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control of foot-and-mouth disease

GLOBAL Monthly Report

Foot-and-Mouth Disease

Foot-and-Mouth Disease Situation | 2019 | May

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

May 2019

MAIN INFORMATION SOURCES USED:

Databases:

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

Other sources:

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

The sources for information are referenced by using superscripts.
The key to the superscripts is in references.

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CONTENTS

Please note that the report contains hyperlinks

I. HIGHLIGHTS

I feel greatly honoured and humbled to be invited as a Guest Editor of this month's Global Monthly Report. This month's issue updates its readers with a detailed and verified information on the global FMD situation.

The demand for animals and their products is increasing globally and the South-East Asian countries are no exception. Southeast Asia (SEA) imports animal products mainly from South Asia, the Pacific and the America, as well as the Middle East and North Africa. A regional study conducted on animal movement organised by OIE SRR-SEA in 2015 concluded that a very big volumes of large ruminants are moved from South Asia to SEA especially Vietnam and China every year. This creates a high likelihood for the incursion of exotic FMDVs in SEA due to several risk factors present in the region such as legal/illegal intra-regional trading of live animal and associated products, free grazing system, different routes and movements of vehicles, humans, and wildlife, limited surveillance and response capacities of the national Veterinary Services, lack of strict enforcement of border control, lack of animal identification and traceability system, poor vaccination coverage etc.

The detection of an exotic serotype Asia1 FMDV in Myanmar in 2017 supports the fact that SEA is at high risk of incursion of exotic FMDVs from South Asia, especially A/Asia/G-VII and Asia 1. On the other hand, it has also raised the question about why/how this serotype remained undetected for so long or if it is a case of a vaccine escape despite the regional effort of vaccinating livestock in the region. Likewise, the possibility of misreporting of quality data or some sort of bias in understanding the epidemiology of the disease must also be considered.

The epidemiology of FMD in East Asia is complex and very dynamic as represented by lineages O/SEA/Mya-98 and O/MESA/PanAsia detected in recent outbreaks in Primorskiy and Zabaikalskiy of Eastern Russia that were closely related to viruses detected in Vietnam and Mongolia respectively. Also, in East and Central Asia, FMD occurs with sporadic clinical outbreak which indicates a continuous circulation of FMDV. To better understand the spatial and temporal distribution of FMDV serotypes and its determinants in this geographical area, as well as to understand the market chains of different susceptible species and livestock products, the development of 'FMD annual risk calendar' has been proposed. This includes information on the main festivities, major animal production events, seasonal grazing or migration trends driving livestock mobility in particular geographic areas. A lot of work has been done in the past two decades already by the South-East Asia and China Foot and Mouth Disease (SEACFMD) Campaign to better understand livestock mobility and market chains in the context of FMD in the region.

Strengthening national laboratory capacities, regional cooperation as well as information sharing among the laboratories are critical elements for effective surveillance and control of FMD. To identify and ensure the improvement of the current situation on FMD molecular diagnosis, evaluate other FMD relevant issues among SEACFMD experts, the inaugural Regional Expert Group meeting on FMD was jointly organised by the Food and Agriculture Organisation of the United Nations Regional Office for Asia and the Pacific (FAO RAP) and the World Organisation for Animal Health (OIE) Sub-Regional Representation for SEA in Bangkok, Thailand during 14-16 May 2019. It succeeded in drafting a sub-regional FMD molecular diagnostic protocol from detection to genotyping, including the selection of suitable primers and probes for pan-serotyping. Likewise, the Progressive Control Pathway Support Officer (PSO) Training workshop will be held in Bangkok between 6-8 August 2019. This PSO system supported by the GF-TADs FMD working group aims at assisting FMD endemic countries with progressive FMD control along the PCP, by developing regional and national capacity and competence.

Thanks again for allowing me to share my thoughts on this comprehensive report.

Kshitiz Shrestha
EuFMD Global Intelligence Focal Point for FMD Pool 1, Thailand
May 2019

II. GENERAL OVERVIEW

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

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

POOL	REGION/COUNTRIES – 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, O and SAT 2**
4	**EASTERN AFRICA** Burundi, Comoros, Djibouti, Eritrea, Ethiopia, Kenya, Rwanda, Somalia, Sudan, South Sudan, United Republic of Tanzania, Uganda, Yemen	**O, A, SAT 1, SAT 2 and SAT 3**
5	**WEST/CENTRAL AFRICA** Benin, Burkina Faso, Cameroon, Cabo Verde, Central Afr. Rep., Chad, Democratic Republic of Congo, Congo, Côte d'Ivoire, Equatorial Guinea, Gabon, Gambia, Ghana, Guinea-Bissau, Guinea, Liberia, Mali, Mauritania, Niger, Nigeria, Sao Tome Principe, Senegal, Sierra Leone, Togo	**O, A, SAT 1 and SAT 2**
6	**SOUTHERN AFRICA** Angola, Botswana, Malawi, Mozambique, Namibia, South Africa, Zambia*, Zimbabwe	**{O, A}**, SAT 1, SAT 2 and SAT 3**
7	**SOUTH AMERICA** Colombia, Venezuela (Bolivarian Republic of)	**O and A**

*REPORTED ONLY IN OMAN IN 2017
** ONLY IN NORTH ZAMBIA AS SPILL-OVER FROM POOL 4

III. IN THIS REPORT

POOL 1- SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA

China [1] **–** Further reports of FMD due to serotype O were notified on May 19th 2019 in cattle of the Mongolian Autonomous Prefecture of Bayingol, Xinjiang.

Vietnam [2] – FMDV serotype O field viruses detected in 2018 and in 2019 did not all obtain good results in the vaccine matching strain differentiation (VMSD) tests in which they were analysed.

POOL 2 - SOUTH ASIA

Bhutan [2] **–** FMDV serotype O field viruses detected during 2019 obtained good results in the vaccine matching strain VMSD tests in which they were analysed.

Nepal [2] **–** FMDV O/ME-SA/Ind-2001/e was the only topotype detected among the positive samples of a total of fifty collected from buffaloes, cattle goats and pigs during 2018 and 2019.

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan [3] – The Central Veterinary Research and Development Laboratory (CVDRL) detected FMDV serotypes Asia 1 and serotype O in the sixty samples analysed.

Israel [2] – A FMD outbreak for which serotyping is pending occurred on May 2nd 2019 occurred in free ranging cattle at Haifa.

Pakistan [4] **–** For the reporting month, 104 outbreaks were reported in the provinces of Baluchistan, Khyber Pakhtunkhwa Punjab and Sindh for which serotyping is ongoing.

Saudi Arabia [2] **-** FMDV serotype O field viruses detected during outbreaks of 2019 obtained good results with the vaccine strains used in the vaccine matching strain VMSD tests.

Turkey [2] **–** A/ASIA/G-VII and O/ME-SA/PanAsia2 were the lineages detected among the forty cattle samples submitted for genotyping.

POOL 3 – NORTH AFRICA

Algeria [1, 2] **–** FMD was notified between January and March 2019 with 56 outbreaks involving small and large ruminants of holdings principally situated in the coastal area of the country. All the episodes were attributed to FMDV serotype O.
FMDV serotype O field viruses detected during 2018 obtained good results with all the vaccine strains used in the vaccine matching strain VMSD tests.

Libya [1] – Ten FMD clinical outbreaks for which serotyping is still pending, occurred during April and May in cattle and sheep in different parts of the country.

Morocco [2] – Six FMDV outbreaks were notified in small and large ruminants at Oriental, Fès-Meknès and Rabat –Salé-Kénitra between end of April and beginning of May 2019.

Tunisia [2] **–** FMDV serotype O field virus detected during 2019 obtained good results with the vaccine strains used in the vaccine matching strain VMSD tests.

POOL 4 - EASTERN AFRICA

Ethiopia [2, 5] – A/AFRICA/G-VI and O/EA- 3 and O/EA-4 were the lineages detected in the thirty-six bovine samples collected during 2018 and 2019. The VMSD tests conducted on some of the field isolates of these lineages obtained good matching results only for those belonging to FMDV serotype O.
Field isolates belonging to FMDV serotypes A O and SAT 2, detected previously in the country between August and December 2018 and tested in the VMSD tests, obtained good matching results only with vaccines strains belonging to the latter serotype.

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

POOL 5 - WEST/CENTRAL AFRICA

Cote d'Ivoire [2] – A field Isolate of 2018 belonging to lineage O/EA-3 obtained good matching results in the VMSD tests.

Guinea [2] **–** Even in this case, a field isolate of 2018 belonging to lineage O/EA-3 obtained good matching results in the VMSD tests.

Nigeria [7] – The National Veterinary Research Institute Vom, Nigeria detected for the reporting month, FMDV serotype A in the samples analysed.

POOL 6 - SOUTHERN AFRICA

Malawi [1] **–** A FMD outbreak due to serotype SAT 2 was notified on February 21st 2019 in cattle of a village of Mzimba.

Mozambique [1] **–** Eight FMD outbreaks were reported on clinical basis in cattle from February 2018 to May 2019 of various villages of the administrative unit of Tete.

Zambia [1] – FMDV O/EA-2 and SAT 1/I were the lineages detected in the twelve bovine samples collected between January and April 2019.

Zimbabwe [1] – Five outbreaks due to FMDV serotype SAT 1 in Midlands and fourteen outbreaks due to FMDV serotype SAT 2 were reported in Mashonaland Central in cattle between March and April 2009.

POOL 7 - SOUTH AMERICA [1, 8]

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

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

IV. DETAILED POOL ANALYSIS

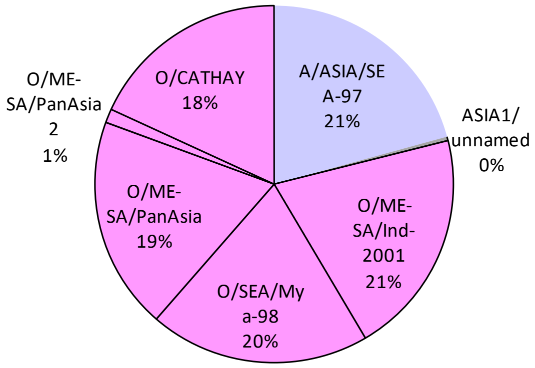
A. *POOL 1 – SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA*

OUTBREAKS	
Country	*Description*
Serotype O in China [1]	Further to the outbreak reported in March 2019, another event still caused by serotype O occurred on May 19th 2019 at Tieqianlike, Ruoqiang in the Mongolian Autonomous Prefecture of Bayingol, Xinjiang, on a cattle farm causing only a low morbidity rate of 3.15% in the 286 animals present. The Lanzhou National Reference Laboratory for Foot and Mouth Disease (OIE Reference Laboratory) confirmed the diagnosis on June 2nd 2019 using reverse transcription - polymerase chain reaction (RT-PCR) and gene sequencing. The source of the outbreaks is attributed to the legal movements of animals and general preventive measures were adopted. The present outbreak is a continuation of the series of events, which commenced in August 2018. Location of outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=30717. 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 an event that first started in July/August 15, 2018.

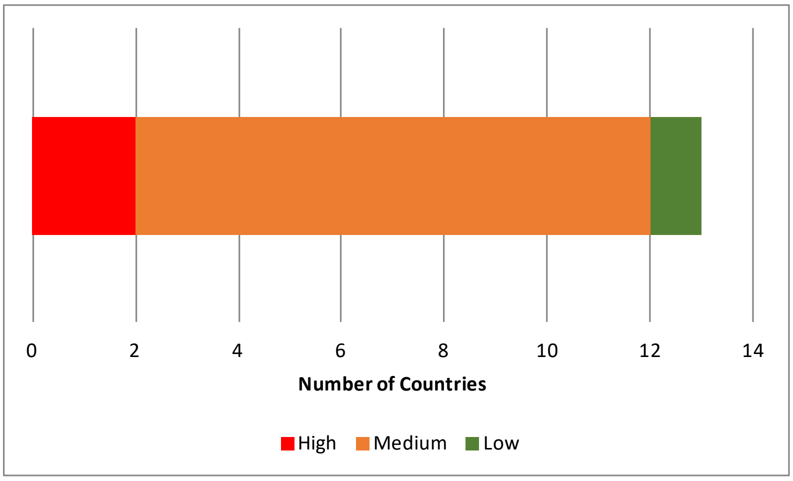
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
Russian Federation [9]	Surv. and Vacc.	The Regional Reference Laboratory for FMD (ARRIAH, Russia) reported the analysis of 1,365 sera of non vaccinated animals and 962 sera of animals for post-vaccination monitoring purposes.
Vietnam [2]	Vacc.	The field isolates belonging to three different lineages analyzed in VMSD tests obtained the following results: - O/VIT/1/2019 (O/SEA/Mya-98) obtained good matching results with O Tur 5/09, while those with O 3039 and O Manisa were at the limit of a good matching result; O/VIT/6/2018 (O/CATHAY) did not obtain good matching results with any of the vaccine strains mentioned above; O/VIT/10/2018 (O/ME-SA/PanAsia) obtained good matching results with all of the previously mentioned vaccine strains.

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

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 13 countries of Pool 1
A	A/ASIA/SEA-97	8
ASIA 1	ASIA1/ unnamed	1
O	O/ME-SA/Ind-2001	8
	O/SEA/Mya-98	6
	O/ME-SA/PanAsia	8
	O/ME-SA/PanAsia2	1
	O/CATHAY	4



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



B. POOL 2 – South Asia

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Bhutan [2]	Vacc.	The two FMDV field isolates O/BHU/1/2019 and O/BHU/1/2019, both belonging to the O/ME-SA/Ind-2001e lineage obtained good matching results in the VMSD tests using vaccine strains O 3039, O Manisa and O Tur 5/09.
India [10]	Surv. and PVM	The ICAR-Directorate of Foot and Mouth Disease, Mukteswar, India examined 472 serum samples collected for epidemiological studies. The sublineages currently circulating in the country are represented by O/ME-SA/2001d and O/ME-SA/2001e as described in the latest issue of the ICAR-DFMD Annual Report of 2017-18.
Nepal [2, 11]	Surv.	FMDV O/ME-SA/Ind-2001/e was the only topotype detected in 44 of the fifty samples collected from buffalo (N° -2), cattle N° - 45), goat (N° - 2) and pig (N° - 1) species from April 2018 to March 2019. The lineage was detected in the samples from all species examined. The field isolates had a high sequence identity (% id) with samples recently collected either from the country or with a field isolate detected in Bhutan in 2018 with the highest % id of 99.8. Location of genotyped samples is reported in Map 1.

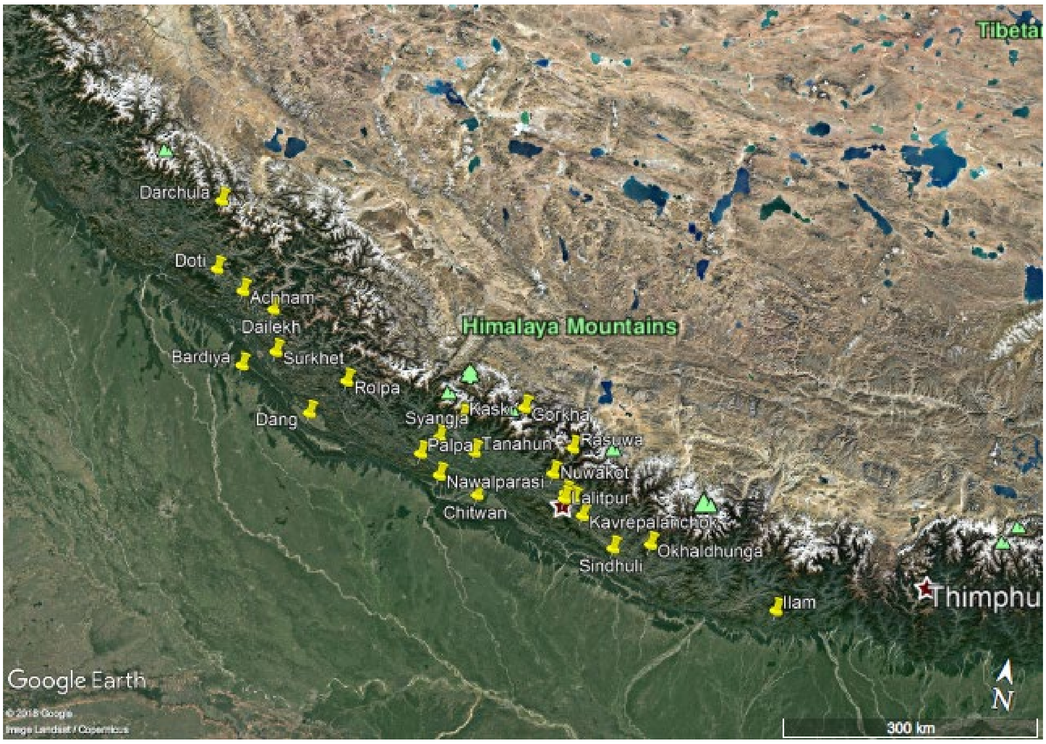
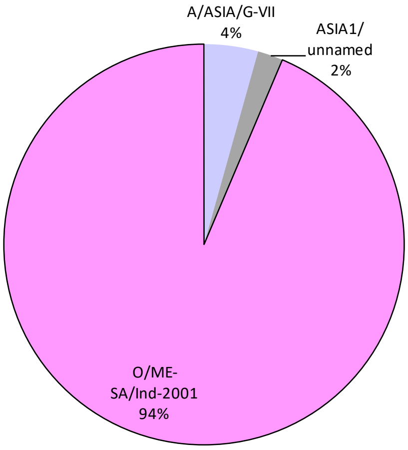
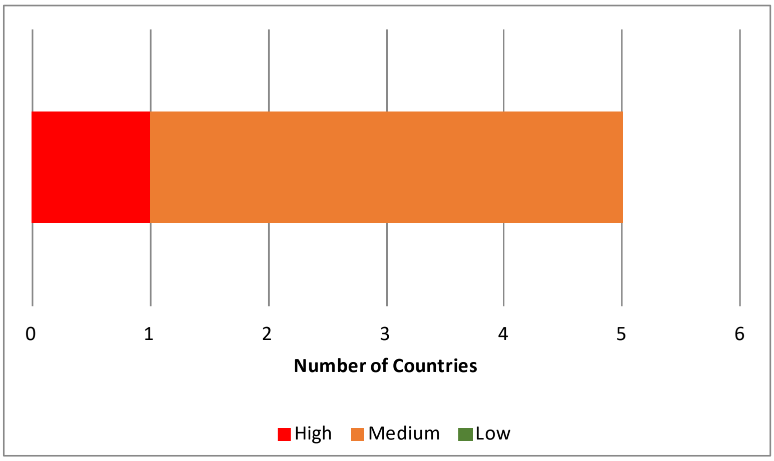
		Map 1: location of genotyped samples collected in Nepal from April 2018 to March 2019. (Source – WRLFMD, Google Earth Pro). 

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

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

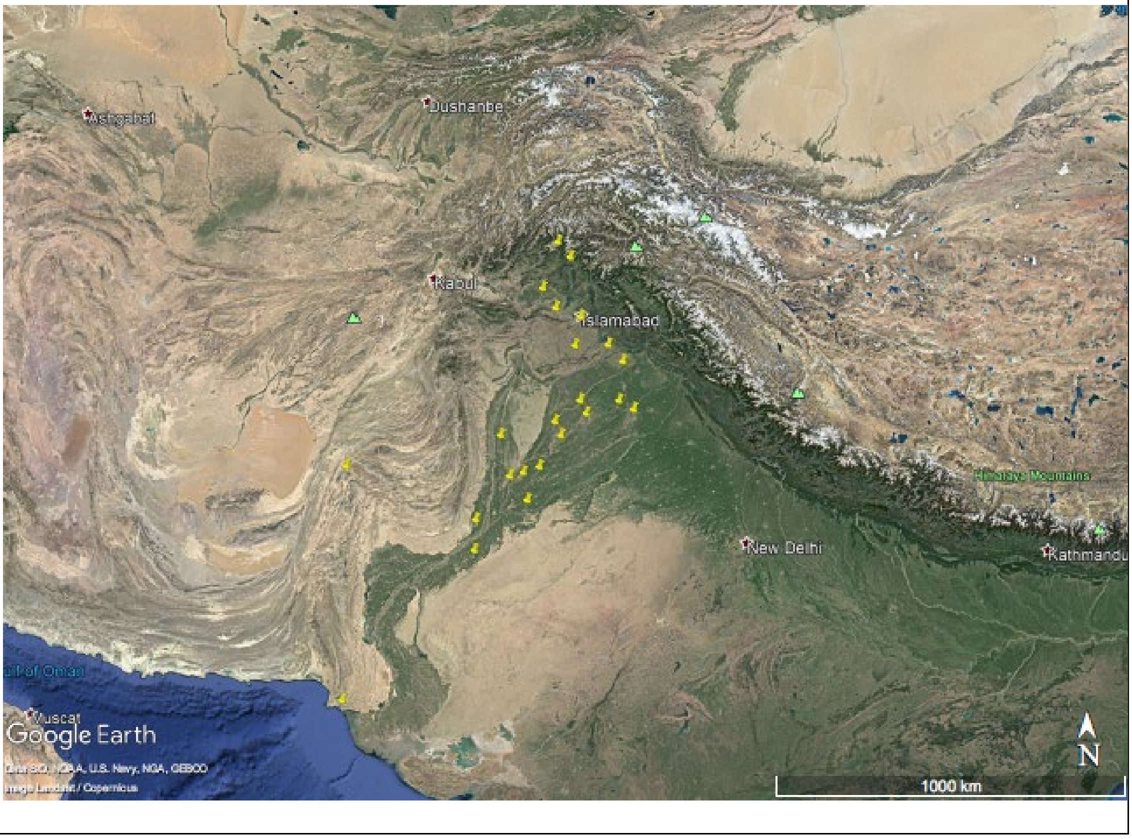


Graph 4: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 2 (see Annex for explanation).



C. POOL 3 – West Eurasia & Middle East

OUTBREAKS	
Country	***Description***
Serotype O in Israel [2]	A new FMD outbreak for which the serotyping is pending occurred on May 2nd 2019 in free ranging cattle at Daliyat Al-Karmel-Isifya, Haifa. This event is the most recent of a series of outbreaks which started on March 17th 2019. The Kimron Veterinary Institute, FMD Laboratory (National laboratory) confirmed the diagnosis of FMD on May 9th using reverse transcription - polymerase chain reaction (RT-PCR) and molecular typing identified the strain as O/ME-SA/PanAsia-2/QOM-15 lineage that is closely related to the isolate from the Tamra outbreak that occurred in Feb 2019. The episode occurred in free ranging beef cattle which presented mouth lesions. The herd presented an apparent morbidity rate of 4.35% with no fatality. The animals were reported as vaccinated a year ago, with a multivalent vaccine including strains O Manisa, O3039, O (Geshur 85) O PanAsia 2, A Iran 05 and A/Asia/G-VII.. The source of the outbreak is not known and general preventive measures were implemented. Location of outbreak is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=30434. *Interpretation:* This report is consistent with previous ones. FMDV is believed to circulate sporadically in the country due to incursions from neighbouring regions with the potential of endemic circulation of the virus, especially in small ruminants and wild species.
Serotyping pending in Pakistan [4]	For the reporting month, 104 outbreaks (for location see Map 2) were reported in the provinces of Baluchistan (N° 5 - 4.8%), Khyber Pakhtunkhwa (N° 5 - 4.8%), Punjab (N° 51 – 49.1%) and Sindh (N° 43 – 41.4%) for which serotyping is ongoing. 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. Different serotypes of FMDV are believed to circulate endemically in the country.

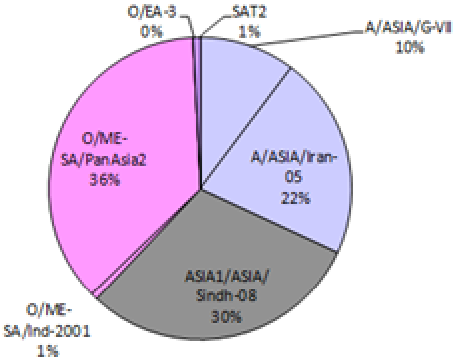
OUTBREAKS	
	Map 2: location of outbreaks reported in Pakistan during May 2019 (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator, Google My Maps). 

SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Afghanistan [3]	Surv.	During the reporting month, the CVDRL, Afghanistan detected FMDV serotypes ASIA 1 and o respectively in 41 (68.33%) and nine (15%) of the samples analysed, while for ten (16.67%) samples serotyping was not achieved. 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.
Pakistan [4]	Surv.	A ring vaccination campaign was carried out in Punjab with the administration of 3,390 doses. A/ASIA/Iran-05, Asia 1/ASIA/Sindh-08 and O/ME-SA/PanAsia-2 are the most recent lineages detected by the WRLFMD in samples collected in the country during 2016 and 2017.
Saudi Arabia [2]		FMDV serotype O field viruses, O/Sau/11/2018 and O/Sau/8/2018, belonging to the O/ME-SA/Ind-2001e lineage obtained good results in the VMSD tests conducted using vaccine strains, O 3039, O Manisa and O TUR 5/09.
Turkey [2]		A/ASIA/G-VII was detected in eight (28.6%) samples and O/ME-SA/PanAsia2^{QOM-15} in 20 (71.4%) samples out of the forty cattle samples collected from January 2016 to April 2019 and submitted for genotyping and phylogenetic analyses. The field isolates belonging to A/ASIA/G-VII, had the % id with samples recently collected either from the country or with a field isolate detected in Armenia, with the highest % id of 98.7. While for field isolates belonging to O/ME-SA/ PanAsia2^{QOM-15}, these also had the % id with either samples recently collected from the country or with field isolates detected in Kuwait, (highest % id of 99.2), in Iran (highest % id of 99.4) and in Israel (highest % id of 99.7). Location of collection of positive samples is represented in Map 3.

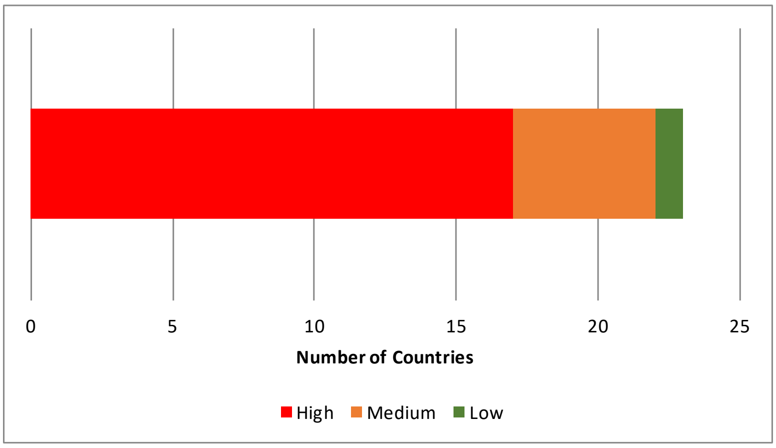
Map 3: location of genotyped samples collected in Turkey from April 2018 to March 2019. Yellow icons refer to location of collection of samples typed as A/ASIA/G-VII and blue icons typed as O/ME-SA/PanAsia2^{QOM-15} (Source – WRLFMD, Google Earth Pro).

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

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 24 countries of Pool 3 - West Eurasia
A	A/ASIA/G-VII	17
	A/ASIA/Iran-05	9
ASIA 1	ASIA1/ASIA/Sindh-08	9
O	O/ME-SA/Ind-2001	6
	O/ME-SA/PanAsia2	21
	O/EA-3	2
SAT2	SAT2	1



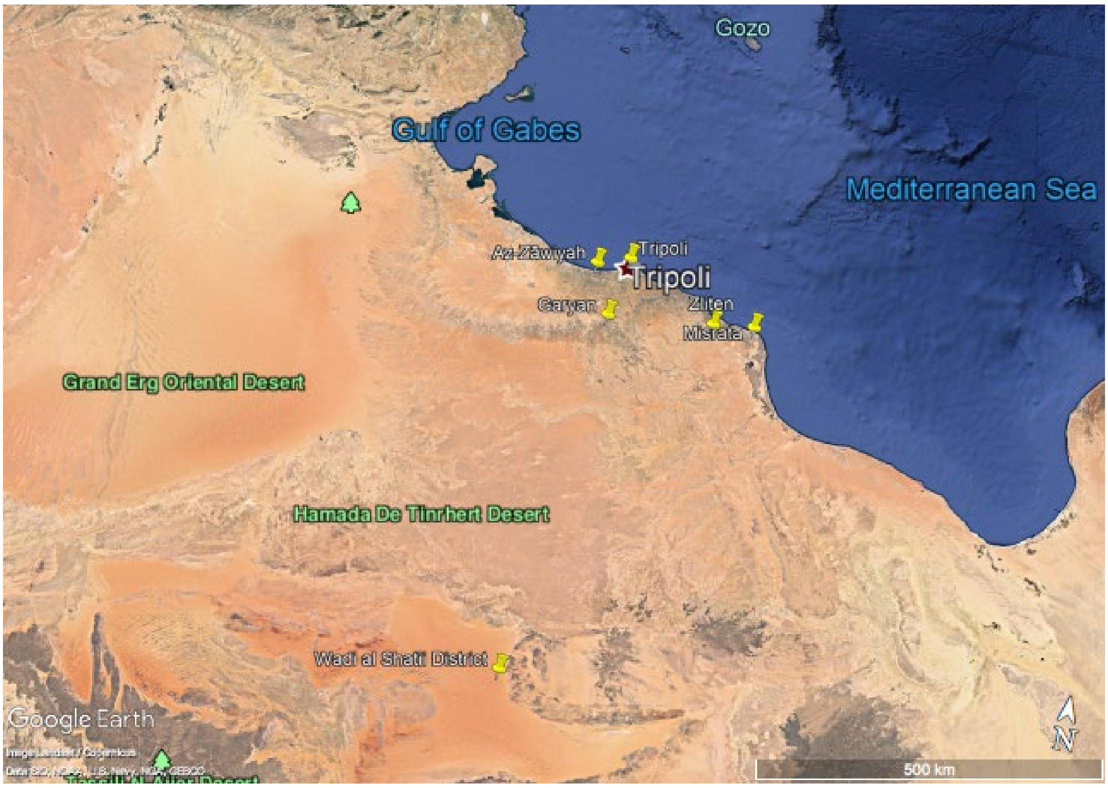
Graph 6: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 3 – West Eurasia & Middle East (see Annex for explanation).



D. POOL 3 – North Africa

OUTBREAKS	
Country	*Description*
Serotype O in Algeria [1]	A number of outbreaks notified between January and March 2019 that reached 171 events, involving small and large ruminants holdings situated in the coastal area of the country. All the episodes were attributed to FMDV serotype O. The source of the outbreaks is not known and a control measure, among others adopted, is that all livestock markets in the country were closed for 30 days from December 25th 2018. Apparent morbidity rate and mortality rate was registered in goats (11.85% and 7.18%) and sheep (15.47% and 9.56%). The location of the outbreaks is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=30405. *Interpretation:* These outbreaks are a continuation of those that were reported in November 2018 after an absence of four years of FMD; the serotype has also been reported in other countries of the same virus pool.
Serotype pending in Libya [1]	Ten FMD clinical outbreaks (Map 4), with one reported as resolved, occurred during April and May in cattle and sheep in different areas of the country. Dairy cattle in different regions presented clinical signs of FMD. The samples required for laboratory diagnosis were collected and as the laboratory diagnosis was not performed locally because of the absence of diagnostic materials these have been forwarded as FTA cards to the OIE/FAO FMD Reference Laboratory of the Istituto Zooprofillatico Sperimentale della Lombardia e dell'Emilia Romagna. Apparent morbidity and mortality were respectively 25.64% and 7.69% for cattle and 23.18% and 9.84% in sheep. *Interpretation:* This report is a continuation of that notified in April 2019. More epidemiological data and information on the serotype involved is required to interpret the significance of the event.

Map 4: location of FMD outbreaks which occurred during April and May in cattle and sheep in Libya. (Source – WRLFMD, Google Earth Pro).



Serotype O in Morocco [1]

Six FMDV outbreaks were notified in small and large ruminants at Oriental, Fès-Meknès and Rabat – Salé-Kénitra between end of April and beginning of May 2019. Diagnosis was carried out for samples taken from all the species involved by the Meknes Regional Laboratory for Analysis and Research on May 5th 2019 using real-time reverse transcriptase/polymerase chain reaction. The disease appeared in a mild form in adult animals principally characterised by lameness, while dead animals were young and their carcasses were destroyed. Further control measures were adopted, including vaccination in cattle only, as reported in Table 4. No details on the type of vaccine used were provided.

Apparent morbidity and mortality were respectively 25.64% and 7.69% for cattle and 23.18% and 9.84% in sheep. Location of outbreaks is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=30505.

Interpretation: These outbreaks are a continuation of those that were reported in January 2019 after an absence of four years of FMD; the serotype has also been reported in other countries of the same virus pool

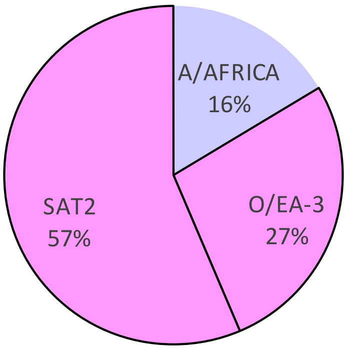
Table 4: details of the vaccination carried out in Morocco reported in May 2019 (Source – Wahis, OIE)

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

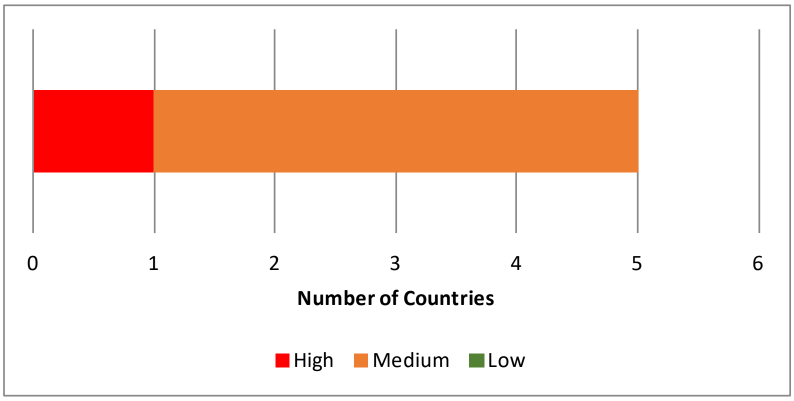
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Algeria [1]	Vacc.	A FMDV serotype O field virus O/ALG/11/2018, belonging to the O(EA-3 lineage, obtained good results in the vaccine matching strain VMSD tests with all the vaccine strains, O 3039, O Manisa and O Tur 5/09, employed.
Tunisia [1, 2]	Surv.	The FMD events, which started in December 2018 due to serotype O, were notified as resolved on March 7th 2019 and no relative reports will be submitted.
	Vacc.	The field virus O/TUN/1/2019 obtained good results in the vaccine matching strain VMSD tests with all the vaccine strains, O 3039, O Manisa and O Tur 5/09, employed.

Table 5 and Graph 7: Conjectured circulating FMD viral lineages in Pool 3 - North Africa (further detail (country-level) in Annex).

Serotype	**Viral lineage**	**Number of countries where strain is believed to circulate in the 5 countries of Pool 3 - North Africa**
A	A/AFRICA	4
O	O/EA-3	5
SAT 2	SAT 2	2



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

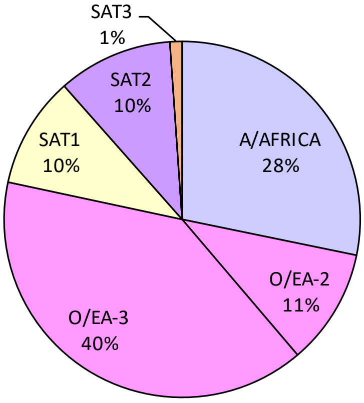


E. POOL 4 – Eastern Africa

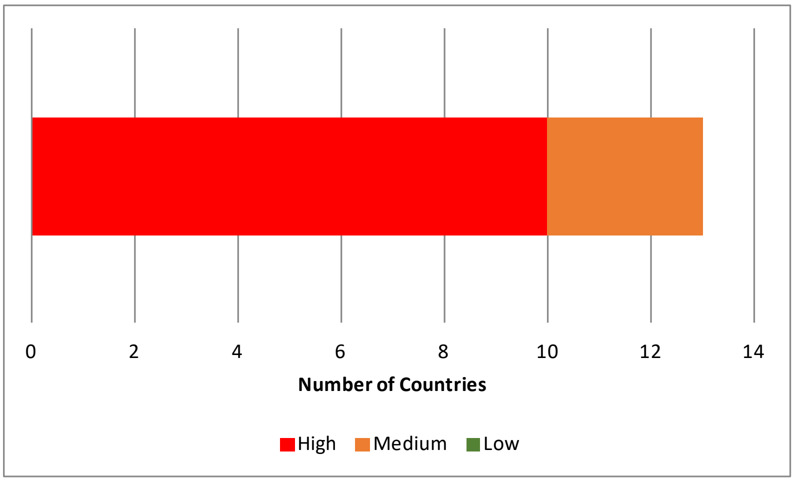
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Ethiopia [2]	Surv.	Field isolates detected in 36 cattle samples collected between August and December 2018 belonging to A/AFRICA/G-IV (N° 13 - 50%), O/EA-3 (N° 12 – 46.2%) and O/EA-4 (N°1 -3.8%) lineages were subjected to VMSD tests with the following results: A/ETH/35/2018 and A/ETH/48/2018 did not obtain good matching results with A Iran 2005, A TUR 20/06, A/ERI/3/98, A/GVII and A22 IRQ; O/ETH/20/2018 and O/ETH/23/2018, both belonging to O/EA-3 obtained good matching results with O 3032, O Manisa and O Tur 5/09.
Kenya [6]	Surv., vacc.	The FMD NRL, Embakasi, Kenya, reported the detection of FMDV serotype SAT 2 in one of the three bovine specimens analysed. The most recent lineages detected in the country are A/AFRICA/G-I and SAT 2/IV/unnamed in samples collected in 2017.
Uganda	Surv. and Vacc.	A ring vaccination was carried out at the border of Uganda and Eastern Democratic Republic of Congo as 200 heads of cattle entred Ugnada and 16 of thesein the area of Makonda village were reported by the Veterinary Officers to present signs of FMD. The vaccine used in the farms around the subcounty was a quadrivalent containing FMDV serotypes A, O, SAT 1 and SAT 2. In addition, the outbreak was contained by quarantine while samples for the identification of virus were not collected due to the delay in reporting.

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



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

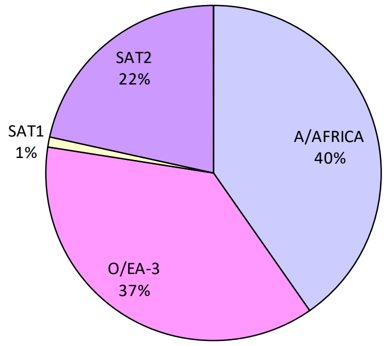


F. *POOL 5 – West / Central Africa*

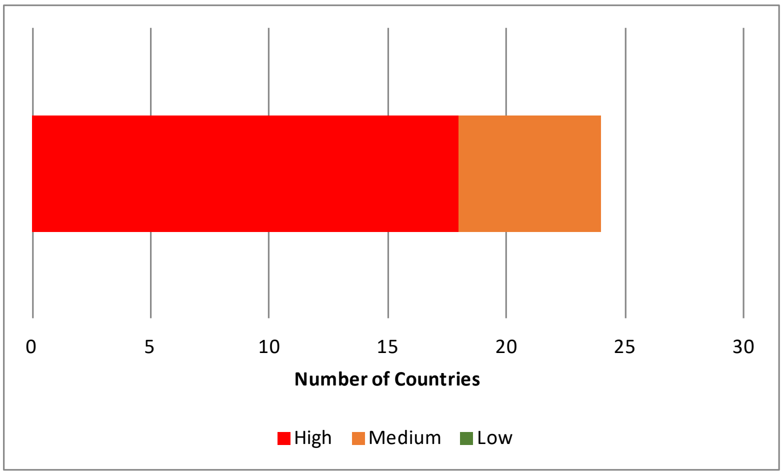
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Cote d'Ivoire [2]	Vacc.	The field isolate O/CIV/3/2018 belonging to lineage O/EA-3 obtained good matching results in the VMSD tests using O 3039, O Manisa and O Tur 5/09 vaccine strains.
Guinea [2]	Vacc.	As for the previous country, good matching results were obtained with O 3039, O Manisa and O Tur 5/09 vaccine strains field when analysing in the VMSD tests field isolate O/GNA/3/2018 that belongs to the O/EA-3 lineage.
Nigeria [7]	Surv.	The NVRI, Vom, Nigeria detected for the reporting month, FMDV serotype A in the five cattle samples analysed using antigen typing Elisa. The samples were collected from animals in the Barakinladi Local Government Area in Plateau State.

Table 7 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 prevalence of circulating serotypes/strains defined for each country of Pool 5 (see Annex for explanation).



G. *POOL 6 – Southern Africa*

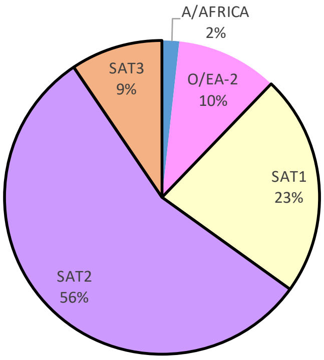
OUTBREAKS	
Country	*Description*
Serotypes A and SAT 2 Malawi[1]	A FMD outbreak due to serotype SAT 2 was notified on February 21st 2019 in cattle of a village of Mzimba. The apparent morbidity presented by the population involved (80,000) was 0.36% with no mortality. The Central Veterinary Laboratory carried out a preliminary serological confirmation of the outbreak on March 1st 2019 while the Botswana Vaccine Institute carried out the serotyping of the virus responsible for the cases reported in this area. Illegal animal movement is the main source suspected for the introduction of infected animals to the area and the population at higher risk is in a communal grazing/watering system. Sera samples collected from Chitipa, area were other FMD outbreaks were reported as positive for serotype A and for this they are being reported as a separate event. Additional cases were observed in Chitipa (7) and Kasungu (32), which is bordering Mzimba. In April, together with other preventive measures, a vaccination programme was instituted in the outbreak areas, including Kasungu, which is close to Mzimba, with the administration of 61,886 doses using a trivalent vaccine, including serotypes SAT 1 SAT 2 and SAT 3, but no serotype A. Booster vaccination is being carried out in May 2019 with 37,906 animals already vaccinated. Location of the outbreak for FMDV SAT 2 is available at the following link: https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=30677. *Interpretation:* More information is needed to interpret the significance of this report, as this is the first notification of FMDV serotype A in the country that is reported to circulate in the neighbouring country of Zambia to study the extent of spread of this serotype and the mechanisms by which it is spreading so as to identify measures for its containment.
Unknown serotype in Mozambique[1]	Eight FMD outbreaks were reported on clinical basis in cattle from February 2018 to May 2019, in Moatize, Doa, Changara and Marara, presenting an apparent morbidity of 4.92% and no mortality. Serotyping of these episodes is pending. The source of the outbreaks reported is attributed to the illegal movement of animals, contact with infected animals at grazing/watering points and through contact with fomites. Preventive measures together with the vaccination of 77,780 cattle using a trivalent vaccine containing serotypes SAT 1, SAT 2 and SAT 3. 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=29899. *Interpretation:* More information is needed to interpret the significance of this outbreak. According to the report no typing of the outbreak has been done. We can extrapolate the Changara outbreak to be SAT 2 from the findings in Mashonaland Central in Zimbabwe where it spread into in June 2018.
SAT 1 and SAT 2 in Zimbabwe[1]	Relative to the five outbreaks due to FMDV serotype SAT 1 that occurred between March and April 2019, in various localities of Shurugwi, Midlands an apparent morbidity of 5.12% was registered in the 1,500 cattle involved. The outbreaks occurred in cattle of varying age groups sharing the same grazing areas and watering points. The infected areas remain under quarantine with weekly livestock inspections on-going in the affected and surrounding area as well as vaccination of 425,000 cattle in Masvingo and 215,000 in Midlands. Other general preventive measures were also applied. 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=29480. For the fourteen outbreaks due to FMDV serotype SAT 2 that were reported in cattle in Bindura, Mazowe and Shamva Mashonaland between March and April 2019 a low apparent morbidity of 1.38% was registered in the population of 22,186 exposed animals that as for the previous case were constituted by cattle of varying age groups sharing grazing and watering points. The outbreaks were due to the illegal movement of animals with spread at grazing areas and watering points.

	Vaccination of cattle was carried out in Mashonaland Central and East with the respective vaccination of 127,265 and 120,000 cattle. The intensive surveillance and implementation of control measures instituted in the infected areas remain in force in the affected districts together with the veterinary checkpoints complimented by the police force in place in strategic points and the destruction of all illegally moved cattle. 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=30382. *Interpretation:* This report is consistent with previous reports. The causative serotype/strain is believed to circulate endemically in the country. A genotyping report is still pending and therefore information about the strain is still missing.

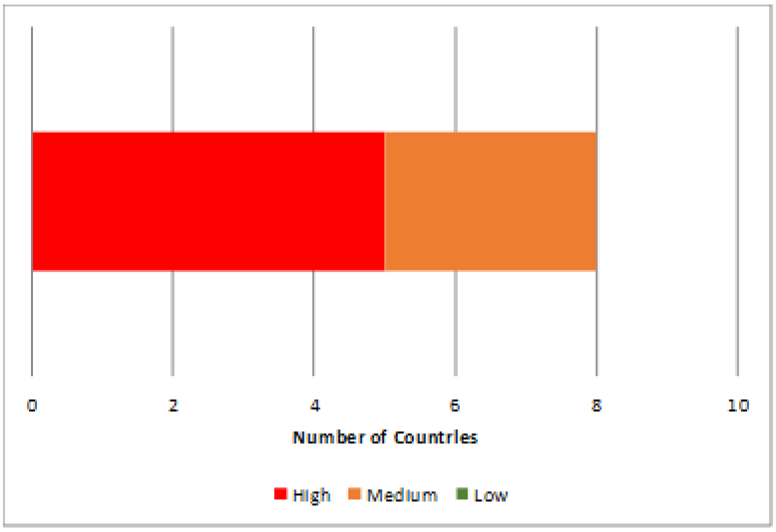
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
South Africa [1], [12]	Surv.	A number of sera collected from African buffalo (Cape buffalo) were tested for movement of these animals and were detected as positive in liquid-phase blocking ELISA for FMDV antibodies.H however serotyping could not be determined. All the buffalo on the farm were these animals were reared were moved into South Africa's FMD Infected Zone by May 10th 2019. Further to this, the Agricultural Research Council, Onderstpoort Veterinary Institute, Transboundary Animal Diseases (OIE Reference Laboratory) examined 5,862 sera in solid-phase competition ELISA and 425 test in non-structural protein ELISA.
Zambia [1]	Surv.	FMDV O/EA-2 and SAT 2/I were detected in the twelve bovine samples collected between January and April 2019. Location of collection of these samples was not provided. For FMDV O/EA-2 all isolates had a high % id close to other isolates detected in the country during 2018 as was also the case the SAT 2/I lineage for isolates of the same country detected in 2019.

Table 8 and Graph 13: Conjectured circulating FMD viral lineages in Pool 6 (further detail (country-level) in Annex).

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



Graph 14: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 6 (see Annex for explanation).

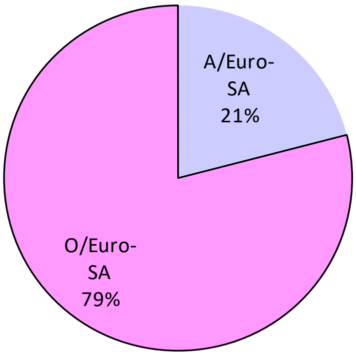


H. POOL 7 – South America

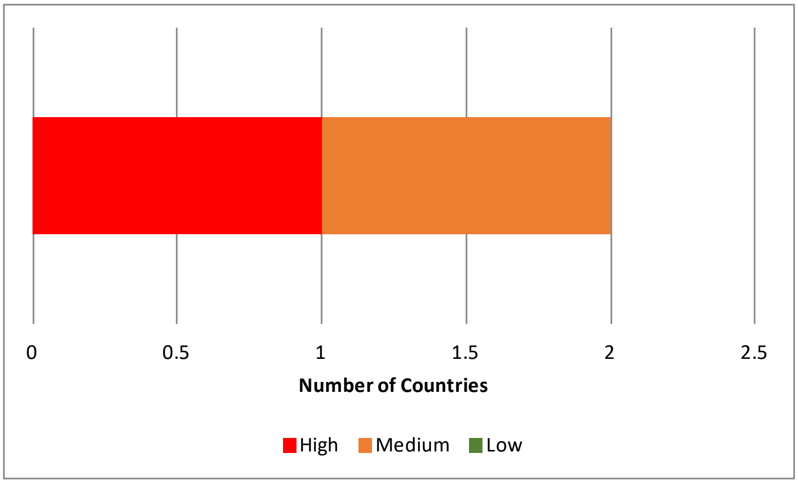
No outbreaks are reported for this Pool during the present month.

Table 9 and Graph 14: 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 15: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 7 (see Annex for explanation).



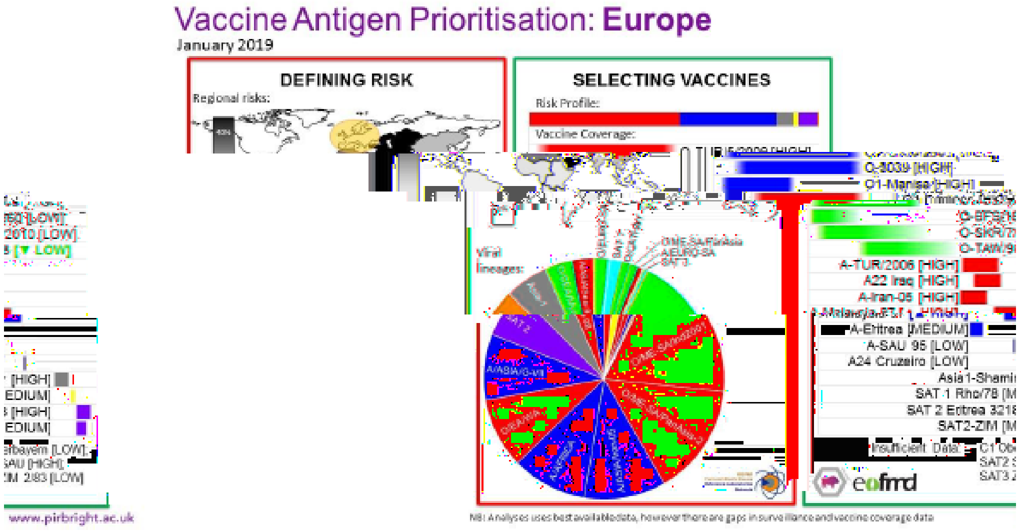
V. OTHER NEWS

[2]The 1st WRLFMD Quarterly Report for the period January – March 2019 contains a new format for recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of Table 16 is contained within the report.

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

This report provides recommendations of FMDV vaccines to be included in antigen banks. These outputs are generated with a new tool (called PRAGMATIST) that has been developed in partnership between WRLFMD® and EuFMD. These analyses accommodate the latest epidemiological data collected by the OIE FAO FMD Laboratory Network regarding FMDV lineages that are present in different *source regions* (see Table below), as well as available *in vitro, in vivo* and field data to score the ability of vaccines to protect against these FMDV lineages.

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



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 e eight *source regions*,
while the figure highlights the importance of these *source regions* fo r **Europe** (using data
collected at the EU-RL Workshop); please contact WRLFMD EuFMD f for assistance to tailor
these outputs to other geographical regions. NB: Vaccine-coverage da ita presented is based
on available data and may under-represent the true performance of ind lividual vaccines.

VI. REFERENCES – Superscripts

1. http://www.oie.int/animal-health-in-the-world/the-world-animal-health-information-system/data-after-2004-wahis-interface/
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3. Central Veterinary Research and Development Laboratory (CVDRL), Aghanistan - *Dr. Wahidullah* Head of Laboratory.
4. Progressive Control of Foot and Mouth Disease in Pakistan - *Dr. Muhammad Afzal*, Project Coordinator.
5. National Animal Health Diagnostic and Investigation Center (NAHDIC) – *Dr. Daniel Gizaw*.
6. National FMD Reference Laboratory, Embakasi, Kenya – *Dr. Kenneth Ketter.*
7. FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria - *Dr. Ularamu Hussaini*
8. OIE/FAO FMD Reference Laboratory Network, Annual Report 2016
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11. Foot and Mouth Disease and TADS Investigation Laboratory, Nepal - Dr. Sharmila Chapagain
12. ARC -Onderstepoort Veterinary Institute, Republic of South Africa - *Dr LE Heath/Ms E Kirkbride*
13. 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
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).
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16. Ibrahim Eldaghayes et al. Exploiting serological data to understand the epidemiology of foot-and-mouth disease virus serotypes circulating in Libya Open Vet J. 2017; 7(1): 1–11 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5283054/

VII. Annex

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

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

__Description of methods__

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

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

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

Pool-level estimates and assumptions:

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

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

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

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

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

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

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

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

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

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

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

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

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

Legend of icons in the following tables

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

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

			Presumed serotype distribution within country			Presumed viral lineage distribution within country								
Country	**Last Outbreak Reported/Serotype#**	**FMD incidence rate**	**A**	**Asia1**	**O**	**A/ASIA/SEA-97**	**ASIA1/ unnamed**	**O/ME-SA/Ind-2001**	**O/SEA/Mya-98**	**O/ME-SA/PanAsia**	**O/ME-SA/PanAsia2**	**O/CATHAY**	**Uncertainty on circulating serotypes**	**Reference**
CAMBODIA	Dec 2016/ A & O	high	◑		◑	◑				◑			medium	2
CHINA	April 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, 13
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 18: Conjectured circulating FMD viral lineages in each country of Pool 2 (current to May 2019).

			Presumed serotype distribution within country			**Presumed viral lineage distribution within country**				
Country	**Last Outbreak Reported/Serotype#**	**FMD incidence rate**	A	Asia1	O	A/ASIA/G-VII	ASIA1/ unnamed	O/ME-SA/Ind-2001	**Uncertainty on circulating serotypes**	**Reference**
BANGLADESH	Dec 2016/A, ASIA 1 and O	high	◔	◔	◕	◔	◔	◕	high	14
BHUTAN	Jan 2019/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 19: Conjectured circulating FMD viral lineages in each country of Pool 3 –West Eurasia (current to May 2019).

			Presumed serotype distribution within country			Presumed viral lineage distribution within country									
Country	**Last Outbreak Reported/Serotype#**	**FMD incidence rate**	A	Asia1	O	sat2	A/ASIA/G-VII	A/ASIA/Iran-05	ASIA1/ASIA/Sindh-08	O/ME-SA/Ind-2001	O/ME-SA/PanAsia2	O/EA-3	SAT2	**Uncertainty on circulating strains**	**reference**
AFGHANISTAN	April 2019/O & Asia 1, Dec 2018/A	high	◑	◔	◑			◑	◔		◑			medium	3
ARMENIA	Dec 2015/A	low/sporadic	◔		◕		◔				◕			high	15
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	May 2019/serityping pendingFeb 2019/O, June2017/A	low/sporadic	◔		◕		◔				◑	◔		low	2
JORDAN	Mar 2017/O	low/sporadic	◕		◑		◕			◔	◔			high	2, as per Saudi Arabia
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	April 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	April 2019/O, Oct 2017/A May 2015/ Asia 1	high	◔		◕		◔				◕			medium	2
TURKMENISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
UNITED ARAB EMIRATES	Sep 2016/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
UZBEKISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran

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

			Presumed serotype distribution within country			**Presumed viral lineage distribution within country**				
Country	**Last Outbreak Reported/Serotype#**	**FMD incidence rate**	**A**	**O**	**SAT 2**	**A/AFRICA**	**O/EA-3**	**SAT 2**	**Uncertainty on circulating serotypes**	**Reference**
ALGERIA	Mar 2019/O, Nov 2016/A, Jun 2016/Sat 2,	medium	◑	◕		◑	◕		medium	2
EGYPT	Nov 2018/Sat 2, Feb 2018/A April 2017/O	high	◔	◔	◕	◔	◔	◕	medium	2
LIBYA	May 2019/serotyping pending, Oct 2013/O	high	◔	◔	◕	◔	◔	◕	high	16, as per egypt
MOROCCO	May 2019/O	low/sporadic		●			●		medium	2
TUNISIA	Feb 2019/O, April 2017/A	low/sporadic	◔	◕		◑	◕		medium	2

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

			Presumed serotype distribution within country					**Presumed viral lineage distribution within country**							
Country	**Last Outbreak Reported/Serotype#**	**FMD incidence rate**	**A**	**O**	**sat1**	**sat2**	**sat3**	**A/AFRICA**	**O/EA-2**	**O/EA-3**	**SAT1**	**SAT2**	**SAT3**	**Uncertainty on circulating serotypes**	**Reference**
BURUNDI	Aug 2013 / not available	high	◑	◔	◔	◔		◑		◔	◔	◔		high	as per Tanzania
COMOROS	March 2019/O	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	April 2019/A, O &SAT 2, Feb 2018/SAT 1	high	◑	◕	◔		○	◔		◕	◔		○	medium	2
KENYA	May 2019/SAT 2, Mar 2019/A, 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 22: Conjectured circulating FMD viral lineages in each country of Pool 5 (current to May 2019).

			Presumed serotype distribution within country				Presumed viral lineage distribution within country					
Country	**Last Outbreak Reported/Serotype#**	**FMD incidence rate**	**A**	**O**	**sat1**	**sat2**	**A/AFRICA**	**O/EA-3**	**SAT1**	**SAT2**	**Uncertainty on circulating serotypes**	**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	
GAMBIA	July 2018/O	high		●				●			medium	1
GHANA	Sep 2018/ O & SAT 2	high		◑		◑		◑		◑	high	2
GUINEA	Sep 2018/O	high		●				●			medium	1
GUINEA-BISSAU	Dec 2018/O	high		●				●			high	as per Guinea
LIBERIA	Not available	high		●				●			high	as per Guinea
MALI	Oct 2016/not reported	high	◑	◑		◑	◑	◑		◑	high	1
MAURITANIA	Aug 2018/O, Dec 2014/SAT 2	high				●				●	medium	2
NIGER	2014/not sampled, May 2015/O	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
NIGERIA	May 2019/A, Sep 2018/O &Sat 2, Sept 2016/ SAT 1	high	◑	◑		◔	◑	◑		◔	high	2
SAO TOME AND PRINCIPE	Not available	0									high	no data available
SENEGAL	Sep 2018/O, Feb 2015/ A, 2014/ SAT 2	high		●				●			medium	2
SIERRA LEONE	Aug 2018/O	high		●				●			medium	as per Senegal
TOGO	2012/O	high	◑	◑		◔	◑	◑		◔	high	1, as per Nigeria

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

			Presumed serotype distribution within country					**Presumed viral lineage distribution within country**						
Country	**Last Outbreak Reported/Serotype#**	**FMD incidence rate**	**A**	O	SAT1	SAT2	SAT3	A/AFRICA	O/EA-2	SAT1	SAT2	SAT3	**Uncertainty on circulating serotypes**	**Reference**
ANGOLA	April 2016/SAT 2	high		◑	◔	○	◔		◑	◔	○	◔	high	as per Zambia
BOTSWANA	July 2018/SAT 2, June 2015/SAT 1	medium				●					●		medium	2
MALAWI	Feb 2019/A, SAT 2, June 2016/SAT 1	medium	◔		◔	◔		◔		◔	◔		high	2
MOZAMBIQUE	May 2019/ 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	April 2019/SAT 2, March 2019/O, Feb 2019/ A, May 2017/SAT 3, Jan 2013/SAT 1	medium	○	◑	○	○	◔	○	◑	○	○	◔	medium	2
ZIMBABWE	April 2019/SAT 1 & SAT 2, Sep2018/typing pending, Jun 2013/SAT 3	high			◑	◑				◑	◑		medium	1, 2

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

			Presumed serotype distribution within country		Presumed viral lineage distribution within country			
Country	**Last Outbreak Reported/Serotype #**	**FMD incidence rate**	A	O	A/Euro SA	O/Euro-SA	**Uncertainty on circulating serotypes**	**Reference**
VENEZUELA	Oct 2018/O	medium	◑	◑	◑	◑	high	7
COLUMBIA	2011/O, 2013/A	medium		●		●	medium	1

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