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 | September

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

September 2019

MAIN INFORMATION SOURCES USED:

Databases:

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

Other sources:

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

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

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

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

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Please note that the report contains hyperlinks

I. HIGHLIGHTS

It is my honour to be invited to write this editorial. Over the past year or so, I have had the pleasure of working with others at the EuFMD to report on the information available about the current FMD situation, with the aim of helping risk managers in free and endemic countries to prevent and/or control FMD.

At the beginning of 2019, we modified the format of the Global Monthly Report (GMR) to include a measure of relative prevalence of the virus strains circulating in each virus pool. This information is needed to make risk-based vaccine choices, which can be facilitated by the PRAGMATIST[1] framework. We recognise that our prevalence estimates are based on incomplete surveillance data, and thus there is a significant level of uncertainty around them. However, we hope that structured, regular reporting of the estimates will assist in highlighting important surveillance gaps and encourage these to be filled.

Also this year, we have benefitted from the insights and contributions of four Global Intelligence Focal Points, who have shared insights on the special features of their regions and illustrated that many of the challenges faced are common, such as FMD spread through uncontrolled animal movements, knowledge gaps and resource constraints. Reviewing the report, I am struck by the great level of detail provided in some aspects, and the absence of contextual information needed to make sense of it. It is like looking at the detail of a photograph, for example zooming in on the pattern of a woman's dress, without being able to see the woman herself nor her surroundings or whom she was with when the picture was taken. Is she a woman typical of the place and time? Or was she photographed because she is unusual in some way?

In the GMR, we sometimes find ourselves in a similar situation; we are provided with detailed information such as the serotype or even genotype of a FMD virus detected in a laboratory sample, but are missing important elements needed to appreciate the significance of the result, such as how and why the animal was selected for sampling, from specifically which place and time, and what events are going on around.

To take the whole FMD picture, field veterinarians and paraveterinarians, epidemiologists and laboratory experts must coordinate and work together. With the massive opportunity provided by new technologies such as smartphones that can act as a camera, spreadsheet and GPS, this vision should be well within reach. Of course, the FMD picture is even broader than that; to fully understand and manage FMD risks we also need to zoom out and include those who can inform us about the drivers for disease spread (such as animal movements) as well as the wider impact of clinical disease on economies and livelihoods. As such, the full canvas will include information originating from livestock owners, traders, socio-economists and pharmaceutical companies.

As we reach the end of 2019, EuFMD is embarking on a new workplan. We will continue to endeavour to improve how we share and communicate information about FMD outbreaks, surveillance and control at the global level. As we strive to capture an accurate snapshot of FMD, we invite you to share your knowledge and ideas.

Melissa McLaws
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[1] Pragmatist_McLaws.pdf

II. GENERAL OVERVIEW

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

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

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

*REPORTED ONLY IN OMAN IN 2017

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

III. IN THIS REPORT

POOL 1- SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA

China (Hong Kong, SAR) [1] **–** The FMDVs detected in porcine samples collected during 2019 were genotyped as O CATHAY.

Myanmar [2] **–** Following the outbreaks due to FMDV serotype O that were first reported in 2018, a vaccination campaign was carried out in the administrative region of the Rakhine State.

Thailand [1] **–** FMDV serotypes A and O were detected in the bovine samples collected in the country between 2018 and 2019.

POOL 2 - SOUTH ASIA

No FMD outbreaks were notified for this Pool for the reporting month.

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan [3] – FMDV ASIA 1 was the serotype detected among the samples analysed by the Central Veterinary Research and Development Laboratory (CVDRL) during the reporting month.

Pakistan [1, 2, 15] **–** Four FMD outbreaks between December 2018 and April 2019 at Punjab and Khyber Pakhtoon Khuwa that were caused by an exotic topotype of FMDV serotype O.
The vaccine matching strain differentiation (VMSD) tests conducted on field FMDVs belonging to serotypes A, ASIA 1 and O obtained overall good matching results with the vaccine strains employed.
FMDV Asia 1 and O were the serotypes that were reported among the 42 outbreaks notified in two different provinces of the country.

POOL 3 – NORTH AFRICA

Morocco [2] **-** A vaccination campaign was conducted in various administrative units in response to the outbreaks caused by topotype O/EA-3 which occurred in the country during 2019.

POOL 4 - EASTERN AFRICA

Ethiopia [4] **–** FMDV serotype O was detected by the National Animal Health Diagnostic and Investigation Center (NAHDIC) in samples collected from clinical outbreaks.

Kenya [5] - FMDV serotypes O and SAT 2 were detected in bovine samples analyzed by the FMD National Reference Laboratory (FMDNRL), Embakasi, Kenya.

POOL 5 - WEST/CENTRAL AFRICA

Nigeria [16] **–** The FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria detected FMDV in clinical samples collected from Ogun and Keebi States.

POOL 6 - SOUTHERN AFRICA

Malawi [2] **–** Primer and booster vaccination was carried out in the Mchinji district due to the outbreaks caused by FMDV SAT 2 that were notified in February 2019.

Namibia [2] **–** A FMD outbreak was reported on clinical basis in August 2019, in cattle of a village of Kabwe North, Zambezi.

South Africa [2, 6] – A FMD outbreak due to serotype SAT 2 occurred in September 2019, in cattle at Musina, Limpopo due to contact with wild animals.

Zambia [2] **–** Fourteen FMD outbreaks due to serotype O occurred between March and August 2019 in the eastern area of the country.

POOL 7 - SOUTH AMERICA [2, 7]

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

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

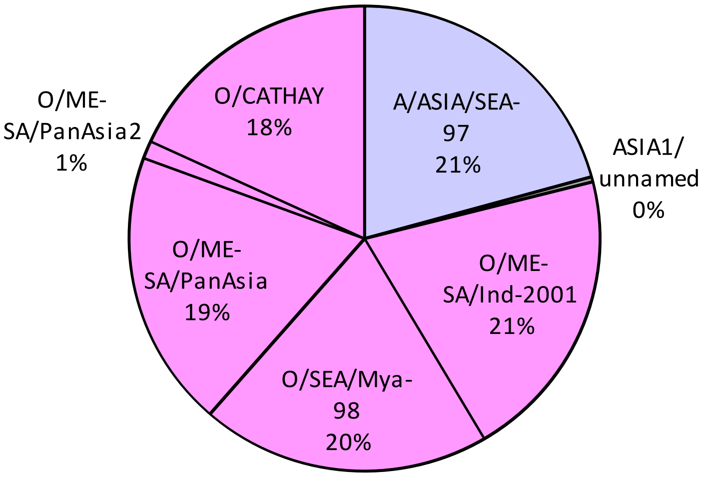
IV. DETAILED POOL ANALYSIS

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

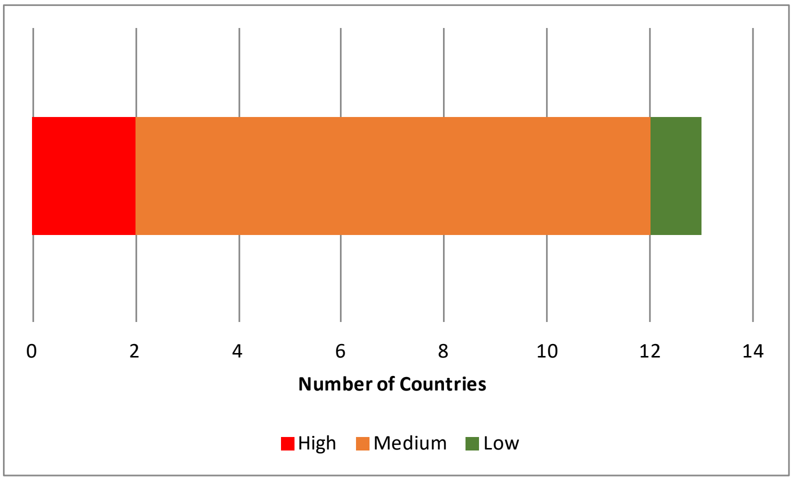
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	***Activity***	***Description***
China (Hong Kong, SAR) [1]	***Surv.***	The FMDVs detected in the porcine samples collected at Sheung Shui, New Territories between March and May 2019 were genotyped as O CATHAY with the highest sequence identity to that of viruses belonging to field strains that were circulating in the country during 2018. Since 2012, O CATHAY is the only topotype detected in this Special Administrative Region as reported from viruses detected in the samples analyzed by the WRLFMD.
Myanmar [2]	***Surv. & Vacc.***	Following the outbreaks that were first reported in April 2018 due to FMDV serotype O, where the animals had contracted the infection due to contact with animals at grazing and watering points, a vaccination campaign was carried out in 28 villages of the administrative region of the Rakhine State with the inoculation of 4,400 cattle. The type of vaccine used was not reported. Other preventive measures are still in place even if no new outbreaks have occurred. The topotypes detected by the WRLFMD belonging to the serotype responsible for the latest outbreaks are O/ME-SA/Ind-2001e, detected for the first time in the country, O/ME-SA/Ind-2001d and O/SEA/Mya-98. These viruses were detected in the last samples collected that refer to 2017 and 2018.
Russian Federation [8]	***PVM***	The Regional Reference Laboratory for FMD (ARRIAH, Russia) carried out the analysis of 470 sera for post vaccination monitoring purposes and of 10,430 sera from unvaccinated animals.

Table 2 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).

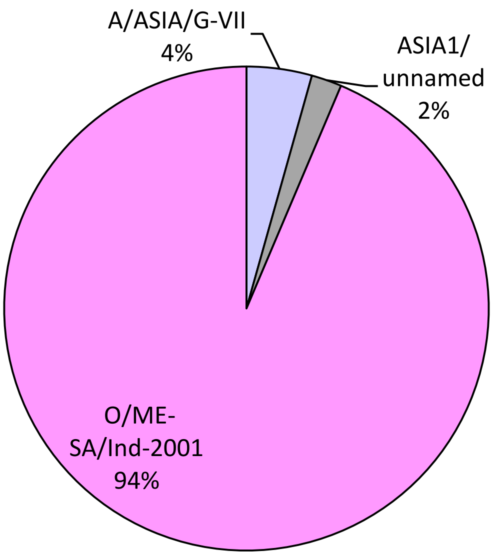


B. POOL 2 – South Asia

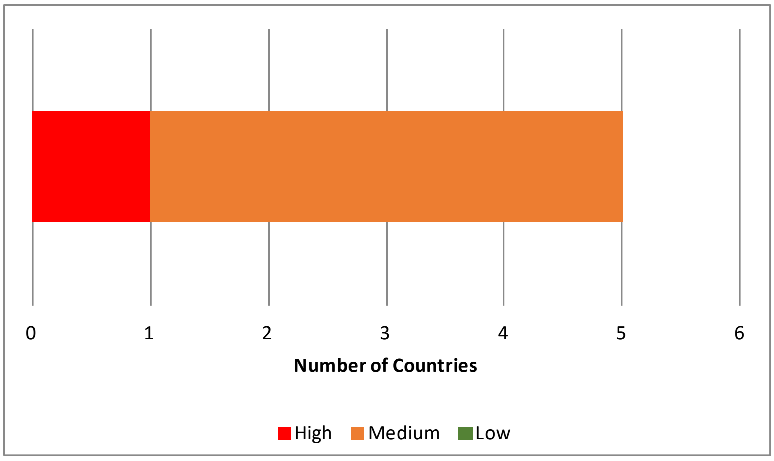
No FMD outbreaks were notified for this Pool for the reporting month.

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



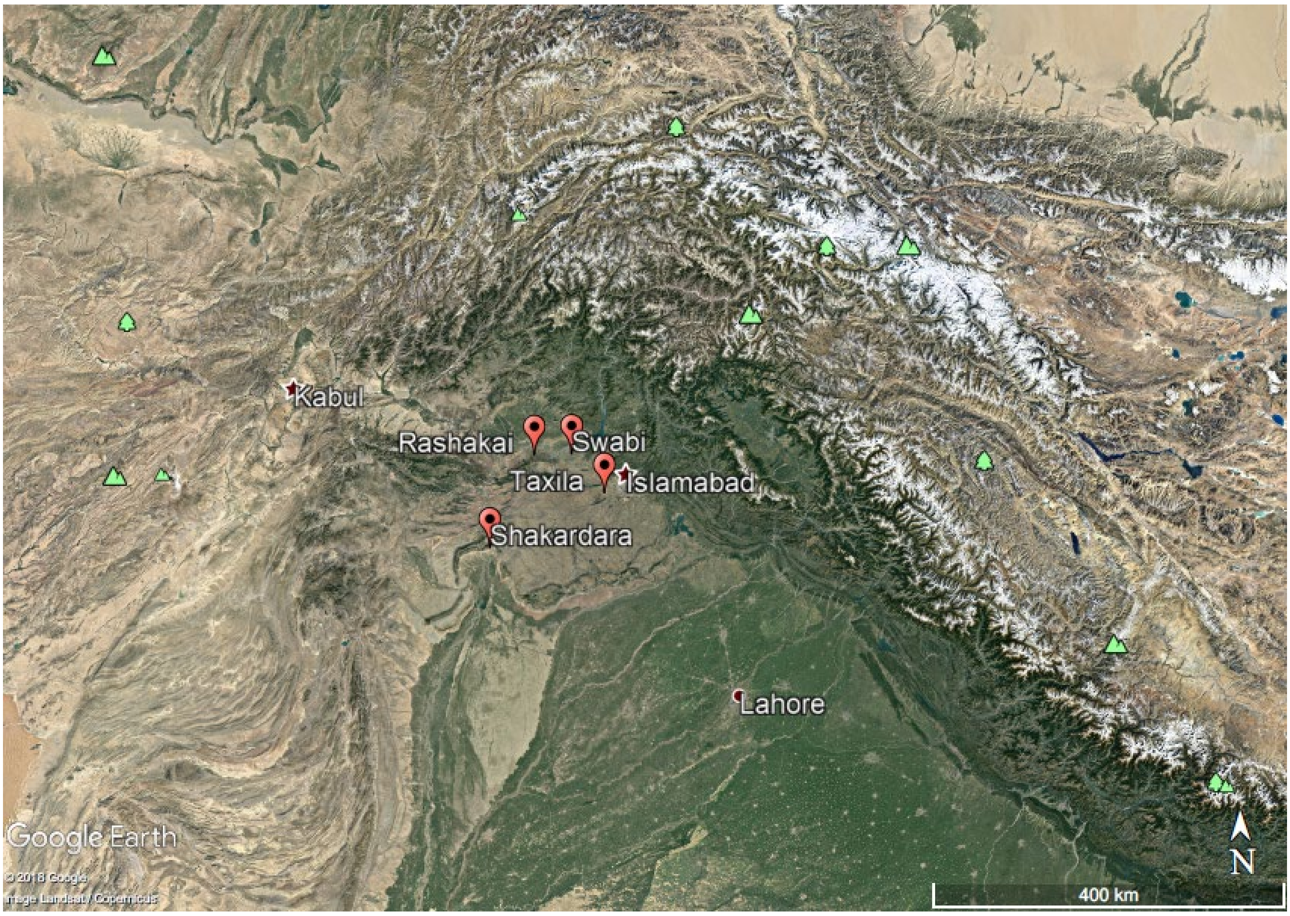
Graph 4: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 2 – see Annex for explanation).



C. POOL 3 – West Eurasia & Middle East

OUTBREAKS	
Country	*Description*
Serotype O in Pakistan [1]	As reported in the previous issues of this report, O/ME-SA/Ind2001e was detected in Pakistan for the first time between December 2018 and April 2019, and specifically on farms of the villages of Punjab and Khyber Pakhtoon Khuwa (Map 1), where cattle and buffaloes were present. An apparent morbidity of 25%, without any mortality, was registered in the 36 cattle present. All the outbreaks are reported as resolved and a study is being planned to determine the source and extent of spread of the topotype O/Me-sa/Ind-2001/e.

Map 1: location of the areas of the FMD outbreaks caused by the new topotype O/ME-SA/Ind2001e detected in Pakistan which occurred between December 2018 and April 2019 (Source – WAHIS and Google Earth Pro).



SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	***Activity***	***Description***
Afghanistan [3]	***Surv.***	FMDV ASIA 1 was the only serotype detected six of the 20 samples analysed during September by the Central Veterinary Research and Development Laboratory (CVDRL). A/ASIA/Iran-05, Asia 1/ASIA/Sindh-08 and O/ME-SA/PanAsia-2 are the most recent topotypes detected by the WRLFMD in last samples analysed that were collected in the country during 2016 and 2017.
Pakistan [1]	***Vacc.***	The FMDV field strains belonging to serotypes A, ASIA 1 and O analysed in the VMSD obtained the following matching results: • Strains A/PAK/1/2018 and A/PAK/24/2019, genotyped as A/ASIA7Iran-05^{SIS13}

<table>
<tr><td></td><td></td><td>obtained good matching results with A Iran 2005, A TUR 200706 but not with A/GVII,
Strains ASIA 1/PAK/10/2019, ASIA 1/PAK/11/2019 and ASIA 1/PAK/14/2019, genotyped as Asia 1/ASIA/Sindh-08 obtained good matching results with Asia 1 Shamir,
Strains O/PAK/1/2019 genotyped as O/ME-SA/Ind-2001e and strains O/PAK/12/2019 and O/PAK/23/2019 genotyped as O/ME-SA/PanAsia-$2^{\text{ANT-10}}$ obtained good matching results with O 3039, O Manisa and O Tur5/09.</td></tr>
<tr><td>Pakistan [15]</td><td><i>Surv.</i></td><td>A summary of the results of the surveillance conducted under the project “The enhancement of FMD control in Pakistan” funded by Government of Japan and executed by FAO is reported in Table 4 and location of outbreaks is reported in Map 2. FMDV Asia 1 and O were the serotypes were reported among the 42 outbreaks notified in two different provinces of the country.

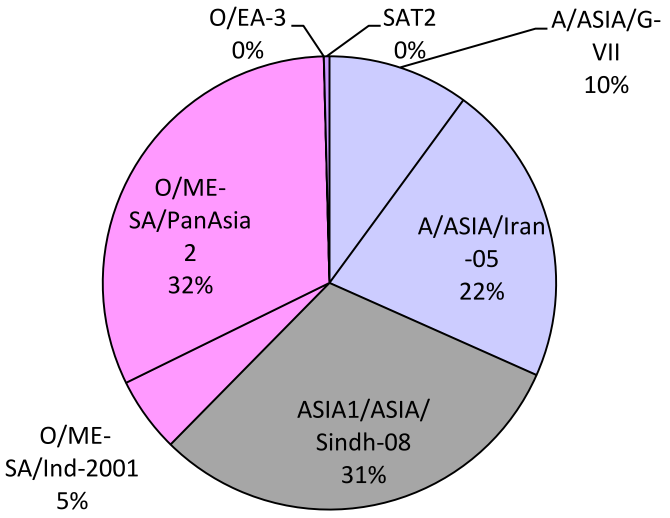
Table 4: summary of the outbreaks reported in different provinces of Pakistan during September 2019 (Source – “The enhancement of FMD control in Pakistan” - <i>Dr. Muhammad Afzal</i>, Project Coordinator).

<table>
<tr><th rowspan="2">Province</th><th rowspan="2">District</th><th rowspan="2">Number Outbreaks</th><th colspan="5">Number of Outbreaks due to FMD Virus Serotypes</th></tr>
<tr><th>O</th><th>‘Asia-1</th><th>Mixed</th><th>Un-Typed/NYT</th><th>Negative</th></tr>
<tr><td rowspan="4">Sindh</td><td>Sargodha</td><td>1</td><td>-</td><td>1</td><td>-</td><td>-</td><td>-</td></tr>
<tr><td>Chakwal</td><td>1</td><td>-</td><td>1</td><td>-</td><td>-</td><td>-</td></tr>
<tr><td>Jhung</td><td>1</td><td>-</td><td>-</td><td>-</td><td>1</td><td>-</td></tr>
<tr><td>Karachi</td><td>32</td><td>-</td><td>-</td><td>-</td><td>32</td><td>-</td></tr>
<tr><td rowspan="4">Balochistan</td><td>Uthal</td><td>1</td><td>-</td><td>-</td><td>-</td><td>1</td><td>-</td></tr>
<tr><td>Lasbella</td><td>1</td><td>-</td><td>-</td><td>-</td><td>1</td><td>-</td></tr>
<tr><td>Hub</td><td>1</td><td>-</td><td>-</td><td>-</td><td>1</td><td>-</td></tr>
<tr><td>Quetta</td><td>4</td><td>3</td><td>-</td><td>-</td><td>-</td><td>1</td></tr>
<tr><td colspan="2">Total</td><td>42</td><td>3</td><td>2</td><td>-</td><td>36</td><td>1</td></tr>
</table>
</td></tr>
</table>

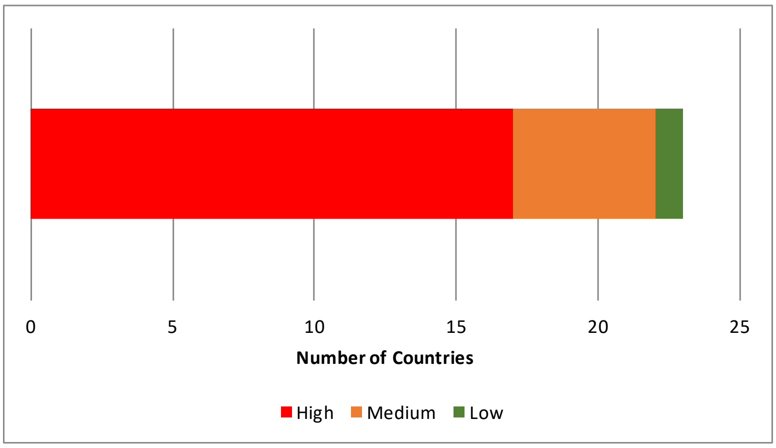
Map 2: location of the areas of the FMD outbreaks that were notified in Pakistan during September 2019 (Source – "The enhancement of FMD control in Pakistan" - *Dr. Muhammad Afzal*, Project Coordinator, Google Earth Pro).

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

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 24 countries of Pool 3 - West Eurasia
A	A/ASIA/G-VII	17
	A/ASIA/Iran-05	9
ASIA 1	ASIA1/ASIA/Sindh-08	9
O	O/ME-SA/Ind-2001	8
	O/ME-SA/PanAsia2	22
	O/EA-3	2
SAT2	SAT2	1



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



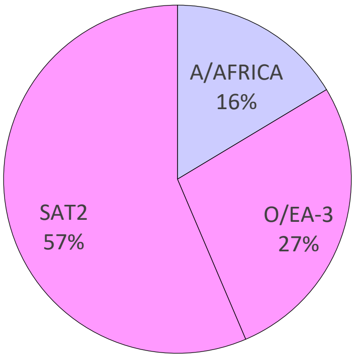
D. POOL 3 – North Africa

<table>
<tr><th colspan="3">SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)</th></tr>
<tr><td><i>Country</i></td><td><i>Activity</i></td><td><i>Description</i></td></tr>
<tr><td>Morocco [2]</td><td>Surv.</td><td>Following the outbreaks which occurred in the country during 2019 due to topotype O/EA-3, a vaccination campaign was conducted with the activity carried out as represented in Table 6. Other preventive measures are still in place even if no new outbreaks were reported.

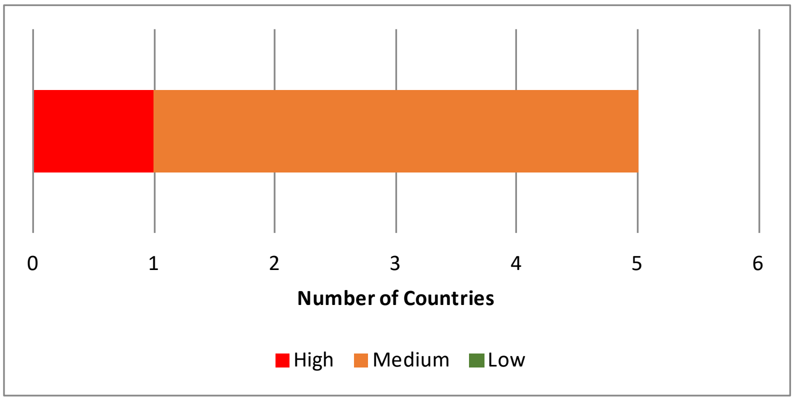
Table 6: vaccination activity carried out in Morocco following the outbreaks which occurred in the country during 2019 due to topotype O/EA-3 (Source – WAHIS)
<table>
<tr><th>Administrative division</th><th>Species</th><th>Total Vaccinated</th><th>N° of farms vaccinated</th></tr>
<tr><td>BÉNI MELLAL-KHÉNIFRA</td><td rowspan="7">Cattle</td><td>6,278</td><td>886</td></tr>
<tr><td>CASABLANCA-SETTAT</td><td>41,447</td><td>8,758</td></tr>
<tr><td>FÈS-MEKNÈS</td><td>1,616</td><td>395</td></tr>
<tr><td>MARRAKECH-SAFI</td><td>644</td><td>129</td></tr>
<tr><td>RABAT-SALÉ-KÉNITRA</td><td>597</td><td>62</td></tr>
<tr><td>SOUSS-MASSA</td><td>4,227</td><td>477</td></tr>
<tr><td>TANGER-TÉTOUAN-AL HOCEÏMA</td><td>691</td><td>211</td></tr>
<tr><td colspan="2">Totals</td><td>55,500</td><td>10,918</td></tr>
</table>
</td></tr>
</table>

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

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



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

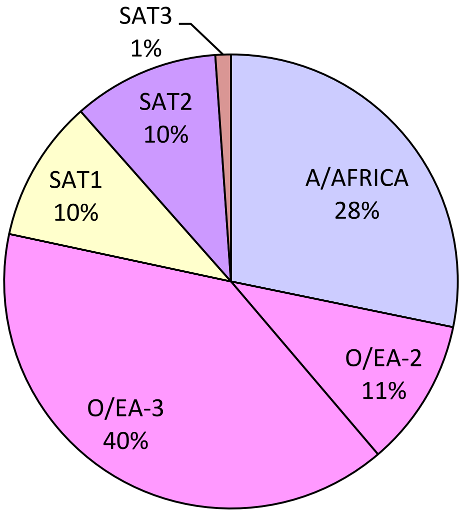


E. POOL 4 – Eastern Africa

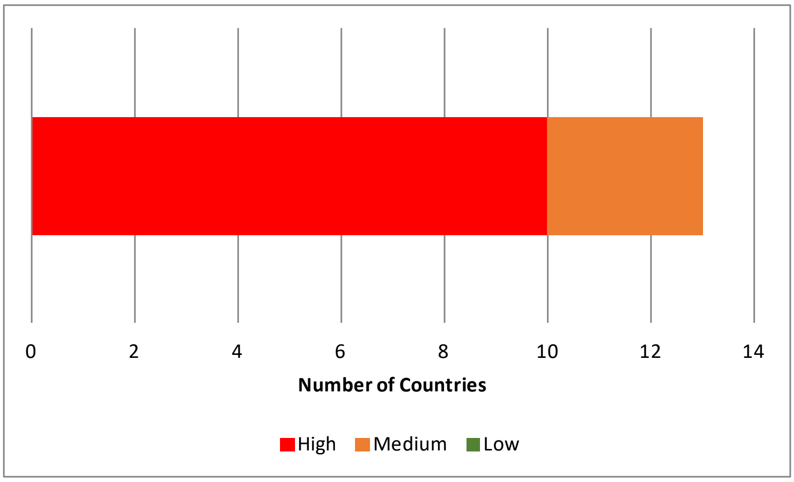
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Ethiopia [4]	**Surv.**	The NAHDIC detected FMDV serotype O using antigen detection ELISA in the three vesicular tissue samples collected from clinical outbreaks that occurred at the Fininfine Leyu zone. The most recent topotype belonging to the FMDV serotype responsible for the reported outbreak is O/EA-3 that was detected by the WRLFMD in the most recently collected samples of 2019.
Kenya [5]	**Surv.**	The FMD NRL, Embakasi, Kenya detected FMDV serotypes O (N°3 samples – 25%) and SAT 2 (N° 8 samples – 75%) among the 12 bovine samples analysed using PCR. This report is consistent with previous reports. The causative serotypes are believed to circulate endemically in the country. The most recent lineages relative to the above serotypes detected in the country are A/AFRICA/G-I, SAT 1/I (NWZ) and SAT 2/IV/unnamed were in samples collected in 2017.

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	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).

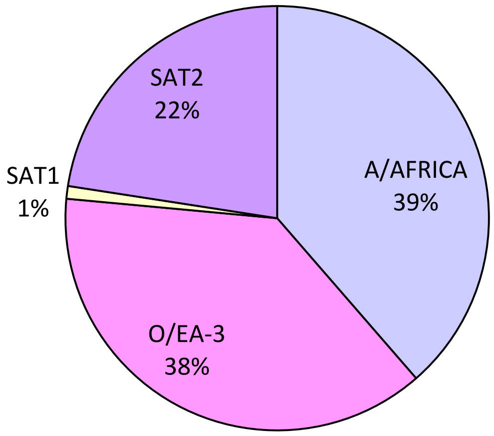


F. POOL 5 – West / Central Africa

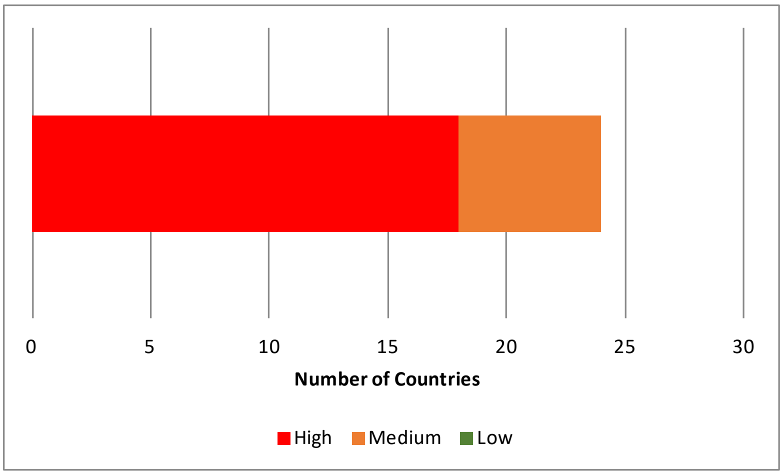
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	*Activity*	*Description*
Cameroon [9]	**Surv.**	The Laboratoire National Vétérinaire (LANAVET), Garoua analyzed 450 serum samples using FMD non-structural protein (NSP) ELISA of which 224 (49.7%) resulted positive while another set of 745 NSP positive sera resulted tested positive for serotype A (N° 281 – 37.9%) and for serotype O (N°464 - 62.5%). The last lineages reported by the WRLFMD as circulating in the country are A/AFRICA/G-IV and SAT 2/VII in samples collected in 2013.
Nigeria [16]	**Surv.**	The FMD Research Centre, Virology Research Department, NVRI, Vom, Plateau State, Nigeria detected FMDV in 18 clinical samples collected from Ogun (12 swabs) and Keebi (six epithelium samples) States.

Table 9 and Graph 11: Conjectured circulating FMD viral lineages in Pool 5 (further detail (country-level) in Annex).

Serotype	Viral lineage	Number of countries where strain is believed to circulate in the 24 countries of Pool 5 - West Africa
A	A/AFRICA	13
O	O/EA-3	22
SAT1	SAT1	2
SAT2	SAT2	14



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

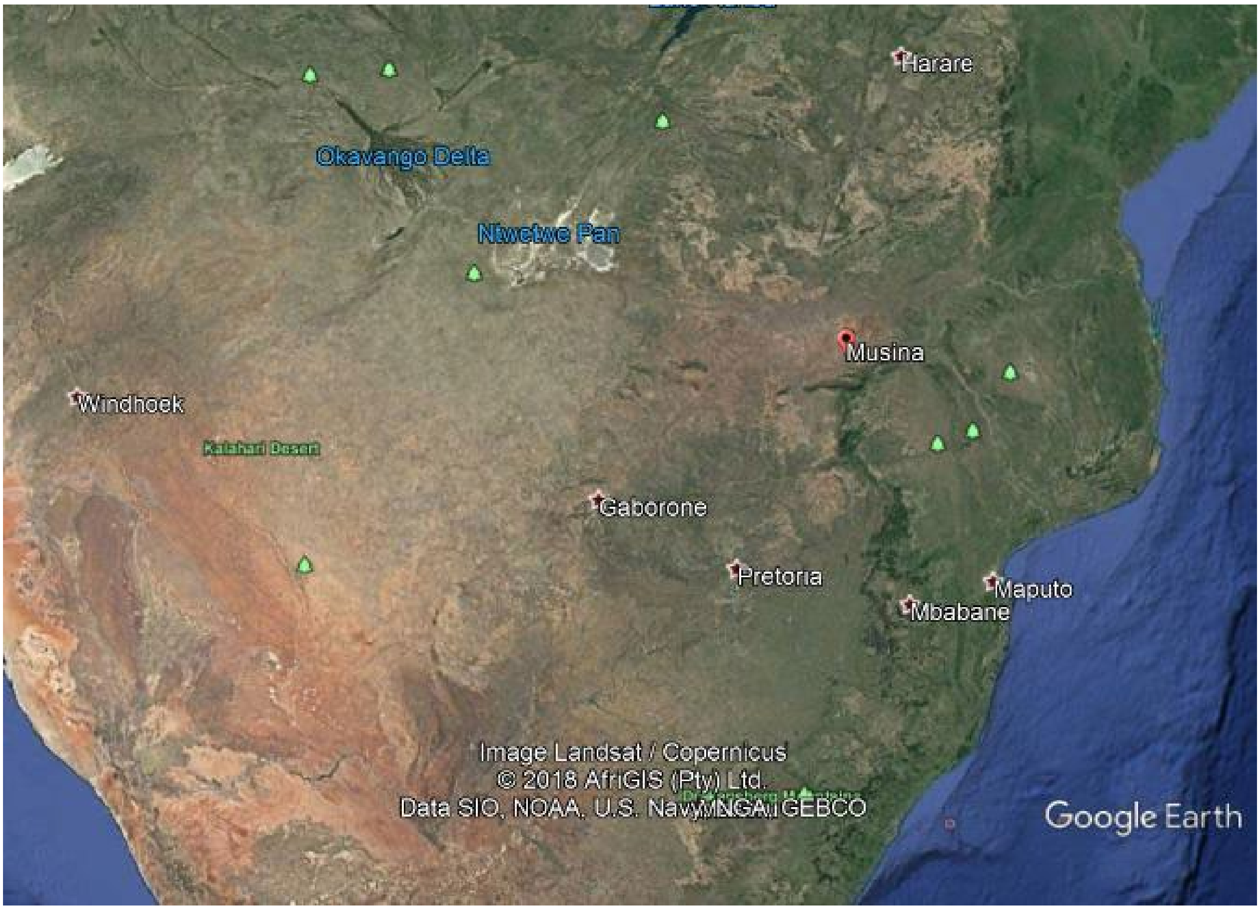


G. POOL 6 – Southern Africa

<table>
<tr><th colspan="2">OUTBREAKS</th></tr>
<tr><td>Country</td><td>Description</td></tr>
<tr><td>Serotype unknown in Namibia[2]</td><td>A FMD outbreak was reported on clinical basis on August 8th 2019 in cattle at Sigwe Crushpen, Katima Mulilo, Kabwe North, Zambezi (Map 3) with 272 cases registered in cattle. The event was attributed to contact with wild species.
Vaccination in response to the outbreaks was among the control outbreaks adopted conducted in 29809 cattle.</td></tr>
<tr><td colspan="2">Map 3: Location of the area where the FMD outbreak notified on clinical basis on August 8th 2019 in cattle at Sigwe Crushpen, Katima Mulilo, Kabwe North, Zambezi, Namibia (Source – WAHIS and Google Earth Pro).

 </td></tr>
<tr><td>Serotype SAT 2 in South Africa[2]</td><td>A FMD outbreak due to serotype SAT 2 was observed on September 2nd 2019 in cattle at Musina, Limpopo (Map 4) with an apparent morbidity rate of 0.88% of the 5,000 cattle involved.
Diagnosis was confirmed by the Agricultural Research Council - Onderstepoort Veterinary Institute (ARC – OVI), Transboundary Animal Diseases Programme (TADP) (OIE Reference Laboratory) on September 6th 2019 by analyzing the biological specimens using PCR and sold-phase competitive ELISA.
The outbreak occurred in South Africa's FMD Protection Zone caused by contact with wild animals.</td></tr>
</table>

Map 4: Location of the area where the FMD outbreak due to serotype SAT 2 was observed on September 2nd 2019 in cattle at Musina, Limpopo, South Africa (Source – WAHIS and Google Earth Pro).



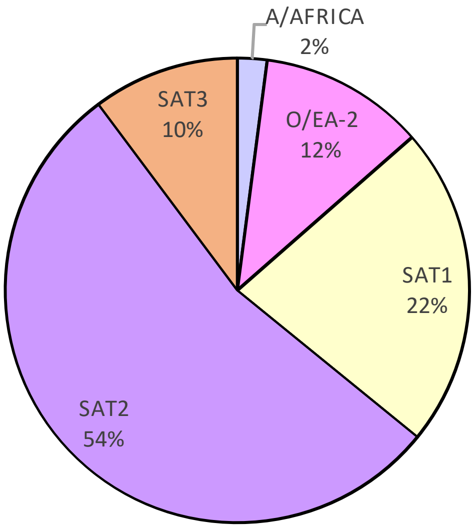
Serotype O in Zambia [2]	Fourteen FMD outbreaks due to serotype O occurred between March and August 2019 in the eastern area of the country Map 5 due to the illegal movement of animals. Five outbreaks were already reported as resolved. The apparent morbidity reported is 2.48% among the 46,778 cattle involved. Two vaccination campaigns were carried out respectively in Central with the ring vaccination of 13,643 cattle and in Southern with the vaccination of 99,855 cattle. Other preventive measures are in place to contain the spread of the disease.

Map 5: Location of the area where fourteen FMD outbreaks due to serotype O occurred between March and August 2019 in the eastern area of Zambia (Source – WAHIS and Google Earth Pro).

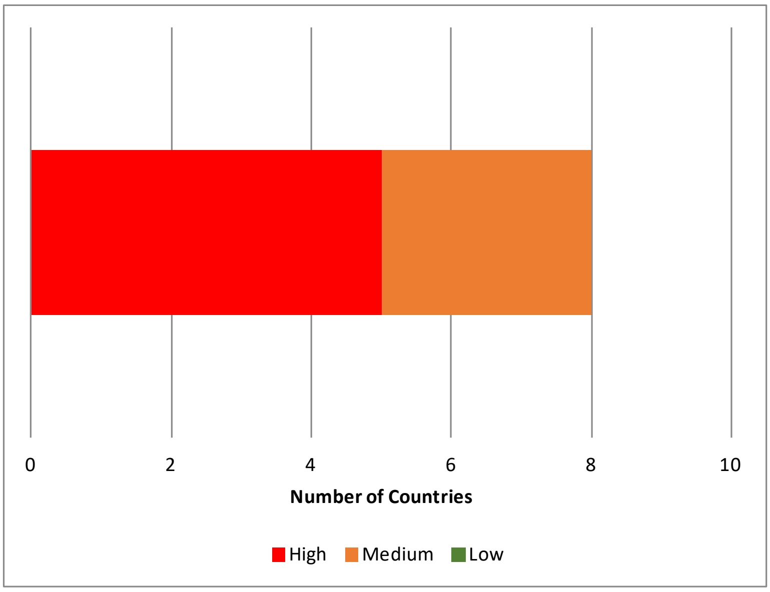
SURVEILLANCE (Surv.), VACCINATION (Vacc.) AND POST VACCINATION MONITORING (PVM)		
Country	**Activity**	**Description**
Malawi [2]	**Vacc.**	Following the FMD episodes due to serotype SAT 2 which were notified in in February 2019, the country conducted primer and booster vaccination campaigns respectively in 11,584 and 11,328 cattle in the Mchinji district. Details of the type of vaccine used were not provided. As no new cases were detected, restrictive measures were lifted on September 11th 2019.
South Africa [6]	**Surv.**	The Agricultural Research Council, Onderstpoort Veterinary Institute, Transboundary Animal Diseases (OIE Reference Laboratory) analysed 7,263 sera in solid-phase competition ELISA for the detection of antibodies against SAT-1, SAT-2 and SAT-3 and 177 sera in (NSP) ELISA.

Table 10 and Graph 13: Conjectured circulating FMD viral lineages in Pool 6 (further detail (country-level) in Annex).

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



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

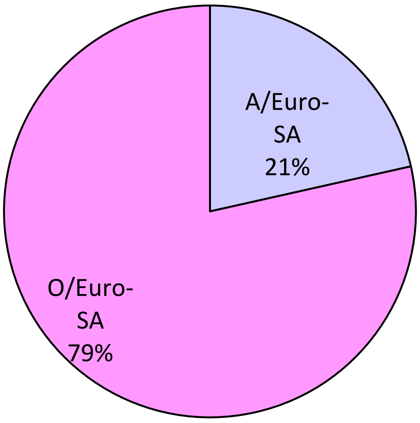


H. POOL 7 – South America

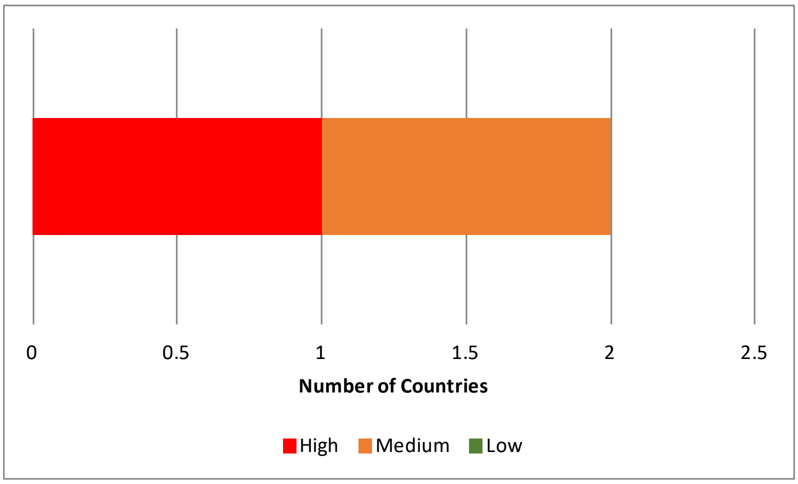
No outbreaks are reported for this Pool during the reporting month.

Table 11 and Graph 15: Conjectured circulating FMD viral lineages in Pool 7 (further detail (country-level) in Annex).

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



Graph 16: Categorization of the level of uncertainty relative to the prevalence of circulating serotypes/strains defined for each country of Pool 7 (see Annex for explanation).



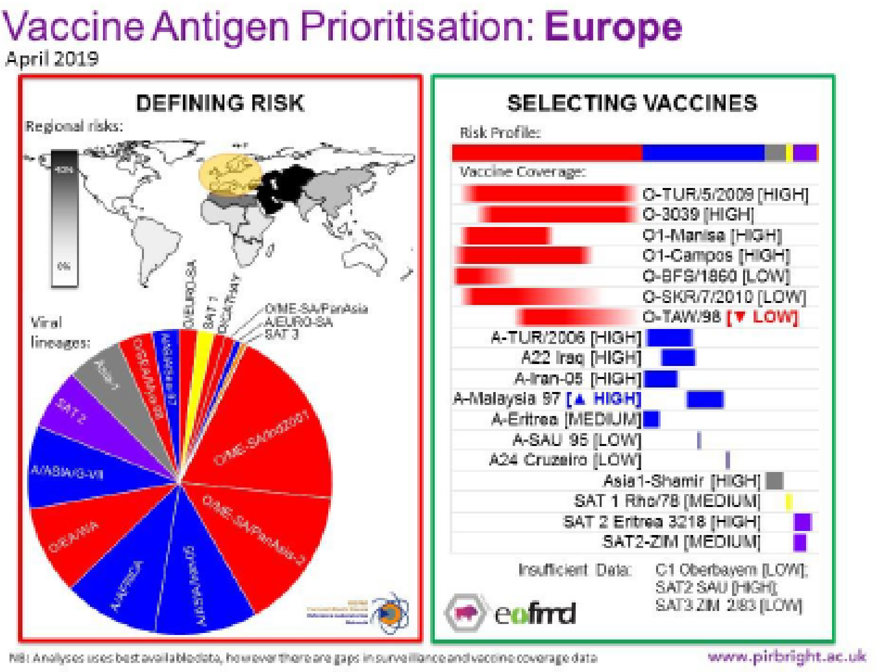
V. OTHER NEWS

[1]The 3rd WRLFMD Quarterly Report for the period April-June 2019 contains the recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of Table 12 is contained within the report.

Table 12: Recommendations from WRLFMD® on FMD virus strains to be included in FMDV antigen banks (for Europe) (Source – WRLFMD).

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**

April 2019

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

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

VI. REFERENCES – Superscripts

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4. National animal health diagnostic and investigation center (NAHDIC), Ethiopia - *Dr. Daniel Gizaw.*
5. National FMD Reference Laboratory, Embakasi, Kenya –*Dr. Kenneth Ketter*
6. OIE/FAO FMD Reference Laboratory Network, Annual Report 2016
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11. 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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14. OIE/FAO FMD Reference Laboratory Network, Annual Report 2017
15. Information collated under project “The enhancement of FMD control in Pakistan” funded by Government of Japan and executed by FAO - *Dr. Muhammad Afzal*, Project Coordinator.
16. FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria - *Dr. Ularamu Hussaini*

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.

<u>Description of methods</u>

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

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

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

Pool-level estimates and assumptions:

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

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

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

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

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

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

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

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

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

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

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

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

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

Legend of icons in the following tables

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

Table 13: Conjectured circulating FMD viral lineages in each country of Pool 1 (current to September 2019).

			Presumed serotype distribution within country			Presumed viral lineage distribution within country								
Country	**Last Outbreak Repoted/Serotype#**	**FMD incidence rate**	**A**	**Asia1**	**O**	**A/ASIA/SEA-97**	**ASIA1/ unnamed**	**O/ME-SA/Ind-2001**	**O/SEA/Mya-98**	**O/ME-SA/PanAsia**	**O/ME-SA/PanAsia2**	**O/CATHAY**	**Uncertainty on circulating serotypes**	**Reference**
CAMBODIA	Aug 2018/O, Aug 2016/ A	high	◑		◑	◑				◑			medium	1
CHINA	July 2019/O, May 2017/A	high	◔		◕	◔		◔	◔	◔		◔	medium	1
CHINA (HONG KONG, SAR)	May 2019/O	high			●							●	medium	1
KOREA, DEMOCRATIC PEOPLE'S REPUBLIC OF	Dec 2016/O	high	◑		◕	◑		◕					high	as per REPUBLIC OF KOREA (SOUTH KOREA)
LAO PEOPLE'S DEMOCRATIC REPUBLIC (LAOS)	Dec 2018/A & O	high	◔		◕	◔			◕	◔			medium	1
MALAYSIA	May 2018/O, August 2016/A	medium			●					●			medium	1
MONGOLIA	Jun 2018/O, Sept 2016/A	medium			●			◑	◑	◑			medium	1
MYANMAR	Dec 2018/O, April 2017/Asia 1, Oct 2015/A	high	◔	◔	◕	◔	◔	◑			◑		medium	1, 10
REPUBLIC OF KOREA (SOUTH KOREA)	Jan 2019/O, April 2018/A	low/sporadic	◑		◕	◑		◕					low	1
RUSSIAN FEDERATION	March 2019/O, Oct 2016/Asia 1, Jan 2016/ A	low/sporadic			●			◑	◑	◑			medium	1
TAIWAN PROVINCE OF CHINA	Jun 2015/A	low/sporadic			●							●	high	as per HONG KONG
THAILAND	Oct 2018 /A & O	high	◔		◕	◔		◔	◔	◔			medium	1
VIETNAM	Jan 2019/O, November 2017/A and not typed	high	◑		◕	◑		◔	◑	◔		◔	medium	1

Table 14: Conjectured circulating FMD viral lineages in each country of Pool 2 (current to September 2019).

			Presumed serotype distribution within country			**Presumed viral lineage distribution within country**				
Country	**Last Outbreak Repoted/Serotype#**	**FMD incidence rate**	A	Asia1	O	A/ASIA/G-VII	ASIA1/ unnamed	O/ME-SA/Ind-2001	**Uncertainty on circulating serotypes**	**Reference**
BANGLADESH	Jun 2018/A, ASIA 1 and O	high	◔	◔	◕	◔	◔	◕	high	11
BHUTAN	Jan 2019/O, Dec 2017/A	high	◔		◕	◔		◕	medium	1
INDIA	July 2019/O, Apr 2015/A, ASIA 1	high	○		●	○		●	medium	1
NEPAL	June 2019/O, Mar 2018/Asia 1, April 2017/A	high			●			●	medium	1
SRI LANKA	Dec 2018/O	high			●			●	medium	1

Table 15: Conjectured circulating FMD viral lineages in each country of Pool 3 –West Eurasia (current to September 2019).

			Presumed serotype distribution within country			Presumed viral lineage distribution within country									
Country	Last Outbreak Repoted/Serotype#	FMD incidence rate	A	Asia1	O	sat2	A/ASIA/G-VII	A/ASIA/Iran-05	ASIA1/ASIA/Sindh-08	O/ME-SA/Ind-2001	O/ME-SA/PanAsia2	O/EA-3	SAT2	Uncertainty on circulating strains	reference
AFGHANISTAN	Aug 2019/O & Asia 1, Juy 2019/A	high	◑	◔	◑			◑	◔		◑			medium	2, 3
ARMENIA	Dec 2015/A	low/sporadic	◔		◕		◔				◕			high	12
AZERBAIJAN	2007/0	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
BAHRAIN	Mar 2015/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
GEORGIA	2001/ASIA 1	low/sporadic	◔		◕		◔				◕			high	as per Turkey
IRAN, ISLAMIC REPUBLIC OF	Dec 2018/A, Asia 1& O,	high	◑	◔	◑		◔	◑	◔		◑			medium	1
IRAQ	Dec 2018/O, Dec 2016/A	high	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
ISRAEL	May 2019/O, June2017/A	low/sporadic	◔		◕		◔				◑	◔		low	1
JORDAN	Mar 2017/O	low/sporadic	◕		◑		◕			◔	◔			high	1, as per Saudi
KUWAIT	April 2016/O	high	◕		◑		◕			◔	◔			high	1, as per Saudi
KYRGYZSTAN	Sep 2014/A, O	low/sporadic	◔	◕	◔			◔	◕		◔			high	as per Pakistan
LEBANON	2010/not typed	low/sporadic	◔		◕		◔				◕			high	as per Turkey
OMAN	Dec 2018/O, May 2015/SAT 2	high			◑	◑				◔	◔		◑	high	1
PAKISTAN	Sep 2019/Asia 1 & O, Aug 2019/ A	high	◔	◕	◔			◔	◕	◔	◔			medium	1, 15
PALESTINE	Mar 2019/Untyped, Dec 2017/O, Mar 2013/Sat 2	low/sporadic			●							●		medium	1
QATAR	Dec 2018/O, Oct 2017/A	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
SAUDI ARABIA	Dec 2018/O & Jun 2018/A	high	◕		◑		◕			◔	◔			high	1
SYRIAN ARAB REPUBLIC (SYRIA)	2002/ A & O	high	◔		◕		◔				◕			high	as per Turkey
TAJIKISTAN	Nov 2013/ not typed	low/sporadic	◔	◕	◔			◔	◕		◔			high	as per Pakistan
TURKEY	April 2019/O, Oct 2017/A, May 2015/ Asia 1	high	◔		◕		◔				◕			medium	1
TURKMENISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran
UNITED ARAB EMIRATES	Jan 2018/O	low/sporadic	◕		◑		◕			◔	◔			high	as per Saudi Arabia
UZBEKISTAN	Not available	low/sporadic	◑	◔	◑		◔	◑	◔		◑			high	as per Iran

Table 16: Conjectured circulating FMD viral lineages in each country of Pool 3 - North Africa (current to September 2019).

			Presumed serotype distribution within country			Presumed viral lineage distribution within country				
Country	**Last Outbreak Repoted/Serotype#**	**FMD incidence rate**	**A**	**O**	**SAT 2**	**A/AFRICA**	**O/EA-3**	**SAT 2**	**Uncertainty on circulating serotypes**	**Reference**
ALGERIA	Mar 2019/O, Nov 2016/A, Jun 2016/Sat 2	medium	◑	◕		◑	◕		medium	1
EGYPT	Nov 2018/Sat 2, Feb 2018/A April 2017/O	high	◔	◔	◕	◔	◔	◕	medium	1
LIBYA	June 2019/O	high	◔	◔	◕	◔	◔	◕	high	13, as per egypt
MOROCCO	July 2019/O	low/sporadic		●			●		medium	1
TUNISIA	Feb 2019/O, April 2017/A	low/sporadic	◔	◕		◑	◕		medium	1

Table 17: Conjectured circulating FMD viral lineages in each country of Pool 4 (current to September 2019).

			Presumed serotype distribution within country					**Presumed viral lineage distribution within country**							
Country	**Last Outbreak Repoted/Serotype#**	**FMD incidence rate**	**A**	**O**	**sat1**	**sat2**	**sat3**	**A/AFRICA**	**O/EA-2**	**O/EA-3**	**SAT1**	**SAT2**	**SAT3**	**Uncertainty on circulating serotypes**	**Reference**
BURUNDI	Dec 2017 / not available	high	◑	◔	◔	◔		◑		◔	◔	◔		high	as per Tanzania
COMOROS	March 2019/O	high		●					●					high	no data
DJIBOUTI	Not available	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
ERITREA	Oct 2018/not reported	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
ETHIOPIA	Sep 2019/ O, April 2019/A &SAT 2, Feb 2018/SAT 1	high	◔	◕	◔		○	◔		◕	◔		○	medium	1
KENYA	Sep 2019/O & SAT 2, May 2018/ SAT 1 , July 2019/A	high	◔	◕	◔	◔		◔	◕		◔	◔		medium	1
RWANDA	Oct 2018/ A, O , SAT 1 & Sat 2	high	◔	◕	◔	◔		◔	◕		◔	◔		high	as per Kenya
SOMALIA	June 2018/not reported	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia
SOUTH SUDAN	June 2017/O & SAT 2, Mar 2018/A Dec 2018/ not sampled	high		●						●				high	1
SUDAN	Dec 2018/ not sampled, May 2017/O	high	◑	◔		◔		◑		◔		◔		medium	1
TANZANIA, UNITED REPUBLIC OF	Dec2018/O, Nov2018/ A & SAT 2, Sep 2018/SAT 1	high	◑	◔	◔	◔		◑		◔	◔	◔		high	1
UGANDA	Feb 2019/A & O, July 2017/SAT1, Jan 2015/SAT 3, July 2015/ SAT 2	high	◑	◑	◔	◔		◑	◑		◔	◔		high	1, as per Kenya
YEMEN	Dec 2016/not sampled	high	◔	◕	◔		○	◔		◕	◔		○	high	as per Ethiopia

Table 18: Conjectured circulating FMD viral lineages in each country of Pool 5 (current to September 2019).

			Presumed serotype distribution within country				Presumed viral lineage distribution within country					
Country	**Last Outbreak Repoted/Serotype#**	**FMD incidence rate**	**A**	**O**	**sat1**	**sat2**	**A/AFRICA**	**O/EA-3**	**SAT1**	**SAT2**	**Uncertainty on circulating serotypes**	**Reference**
BENIN	Dec 2017/O, SAT 1 &SAT 2, Apr 2017/A	high	◔	◔	◔	◔	◔	◔	◔	◔	high	2
BURKINA FASO	Dec 2018/not sampled, Aug2018/O	high	◑	◑		◑	◑	◑		◑	medium	2, as per Mali
CAMEROON	Dec 2019/untyped, Nov 2014/O, SAT 2, May 2014/SAT 1, Apr 2014/ A	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CAPE VERDE	Not available	low/sporadic		●				●			high	as per Senegal
CENTRAL AFRICAN REPUBLIC	Not available	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CHAD	Dec 2018/Not sampled	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CONGO	Not available	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
CONGO, DEMOCRATIC REPUBLIC OF	Jun 2018/A, O & Sat 1	high	◑	◑	◑		◑	◑	◑		high	2
COTE D'IVOIRE	Jun 2018/O	high		●				●			high	2, as per Guinea
EQUATORIAL GUINEA	Jun 2015/Disease suspected	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
GABON	Not available	high	◑	◑		◔	◑	◑		◔	high	
GAMBIA	Dec 2018/O	high		●				●			medium	2
GHANA	Dec 2018/SAT 2, Sep 2018/ O	high		◑		◑		◑		◑	high	1
GUINEA	Dec 2018/O	high		●				●			medium	2
GUINEA-BISSAU	Dec 2018/O	high		●				●			high	as per Guinea
LIBERIA	Not available	high		●				●			high	as per Guinea
MALI	Oct 2018/O, Jun 2018/A & SAT	high	◑	◑		◑	◑	◑		◑	high	2
MAURITANIA	Aug 2018/O, Dec 2014/SAT 2	high				●				●	medium	1
NIGER	Dec 2015/O	high	◑	◑		◔	◑	◑		◔	high	as per Nigeria
NIGERIA	Sep 2019/untyped, June 2019/A, Sep 2018/O &Sat 2, Sept 2016/ SAT 1	high	◑	◑		◔	◑	◑		◔	high	1, 16
SAO TOME AND PRINCIPE	Not available	0									high	no data available
SENEGAL	Nov 2018/A, O & Sat 2, Jun 2018/ Sat 1	high		●				●			medium	1
SIERRA LEONE	Aug 2018/O	high		●				●			medium	as per Senegal
TOGO	Dec 2017/ not sampled, Dec 2016/ O & Sat 1	high	◑	◑		◔	◑	◑		◔	high	2, as per Nigeria

Table 19: Conjectured circulating FMD viral lineages in each country of Pool 6 (current to September 2019).

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

Table 20: Conjectured circulating FMD viral lineages in each country of Pool 7 (current to September 2019).

			Presumed serotype distribution within country		Presumed viral lineage distribution within country			
Country	**Last Outbreak Repoted/Serotype#**	**FMD incidence rate**	A	O	A/Euro SA	O/Euro-SA	**Uncertainty on circulating serotypes**	**Reference**
VENEZUELA	Oct 2018/O	medium	◑	◑	◑	◑	high	2, 6
COLUMBIA	2011/O, 2013/A	medium		●		●	medium	2

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