4]	ICAR-DFMD, Mukteswar, India detected FMDV serotype O among 14 bovine samples examined using FMDV antigen and/or RNA detection methods. *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country.

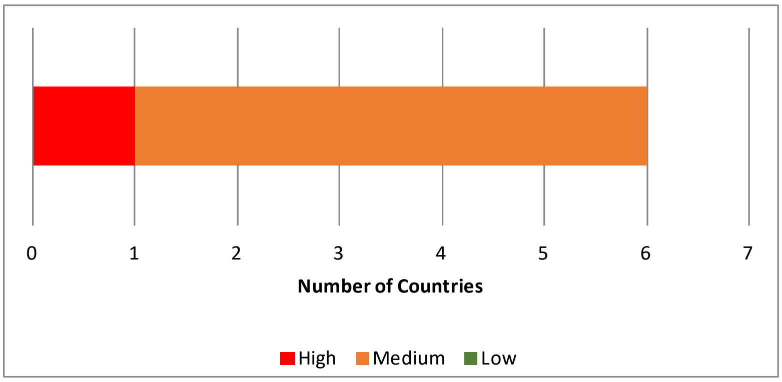
SURVEILLANCE (Surv), VACCINATION (Vacc) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
India [4]	SURV and PVM	The laboratory submitted two field isolates belonging to serotype O for vaccine matching tests. The laboratory also conducted the analyses of 380 sera collected in the course of epidemiological studies for the detection of FMD antibodies. The FMD diagnostics kits employed are those developed at ICAR-PDFMD. The sublineages currently circulating in the country are represented by O/ME-SA/2001d and O/ME-SA/2001e as described in the latest ICAR-DFMD Annual Report of 2017-18.

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

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



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



C. POOL 3 – West Eurasia & Middle East

OUTBREAKS	
Country	*Description*
Serotype O in Afghanistan [4]	The CVDRL, Afghanistan detected FMDV serotype O in seven of the 13 samples examined, with other three samples positive for FMDV but not yet serotyped. A/ASIA/Iran-05 and O/ME-SA/PanAsia-2 are the most recent lineages detected by the WRLFMD in samples collected in the country during 2018. *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country.
Serotype O in Israel [2]	Seven outbreaks due to O/ME-SA/PanAsia2 lineage, diagnosed by the Kimron Veterinary Institute, Virology Department, were reported as resolved during January 2019. The outbreaks occurred in different areas of Hazafon between November 16th and December 19th 2018, on different cattle farms, feedlots and in free ranging animals. The animals had history of recent vaccination. The source of the infection is unknown and different control measures were set up for the containment of the outbreaks. Location of outbreak is reported at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29099 https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29108 *Interpretation* This report is consistent with previous reports; The causative strain is believed circulate endemically in the country. The most recent circulating topotypes belonging to FMDV serotype O reported by the WRLFMD are represented by O/EA-3 and O/ME-SA/PanAsia-2 detected in samples respectively collected during 2017 and 2018.

OUTBREAKS

Serotype O in Pakistan [5]

137 outbreaks were reported in the provinces of Balochistan, Khyber Pakhtunkhwa, Punjab and Sindh due to FMDV serotypes A, ASIA 1 and O. A summary of the outbreaks is reported in Table 4 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.

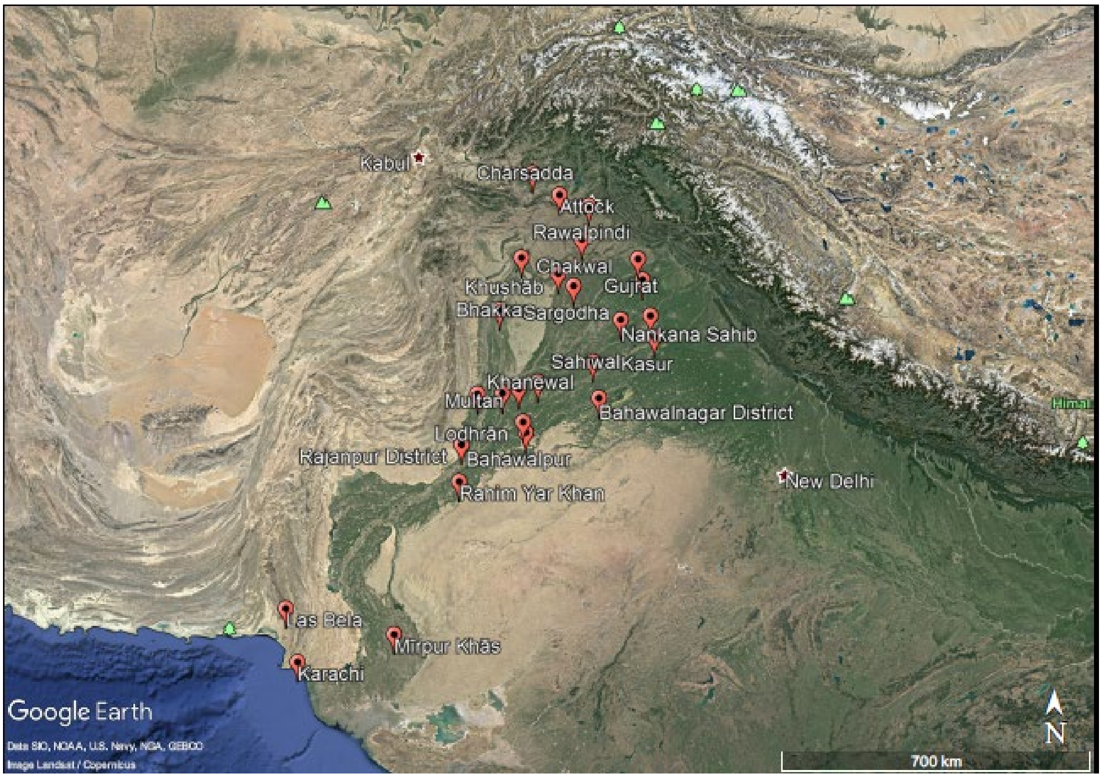
Interpretation This report is consistent with previous reports; The causative serotypes are believed circulate endemically in the country.

Table 4 (Source –Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator)

Province	District	Total number of outbreaks	Number of outbreaks per serotype			
			O	A	ASIA 1	Negative
Punjab	Lodhran	3	3	-	-	-
	Khanewal	7	-	3	-	4
	Multan	16	6	-	3	7
	Rajanpur	1	-	-	-	1
	Muzaffar Grahh	11	2	3	-	6
	DG Khan	1	-	-	-	1
	Sargodha	5	1	1	1	2
	Mianwali	4	1	1	-	2
	Khushab	1	1	-	-	-
	Bhakkar	6	4	1	-	1
	Rahim Yar Khan	2	-	-	-	2
	Attock	2	2	-	-	-
	Rawalpindi	6	4	-	-	2
	Chakwal	4	2	-	-	2
	Gujranwala	2	1	-	-	1
	Lahore	1	1	-	-	-
	Kasur	1	1	-	-	-
	Bahawalpur	2	2	-	-	-
	Sahiwal	3	1	-	-	2
	Nankana sahib	1	1	-	-	-
	Gujrat	3	1	-	-	2
	Bahawalnagar	1	-	1	-	-
Sindh	Karachi	48	13	2	4	29
	Mirpur Khas	1	-	-	-	1
Balochistan	Lasbella	2	-	-	-	2
KPK	Swat	2	1	-	-	1
	Charsada	1	-	-	1	-
Total		**137**	**48**	**12**	**9**	**68**

OUTBREAKS

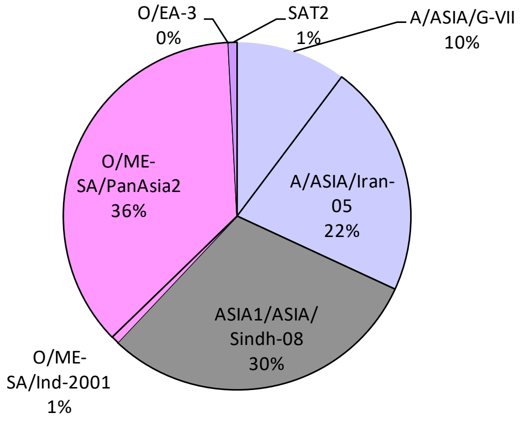
Map 2: red icons indicate location of the areas of the FMD outbreaks reported in Table 4 (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator, Google Earth Pro)



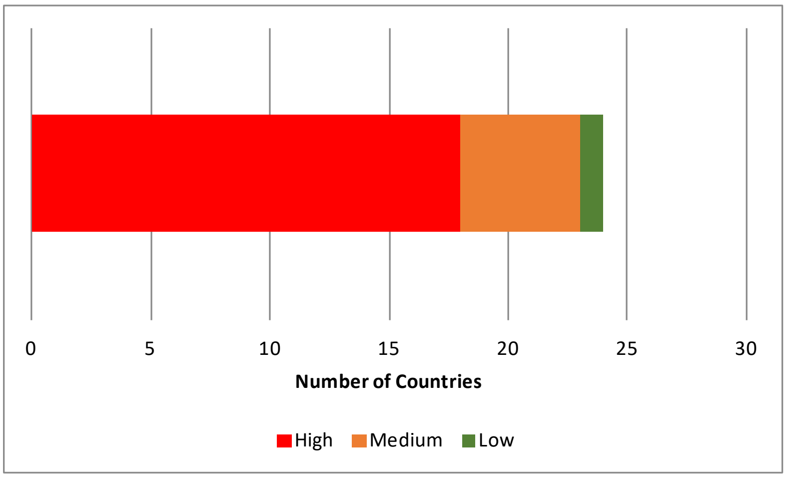
<table>
<tr><th colspan="3">SURVEILLANCE (Surv), VACCINATION (Vacc) AND POST VACCINATION MONITORING(PVM)</th></tr>
<tr><td>Country</td><td>Activity</td><td>Description</td></tr>
<tr><td>Israel [1]</td><td>Surv</td><td>At least one of the two field isolates detected during 2018, belonging to O/ME-SA PAnAsia2$^{\text{QOM-15}}$, obtained good matching results in the VMSD tests with vaccines strains O 3039, O 5911, O Manisa and O TUR 5/09.</td></tr>
<tr><td>Pakistan [5]</td><td>Vacc</td><td>
<table>
<tr><th>Province</th><th>Ring Vaccination (Doses)</th></tr>
<tr><td>Punjab</td><td>5825</td></tr>
<tr><td>Sindh</td><td>10550</td></tr>
<tr><td>KP</td><td>75</td></tr>
<tr><td>Baluchistan</td><td>50</td></tr>
<tr><td>Total</td><td>16500</td></tr>
</table>
A ring vaccination campaign was carried out for the reporting month in some of the Provinces of the country as reported in Table 5. (Source – Progressive Control of Foot and Mouth Disease in Pakistan, Dr. Muhammad Afzal, Project Coordinator)</td></tr>
<tr><td>Palestine [2]</td><td>Surv</td><td>A sheep sample collected at Hebron in July 2018 was genotyped as O/EA-3 with the most closely related virus not pertaining to the country represented by a field sample ISR/15/2017, detected in cattle in Israel with a 99.7% sequence identity (seq id).</td></tr>
</table>

Table 6 and Graph5: 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]	The 16 outbreaks notified during January 2019 on multispecies farms at Béni Mellal-Khénifra, Tanger-Tétouan-Al Hoceïma, Casablanca-Settat, Marrakech-Safi were all reported as resolved. Location of the outbreaks described in this section is available at the following links: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29162 https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29232 https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29321 Only for some of the outbreaks was serotyping carried out by the ONSSA Regional Analysis and Research Laboratory in Casablanca with the detection of FMDV O. Previous reports of FMD in the country were in November 2015 due to O/ME-SA/Ind2001d. The source of the outbreaks is unknown and general control measures were put in place with the vaccination of farms as reported as following.

Administrative division	Species	Total Vaccinated	Details
BÉNI MELLAL-KHÉNIFRA	Cattle	5,676	810 farmers
CASABLANCA-SETTAT	Cattle	8,088	2163 farmers
MARRAKECH-SAFI	Cattle	396	77 farmers
TANGER-TÉTOUAN-AL HOCEÏMA	Cattle	269	21 farmers

Interpretation This is the first report of this serotype in the country in 4 years, however it has been previously reported in other countries in the same virus pool.

Tunisia [1]

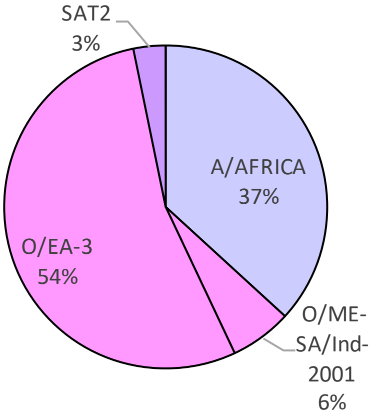
Eight outbreaks due to FMDV serotype O were notified between December 27th 2018 and January 17th 2019 as ongoing or resolved. The outbreaks occurred on multispecies farms at Siliana, Sidi Bouzid, Gafsa, Jendouba, Kasserine. Outbreak samples were sent to the OIE reference laboratory of the French Agency for Food, Environmental and Occupational Health & Safety (Anses), France.
The outbreak declared in El Makarem on December 19th 2018 represents the source of some of the above reported outbreaks.
The launch of the vaccination campaign against FMD in cattle and small ruminants in 2019 is scheduled for January 2019. Date of previous occurrence of FMD in the country was in May 2017 with the circulation of was A/AFRICA /G-IV.
Location of the outbreaks is available at the following links:
https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29158
https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29289
Interpretation This is the first report of this serotype in the country in 5 years, however it has been previously reported in other countries in the same virus pool.

SURVEILLANCE (SURV), VACCINATION (VACC) AND POST VACCINATION MONITORING(PVM)

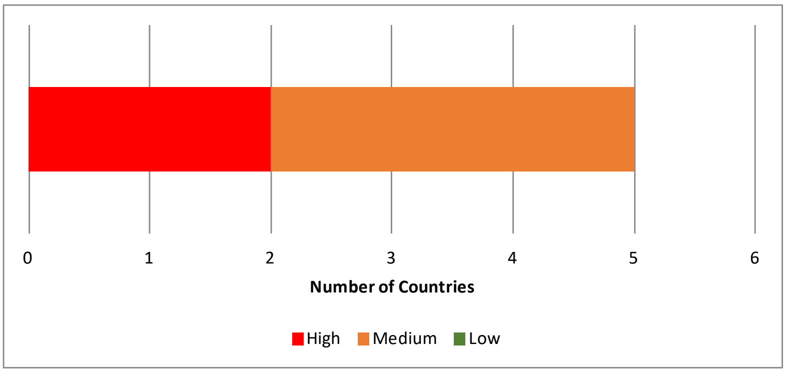
Country	*Activity*	*Description*
Algeria [2]	SURV	FMDV serotypes A and O were detected in eight of the bovine samples collected during December 2018 and January 2019. Genotyping is available only for FMDV serotype O identified as O/EA-3 and the most closely related field viruses are those detected in the country during the outbreaks that occurred in 2018.

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	5
O	O/ME-SA/Ind-2001	1
	O/EA-3	5
SAT 2	SAT 3	1



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



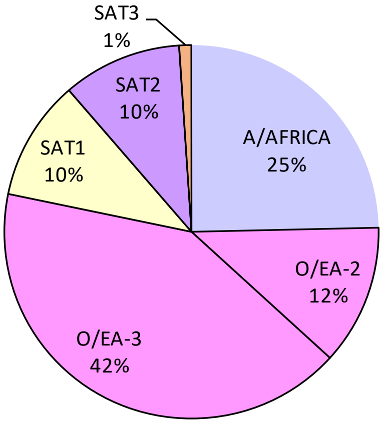
E. POOL 4 – Eastern Africa

OUTBREAKS	
Country	*Description*
SAT 2 **Kenya** [6]	The FMDNRL, Embakasi, Kenya, reported the detection of FMDV serotype SAT 2 in seven of the ten bovine samples analysed for the reporting month. Details on the origin of the samples are not available. The latest lineage circulating relative to the serotype reported is SAT 2/IV/unnamed, detected in 2017. *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country
Uganda **O** [15]	FMDV serotype O by conventional PCR was detected in three of the bovine samples collected during December 2018 and January 2019. The samples well be forwarded to the WRLFMD for genetic characterization. Surveillance activities are continuing in these affected districts. The source of these outbreaks are mainly due to the introduction of new live animals, Illegal movement of animals, animals in transit and contact with infected animals at grazing/watering points in the dry seasons. Controls measures in place include reactive ring vaccinations and quarantines. The last reported lineages by the WRLFMD from outbreak surveillance in the country were O/EA-2 in 2017 and SAT2/VII in July 2017, different from the SAT2/I collected in 2015 from cattle of the district of Isingiro ar the Tanzania/Ugandan boarde. The FMDV serotype O was most closely related to field virus isolates from Tanzania with a 96.2% seq id. SAT3 was last isolated in Uganda in cattle in 2013. *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country.

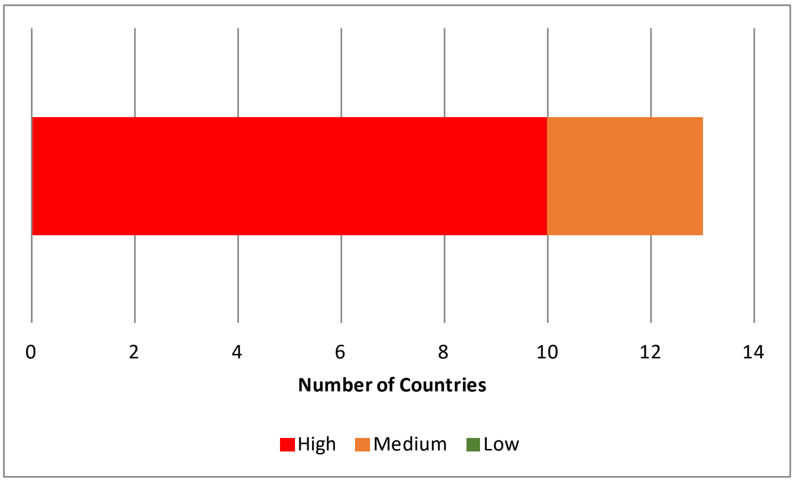
SURVEILLANCE (Surv), VACCINATION (Vacc) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
South Sudan [2]	Surv	The field virus isolated from a sample collected at Jonglei in 2017 was genotyped as O/EA-3. The virus was recovered by transfection of LFBK cells with RNA extracted from one of the 12 bovine fluid samples collected between April – May 2017. The most closely related virus not pertaining to the country is that detected in cattle, in Ethiopia, during the same year with a 98.9% seq id.

Table 8 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

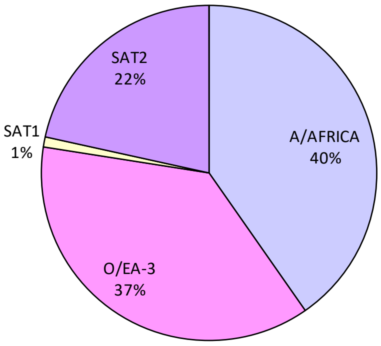
OUTBREAKS	
Country	*Description*
Nigeria [9]	The NVRI Vom, Nigeria, reported a suspicion of an FMD outbreak in Yobe State. Samples were collected to confirm the diagnosis. Support was also provided by the laboratories for the control of the episode. *Interpretation* This report is consistent with previous reports. FMD is believed to circulate endemically in the country. More information on the circulating serotypes is needed to interpret the significance of this report.

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Burkina Faso [2]	Surv.	O/EA-3 was the lineage detected in seven of the 18 cattle samples collected in the country between June and August 2018. The FMDV was detected in Boulkiemde, Kadiogo and Oubritenga (Map 3. Source – Google Earth Po). The most closely related virus not pertaining to the country is that detected in cattle, in Senegal during the same year with a seq id of at least 99.4%. **Map 3**: Red icons indicate location of were the genotyped samples were collected in Burkina Faso between June and August 2018. 
Cameroon [7]	Surv.	The LANAVET, Garoua Cameroon detected FMDV in 4 (2.3%) of the 177 environmental soil and air samples examined. The laboratory tested and serotyped 550 serum samples of which 255 were positive for serotype O and 224 were positive for serotype A. Details on the history vaccination of the animals from which the sera were collected were not provided.
Côte d'Ivoire [2, 8]	Surv.	The three VP1 sequences of FMDVs detected in porcine samples collected at Bingerville, Port-Bouet and Yopougon Azito (Map 4. Source – Google Earth Pro) in June 2018 and submitted by ANSES, France were genotyped as O/EA-3. The most closely related virus not pertaining to the country to these viruses were those detected in cattle, in Senegal and in Gambia during the same year with a seq id of at least 99.2%.

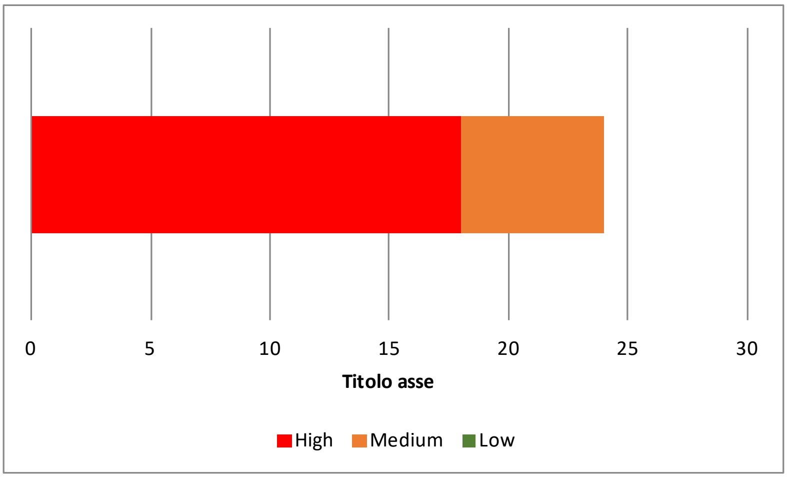
		Map 4: Red icons indicate location of where the genotyped sample were collected in Sierra Leone between in August 2018. 
Gambia [2]	Surv.	The VMSD tests carried out on a field isolate genotyped as O/EA-3 that was detected during 2018 produced good matching results with vaccine strains O 3039, O Manisa and O TUR 5/09.
Sierra Leone [2]	Surv.	The FMDV detected in a sample collected from cattle at Quidadu, Kono, Eastern in August 2018 and recovered by transfection of LFBK cells with RNA was genotyped as O/EA-3. The most closely related virus not pertaining to the country to these viruses were those detected in cattle, in Senegal and in Gambia during the same year with a seq id of at least 99.2%. **Map 5**: Red icon indicates location where the genotyped sample were collected in Sierra Leone between in August 2018. 

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	14
O	O/EA-3	22
SAT1	SAT1	2
SAT2	SAT2	14



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



G. POOL 6 – Southern Africa

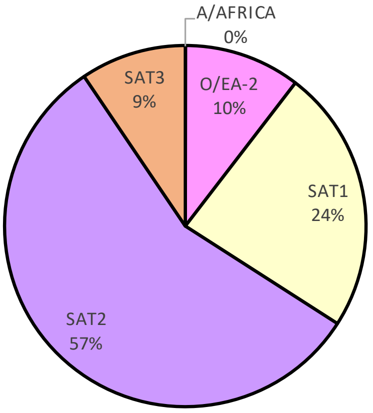
OUTBREAKS	
Country	*Description*
Serotype SAT 2 in [Malawi 1]	The disease is continuing in the country with 42 cases reported in December 2018. Samples were collected on December 21st 2018 and sent for typing to the Botswana Veterinary Institute. Surveillance activities are continuing in the area. The source of the outbreaks is due to introduction of new live animals, Illegal movement of animals, animals in transit and contact with infected animals at grazing/watering points. Controls measures are in place including vaccination in response to the outbreaks. Date of previous occurrence of the disease was in August 2018. Location of outbreaks is reported at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29127 *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country.
Serotype SAT 2 in	Five FMD outbreaks due to serotype SAT 2 were reported between September 2018 and January 2019 in cattle of Cabane, Makhado and Greater Giyani, Limpopo. These events have caused the suspension of the

South Africa [1], [11]	country's FMD Free Zone. ARC-Onderstepoort Veterinary Institute carried out diagnosis. The source of the outbreaks was attributed to contact with wild species. Control measures are put into place, but not vaccination which at present is prohibited. Location of outbreaks is available at the following links: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29130 https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29202 https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=29331 *Interpretation* This report is consistent with previous reports. The causative serotype is believed to circulate endemically in the country within wildlife in the Kruger National park. The affected areas surround the park and therefore the event is not unexpected given the country's policy of non-vaccination even in the high-risk areas. Infection is likely a spillover from wildlife in the Kruger national Park. Affected area is their surveillance zone outside the clean zone.
Serotype A and O in Zambia [1]	The FMD outbreak reported in cattle in January 2018, at Central was caused by serotype O diagnosed by the Central Veterinary Research Institute The affected cattle are mainly on commercial farms in Chisamba, District of Central Province and the source of the outbreak is unknown. A ring vaccination was carried out with the administration of the vaccine to 13,643 cattle. Another two outbreaks occurred in the country in September 2018 and in January 2019, at Northern that were caused by serotype A. The outbreaks were due to illegally introduced animals into the area. Containment measures are in place. Location of outbreaks is available at the following links: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29354 https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29353 *Interpretation* This serotype has not been previously reported in this district/province although it has been previously reported elsewhere in the country. This report suggests that there has been spread within the country.
Serotype SAT 1 and SAT 2 in Zimbabwe [1]	Two outbreaks due to FMDV serotype SAT 1 occurred on two cattle farms on January 15th and 19th January respectively at Masvingo and Matabeleland. These episodes are a continuation of that notified in July 2017. Vaccination of cattle was carried out for 425,000 heads at Masvingo and 215,000 at Midlands together with other restrictive and control measures. The FMD outbreaks due to SAT 2 that were first notified in June 2018 at Mashonaland Central are continuing. The above outbreaks are due to illegal movement of animals and contact with infected animals at grazing/watering points. Intensive surveillance and implementation of control measures remain in force in the affected districts together, with veterinary checkpoints at strategic points in the infected areas and destruction of illegally moved cattle. Location of outbreaks is available at the following links: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29353 https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=29403 *Interpretation* This report is consistent with previous reports. The causative serotypes are believed to circulate endemically in the country. Outbreaks that occurred in the south of the country relate more to the events in the south-eastern lowveld, characterised by huge buffalo populations in the Gonarezhou National Park. These outbreaks are not related to the outbreaks that occurred in June 2018 in the north of the country. The later outbreaks have contacts that are traceable to the outbreaks in Tete province of Mozambique in the first quarter of 2018. The two countries share a border that allows cattle to share grazing and watering points between the two countries and animal settlements are rural and unfenced. There is no information to confirm that the same virus causes the two outbreaks.

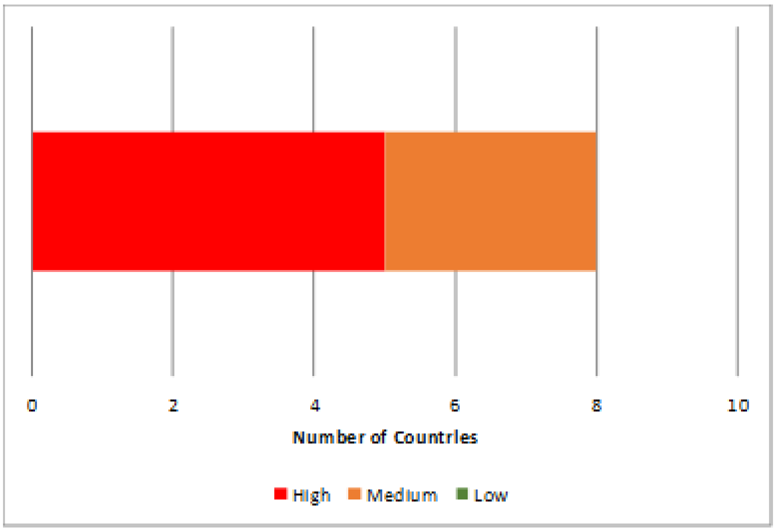
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
South Africa [11]	Surv.	The ARC-Onderstepoort Veterinary Institute reported the detection of FMDV in 12 of the 18 samples examined. The laboratory analysed 3,498 sera using liquid-phase blocking ELISA for the detection of antibodies against SAT 1, SAT 2 and SAT 3 and 48 sera using a non–structural protein antibody ELISA.
Zambia [2]	Surv.	The detection of FMDV serotype A in three bovine samples collected in October 2018 was confirmed by the WRLFMD as belonging to A/AFRICA/G-1 lineage. The most closely related field virus not pertaining to the country was identified as that detected in cattle Kenya in 2008 with a 94.6% seq id. The VMSD tests carried out on two of the field isolates cited above produced good matching results with A IRN/2005 and A22 IRQ/24/64, but not with A/ERI/3/98 and A/TUR/20/2006.

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	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).

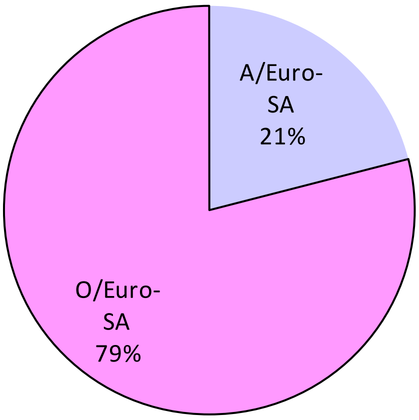


H. POOL 7 – South America

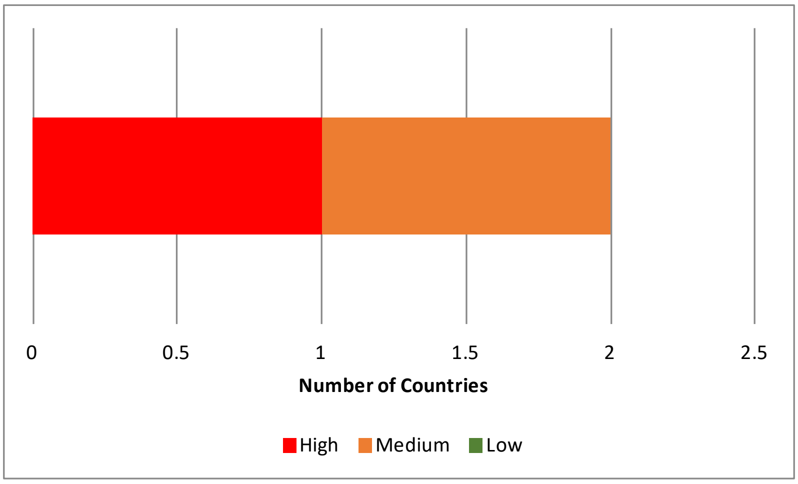
SURVEILLANCE (Surv), VACCINATION (Vacc) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
Colombia [1]	Surv	Following the outbreaks that occurred in the country due to FMDV serotype O, last notified in October 2018, the veterinary services have started with the introduction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

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



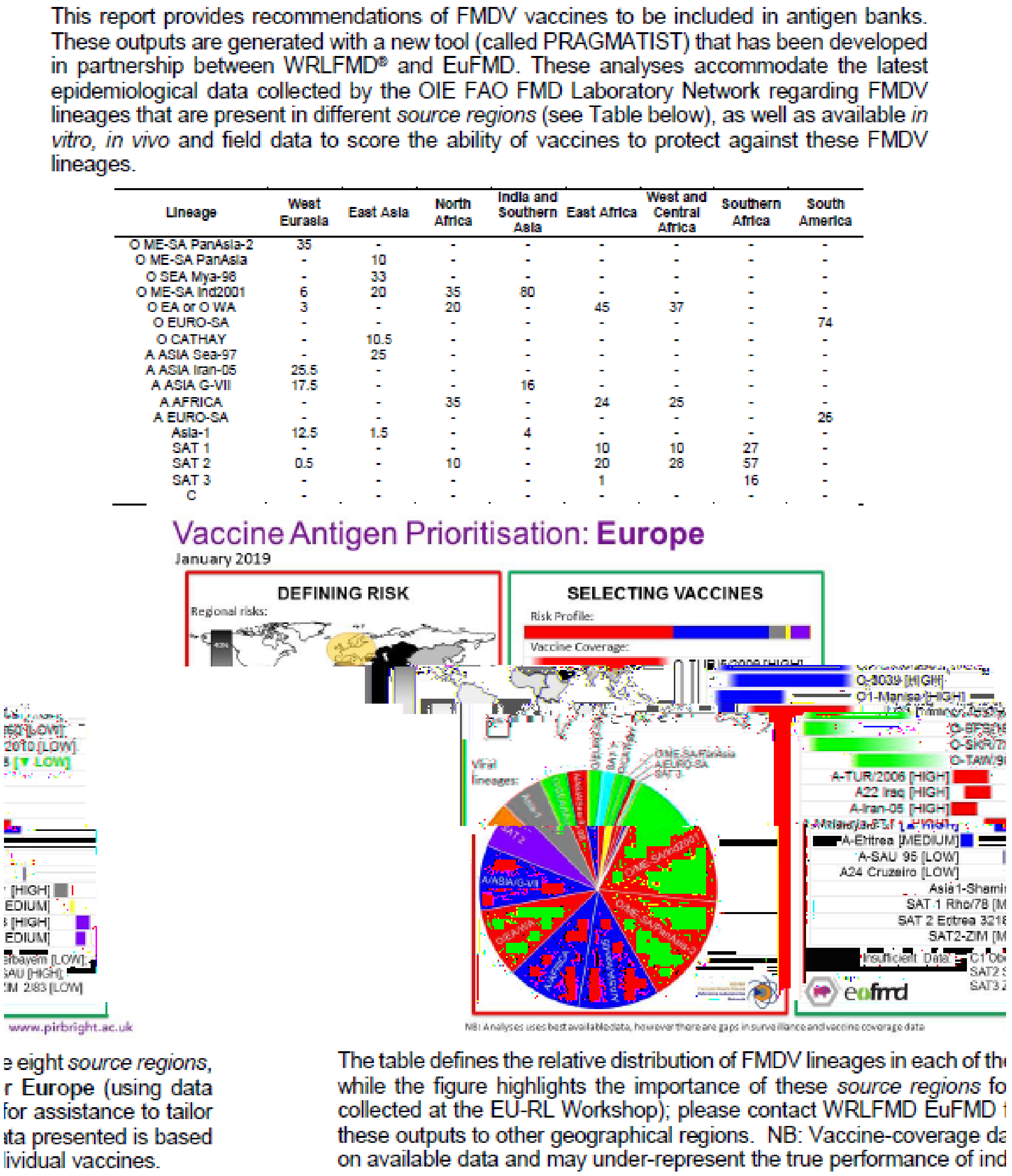
Graph 16 - categorization of the level of uncertainty relative to the FMD epidemiological situation defined for each country of Pool 7 (see Annex for explanation).



V. OTHER NEWS

[1]The 4th WRLFMD Quarterly Report for the period October – December 2018 contains a new format for recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of Table 12 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	-	-	-	-	-	-	-	-

Vaccine Antigen Prioritisation: **Europe**

January 2019

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
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
ita presented is based
lividual vaccines.

VI. REFERENCES – Superscripts

1. http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home
2. World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD), www.wrlfmd.org.
3. Project Directorate on Foot and Mouth Disease (PD-FMD), Indian Council of Agricultural Research, Mukteswar, India - *Dr. S. Saravanan*.
4. Central Veterinary Research and Development Laboratory **(**CVDRL), Aghanistan - *Dr. Wahid Bahir* Head of Laboratory
5. Progressive Control of Foot and Mouth Disease in Pakistan - *Dr. Muhammad Afzal*, Project Coordinator.
6. National FMD Reference Laboratory, Embakasi, Kenya – *Dr. Kenneth Ketter, Miss Helen Mutua*
7. Laboratoire National Vétérinaire (LANAVET) - Garoua, Cameroon - *Dr. Simon Dickmu Jumbo*.
8. OIE Reference Laboratory for FMD - Agence Nationale de Sécurité de l'Alimentation, de l'Environnement et du Travail (Anses), France
9. FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria - *Dr. Ularamu Hussaini.*
10. Regional Reference Laboratory for FMD (ARRIAH, Russia) - *Dr. Svetlana. Fomina.*
11. ARC -Onderstepoort Veterinary Institute, Republic of South Africa - *Dr LE Heath/Ms E Kirkbride*
12. OIE/FAO FMD Reference Laboratory Network, Annual Report 2016
13. OIE/FAO FMD Reference Laboratory Network, Annual Report 2017
14. Islam, M. S., et al. "Distribution of foot and mouth disease virus serotypes in cattle of Bangladesh." SAARC Journal of Agriculture 15.1 (2017): 33-42. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5283054/ and neighbouring countries (A lineage).
15. The National Animal Disease Diagnostic and Epidemiology Centre, Entebbe Uganda - *Dr. Deo Ndumu*
16. FMD Situation in SEACFMD Countries 2015-2016; presentation at the The 23rd SEACFMD Sub-Commission Meeting 9-10 March 2017, Siem Reap, Cambodia, http://www.rr-asia.oie.int/fileadmin/sub_regional_representation/sub_regional_programme/seacfmd/SEACFMD_Activities/sub_com/23nd_Meeting__2017_/presentations/1.3_Regional_FMD_situation.pdf

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 strian circulating

Table 13 – Conjectured circulating FMD viral lineages in each country of Pool 1 (current to January 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	Oct 2018/O, May 2017/A	high	◔		◕	◔		◔	◔	◔		◔	medium	2
CHINA (HONG KONG, SAR)	July 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 2017/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, 17
REPUBLIC OF KOREA (SOUTH KOREA)	Jan 2019/O, April 2018/A	low/sporadic	◑		◕	◑		◕					low	2
RUSSIAN FEDERATION	Jan 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	November 2017/A, Jan 2018/O and not typed	high	◑		◕	◑		◔	◔	◔		◔	medium	2

Table 14 – Conjectured circulating FMD viral lineages in each country of Pool 2 (current to January 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	14
BHUTAN	Apr 2018/O, Sep 2017/A	high	◔		◕	◔		◕	medium	2
INDIA	Jan 2019/O, Apr 2015/A, ASIA 1	high		○	●		○	●	medium	2
NEPAL	Nov 2018/O, Mar 2018/Asia 1, April 2017/A	high	◔	◑	◕	◔	◑	◕	medium	2
SRI LANKA	May 2018/O	high			●			●	medium	2

Table 15 – Conjectured circulating FMD viral lineages in each country of Pool 3 –West Eurasia (current to January 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	Jan 2018/O, Dec 2018/A, July 2018/ Asia 1	high	◑	◔	◑			◑	◔		◑			medium	4
ARMENIA	Dec 2015/A	low/sporadic	◔		◕		◔				◕			high	14
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	Jan 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	Jan 2019/ A, O & Asia 1	high	◔	◕	◔			◔	◕		◔			medium	2
PALESTINE	July 2018/Untyped, Dec 2017/O, Mar 2013/Sat 2	low/sporadic			●							●		medium	2
QATAR	Dec 2013/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
SAUDI ARABIA	Oct 2016/A & April 2016/O	high	◕		◑		◕			◔	◔			high	2
SYRIAN ARAB REPUBLIC (SYRIA)	2002/ A & O	high	◔		◕		◔				◕			high	as per Turkey
TAJIKISTAN	Nov 2012/ not typed & Nov 2011/Asia 1,	low/sporadic	◔	◕	◔			◔	◕		◔			high	as per Pakistan
TURKEY	Oct 2015/ A May, 2014-2015/ Asia 1 and O	high	◔		◕		◔				◕			medium	2
TURKMENISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
UNITED ARAB EMIRATES	Sep 2016/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
UZBEKISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran

Table 16 – Conjectured circulating FMD viral lineages in each country of Pool 3 - North Africa (current to January 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	Jan 2018/O, Nov 2016/A May-Jun 2016/Sat 2, Aug 2016/typing pending	medium	◕	◔		◕		◔		medium	2
EGYPT	April 2017/O, Nov 2016/A May-Jun 2016/Sat 2, Aug 2016/typing pending	high	○	◕	◔	○		◕	◔	medium	2
LIBYA	Oct 2013/O	high	◑	◑		◑	◔	◔		high	15
MOROCCO	Jan 2019/Not typed, Oct 2015/O	low/sporadic	◕	◔		◕		◔		high	as per Algeria
TUNISIA	Jan 2019/O, April 2017/A	medium	◑	◑		◑		◑		medium	2

Table 17 - Conjectured circulating FMD viral lineages in each country of Pool 4 (current to January 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	Dec 2018/untyped,Nov 2018/A& O, April 2018/ SAT 2, Feb 2018/SAT 1	high	◔	◕	◔		○	◔		◕	◔		○	medium	2
KENYA	Jan 2019/SAT 2, Nov 2018/O, Oct 2018/ A, 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	Jan 2019/O Nov 2014/SAT1, Jan 2015/A and SAT 3, July 2015/ SAT 2 and untyped	high	◔	◕	◔	◔		◔	◕		◔	◔		high	2, as per Kenya
YEMEN	2009/O	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia

Table 18 - Conjectured circulating FMD viral lineages in each country of Pool 5 (current to January 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	Jan 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 19 - Conjectured circulating FMD viral lineages in each country of Pool 6 (current to January 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, July 2015/ SAT 2	high		◑	◔	◔	◑		◑	◔	◔	◑	high	as per Zambia
BOTSWANA	July 2018/SAT 2, June 2015/SAT 1	medium				●				○	●		medium	2
MALAWI	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	Jan 2019/ A &O, May 2017/SAT 3, Mar 2017/SAT 2, Jan 2013/SAT 1	low/sporadic	◔	◑	◔	◔	◑	◔	◑	◔	◔	◑	medium	2
ZIMBABWE	Jan 2019/SAT 1 & SAT 2, Sep2018/typing pending, Jun 2013/SAT 3	high			◑	◑				◑	◑		medium	1, 2

Table 20 - Conjectured circulating FMD viral lineages in each country of Pool 7 (current to January 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	12
COLUMBIA	2011/O, 2013/A	medium		●		●	medium	1

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