September

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MONTHLY REPORT
FOOT-AND-MOUTH DISEASE SITUATION

Food and Agriculture
Organization of the
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European
Commission

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

Foot-and-Mouth Disease Situation

Food and Agriculture Organization of the United Nations
Monthly Report

September 2018

Guest Editor:
Donald King: WRLFMD, Pirbright

#INFORMATION SOURCES USED:

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

Other sources:
FAO/EuFMD supported FMD networks
FAO/EuFMD projects and field officers

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

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

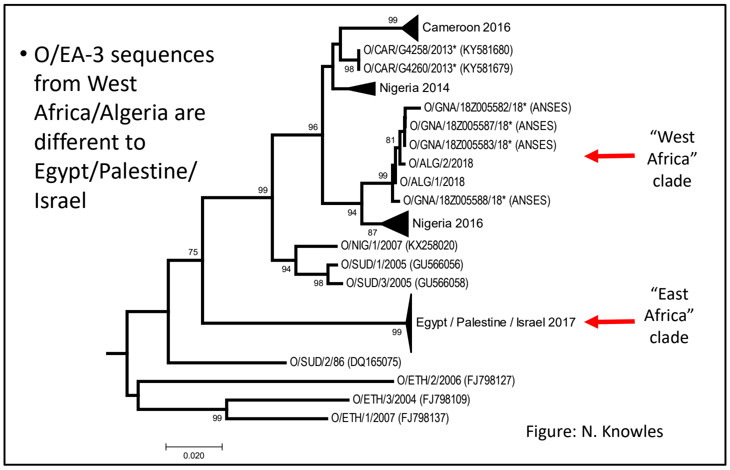
September 2018

Contents

Guest Editor’s comments:

I am very happy to be asked to write this short editorial to introduce the FMD monthly situation report, and I look forward to catching up with many of you all at the EuFMD Open Session in Puglia next week. Since my last editorial contribution in June, the WRLFMD has tested sample submissions from Algeria, Kenya, Malaysia, Mongolia, South Sudan and Sudan. Sequence data generated by ANSES, France, LVRI, China and BVI, Botswana for samples collected in Chad, China, Guinea, Mauritania and Zimbabwe were also analysed. Detailed reports for these samples can be retrieved from http://www.wrlfmd.org/.

In my last report, we described new cases of FMD in Algeria due to the O/EA-3 topotype (samples received to Pirbright on 03/07/18). There have now been >50 outbreaks of FMD in the country (reported to OIE). At the same time, there has been an apparent upsurge in FMD cases across a range of West African countries (reports from Sierra Leone, Burkina Faso, Guinea, Guinea Bissau, Senegal and The Gambia). Sequence data provided to the WRLFMD (from the OIE Reference Laboratory at ANSES, France) for samples collected from Guinea were very closely related to the viruses recovered from the Algerian outbreaks; findings which reinforce the idea that circulation of FMD in West African countries is now posing an important risk for onward spread into North Africa. The spread of the O/EA-3 topotype in Algeria appears to parallel the emergence of the A/AFRICA/G-IV lineage in Algeria and Tunisia that occurred for the first time in 2017. It is perhaps noteworthy that there is now evidence that exotic outbreaks in North Africa (either in the Maghreb or Egypt) caused by the O/EA-3 and A/AFRICA/G-IV lineages are due to separate genetic clades with origins to viruses that are independently circulating in East African and West African countries (see figure).



- O/EA-3 sequences from West Africa/Algeria are different to Egypt/Palestine/Israel

Figure: N. Knowles

Elsewhere, we continue to monitor the spread of the “pandemic” O/ME-SA/Ind-2001 lineage that has emereged from South Asian countries. In partnership with fourteen other FMD Reference Laboratories, the WRLFMD has recently reconstructed the global transmission history of the O/ME-SA/Ind-2001 lineage providing evidence of at least 15 independent escapes during the period 2013–2017 that have led to FMD outbreaks in North Africa, the Middle East, Southeast Asia, the Far East and the FMD-free islands of Mauritius (See Bachanek-Bankowska et al., 2018 – Scientific Reports). Recent FMDV-positive samples received from Malaysia were characterised as belonging to the O/ME-SA/Ind-2001e lineage, which represent further spread of this lineage in Southeast Asia.

There are still important gaps in (i) our understanding of the way that FMDV lineages are maintained in endemic countries, as well as (ii) robust evidence to demonstrate that vaccines confer protection against different viral lineages that are present. The OIE/FAO FMD Laboratory Network (https://www.foot-and-mouth.org) encourages countries to submit appropriate clinical samples for laboratory analyses – testing is free-of-charge, for further information or assistance with shipments, please contact donald.king@pirbright.ac.uk.

Don King (Pirbright, October 2018)

I. GENERAL OVERVIEW

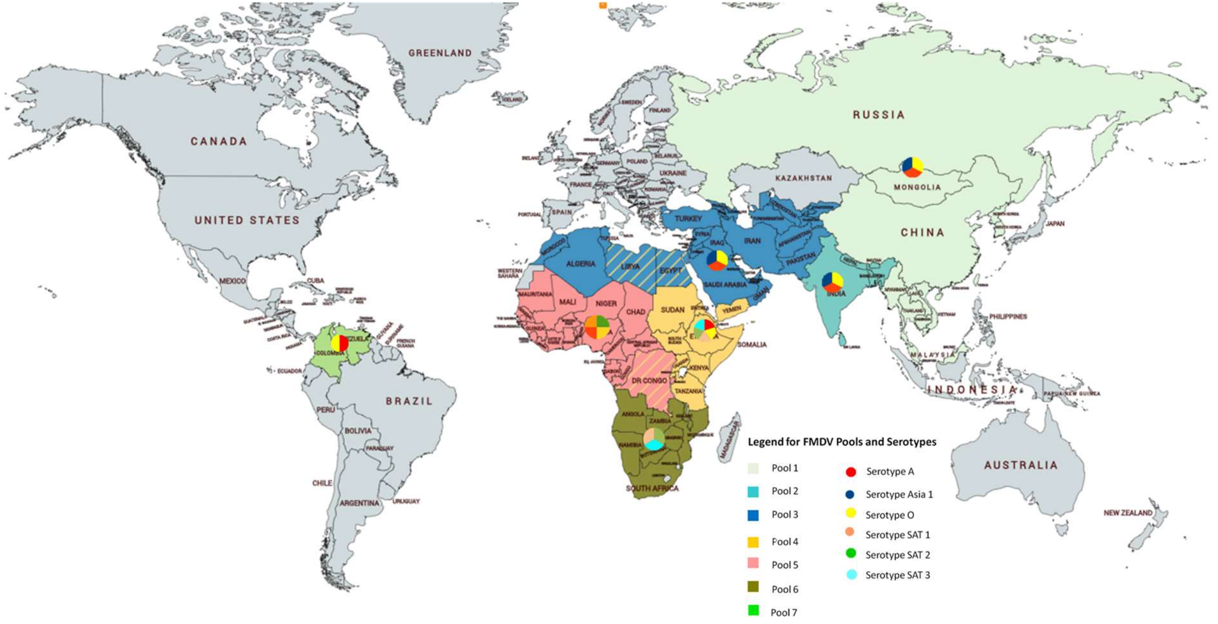
Pools represent independently circulating and evolving foot-and-mouth disease virus (FMDV) *genotypes; within the pools, cycles of emergence and spread occur that usually affect multiple countries in the region. In the absence of specific reports, it should be assumed that the serotypes indicated below 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 2013 – 2017 (source EuFMD)

POOL	REGION/COUNTRIES – colour pools as in Map	SEROTYPES
1	**SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA** Cambodia, China, China (Hong Kong, SAR), Taiwan Province of China, Democratic People's Republic of Korea, Republic of Korea, Laos People's Democratic Republic, Malaysia, Mongolia, Myanmar, Russian Federation, Thailand, Viet Nam	**A, Asia 1 and O**
2	**SOUTH ASIA** Bangladesh, Bhutan, India, Mauritius, Nepal, Sri Lanka	**A, Asia 1 and O**
3	**WEST EURASIA & MIDDLE EAST** Afghanistan, Algeria, Armenia, Azerbaijan, Bahrain, **Egypt**, Georgia, Iran (Islamic Republic of), Iraq, Israel, Jordan, Kazakhstan, Kuwait, Kyrgyzstan, Lebanon, **Libya**, Morocco, Oman, Pakistan, Palestine, Qatar, Saudi Arabia, Syrian Arab Republic, Tajikistan, Tunisia, Turkey, Turkmenistan, United Arab Emirates, Uzbekistan	**A, Asia 1 and O**
4	**EASTERN AFRICA** Burundi, Comoros, **Democratic Republic of Congo**, Djibouti, **Egypt**, Eritrea, Ethiopia, Kenya, **Libya**, 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, **Congo D. R.,** 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**

Egypt, Libya and **Democratic Republic of Congo** (highlighted in bold) are indicated as being in multiple pools, since they have evidence of FMDV originating from two or more pools. * ONLY IN NORTH ZAMBIA AS SPILL-OVER FROM POOL 4

MAP 1: Foot-and-mouth disease (FMD) virus pools: world distribution by serotype in 2013-2017 (source EuFMD, https://mapchart.net/world.html)



II. HEADLINE NEWS

POOL 1- SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA

China [1] – FMDV serotype O was responsible for the outbreak that was notified during September 2018 on a cattle farm at Zhangye, Gansu.

China (Hong Kong, SAR) [2] – FMDV O/CATHAY was detected in the batch of suspect pig samples collected during June and July 2018.

Malaysia [2] – O/SEA/Mya-98 and O/ME-SA/Ind-2001/e were the viral lineages present in the cattle and water buffalo field samples collected between May 2016 and 2018.
The FMD vaccine matching strain differentiation (VMSD) tests conducted on some of the field isolates belonging to the previous mentioned lineages gave good matching results with all the vaccine strains employed.

Mongolia [2] - O/SEA/Mya-98, O/ME-SA/PanAsia and O/ME-SA/Ind-2001/e were the viral lineages detected in the field samples of different species collected between January and April 2018.

POOL 2 - SOUTH ASIA

India [3] – The ICAR-Directorate of Foot and Mouth Disease, Mukteswar, India continues to report the detection of FMDV O as the only serotype circulating in the country since 2015.

Nepal [4] – The National Foot and Mouth Disease and TADS, Nepal has reported the presence of FMDV serotype O during the reporting month.

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan [5] - The Central Veterinary Research and Development Laboratory (CVDRL), Afghanistan detected FMDV serotypes A and O among the samples examined.

Israel [1] **–** A FMD outbreak which occurred in September 2018, due to serotype O, was diagnosed on a cattle and goat farm at Kineret, Hazafon.

Pakistan [6] **–** An outbreak due to FMDV serotype O was reported for the current month in Rawalpindi, Punjab.

POOL 4 - EASTERN AFRICA

Ethiopia [7] - The National Animal Health Diagnostic and Investigation Center (NAHDIC) notified a FMD outbreak on clinical basis in the Tigray Region.

Kenya [2, 8] – For the reporting month, the FMD National Reference Laboratory (FMDNRL), Embakasi, Kenya detected FMDV A and O among the cattle samples collected from outbreaks, while A/AFRICA/G-I, O/EA-2, SAT 1/I and SAT 2/IV were the lineages detected by the WRLFMD in bovine samples collected between January 2017 and June 2018.

South Sudan [2] **-** FMDV genome was detected in seven of the 29 bovine samples collected in the country between April and June 2017 without giving positive results in the cell/culture and antigen ELISA serotyping techniques.

Sudan [2] - The VMSD tests conducted on field isolates detected in samples, collected in 2017 and 2018, belonging to A/AFRICA/G-IV, O/EA-3 and SAT2/VII/ALx-12 lineages gave variable levels of matching results with the vaccine strains employed.

POOL 5 - WEST/CENTRAL AFRICA

Cameroon [9] **-** The Laboratoire National Vétérinaire (LANAVET), Garoua Cameroon found FMDV among the 264 bovine samples examined.

Guinea Bissau [1, 2, 10] **–** Four FMD outbreaks due to serotype O were notified on cattle farms in Oio, during August 2018.

Guinea [2, 10]

The FMDV VP1 sequence of samples collected during outbreaks that occurred in the previous month of July 2018, and submitted by ANSES Paris France, on behalf of the country, to the WRLFMD, was identified as belonging to O/EA-3 lineage.

Nigeria [11] **–** FMDV serotype O was detected during the reporting month in cattle samples examined by the National Veterinary Research Institute (NVRI) Vom, Nigeria.

Senegal [12] **–** The Laboratoire National d'Elevage et de Recherches Vétérinaires (LNERV), Senegal reported the occurrence in the country of three FMD outbreaks and the detection of FMDV serotype O.

Sierra Leone [1] **–** Two clinical FMD outbreaks for which serotyping is still pending were notified during September 2018 in cattle of villages of Kambia and Kono.

POOL 6 - SOUTHERN AFRICA

Malawi [5] **–** Another FMD outbreak due to serotype SAT 2 was reported during August 2018 in cattle of some villages in Lilongwe.

South Africa [13]**–** For the reporting month, the ARC Onderstepoort Veterinary Institute detected the presence of FMDVs belonging to serotype SAT 2.

Zimbabwe [1] **–** Fifty FMD outbreaks were reported in cattle in different areas of the country between July and September 2018 due to FMDV serotypes SAT 1 and SAT2 and also with some of these outbreaks with serotyping pending.

POOL 7 - SOUTH AMERICA [1, 14, 15]

Columbia [1] – Following the outbreaks of 2017 due to FMDV O, the country notified a new episode that occurred during September 2018 due to the same serotype on a cattle farm in Boyacá, which is located in the central area of the country.

FMD in Latin America was last detected in Colombia in July 2017 with outbreaks due to FMDV serotype O, while PANAFTOSA reported historical outbreaks due to serotype A that occurred in Venezuela in 2013.

COUNTER

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

III. DETAILED POOL ANALYSIS

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

China [1]

Further to the event that started in April 2018, another FMD outbreak has occurred on September 6th 2018 on a cattle farm in Zhangye, Gansu.

The episode was diagnosed on September 14th 2018 by the Lanzhou National Reference Laboratory for Foot and Mouth Disease (OIE Reference Laboratory) using reverse transcription - polymerase chain reaction (RT-PCR) followed by gene sequencing.

The source of the outbreak is unknown and the containment measures adopted were movement control inside the country, screening, traceability, quarantine, official destruction of animal products, official disposal of carcasses, by-products and waste, stamping out, disinfection while vaccination is prohibited and no treatment is being administered to the affected animals.

A summary of the animals involved and location of the outbreak are reported in Table 2 and Map 2.

The most recent lineages reported by the WRLFMD as circulating in the country belonging to the serotype responsible for the present outbreak are O/ME-SA/Ind-2001e and O/Cathay respectively detected in samples collected in 2017 and 2018.

Table 2: summary of the cattle involved in the FMD outbreak that occurred during September 6th 2018 on a cattle farm in Zhangye, Gansu. (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	47	8	0	47	0	17.02%	0.00%	0.00%	100.00%

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

Map 2: location of the FMD outbreak which occurred on September 6th 2018 on a cattle farm in Zhangye, Gansu. (Source – WAHIS)

China (Hong Kong, SAR) [2]

FMDV O/CATHAY was detected in seven of the eight pig samples collected during June and July 2018at Sheung Shui Slaughterhouse, Sheung Shui, New Territories. All the viruses clustered within one group and were closely related to field isolates detected in the same autonomous region during 2017 and 2018.

O/CATHAY is the only lineage that has been detected in the country since 2010.

Malaysia [2]

The FMD VMSD tests conducted on field isolates, O/MAY/12/2016, O/MAY/1/2018 (detected in cattle samples) and O/MAY/5/2018 (detected in a water buffalo sample) respectively belonging to lineages O/SEA/Mya-98 and O/ME-SA/Ind-2001/e gave good matching results with all the vaccine strains employed represented by O 3039, O Manisa and O TUR 5/09.

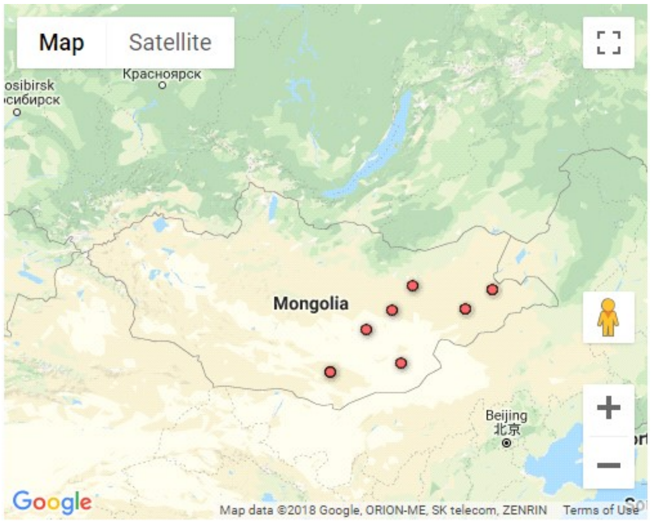
Mongolia [2]

Three different lineages belonging to FMDV serotype O and represented by O/SEA/Mya-98, O/ME-SA/PanAsia and O/ME-SA/Ind-2001/e were present in the field samples of different species, including a camel, collected between January and April 2018. The genotyping results and location of were the positive samples were collected are reported in Table 3 and Map 3.

Table 3: genotyping results of the FMDV positive bovine samples collected in Mongolia between January and April 2018 (source – WRLFMD)

Sample Identification	Location origin of sample	Species in which sample was collected	Date of collection	Genotype	Most Closely Related Viruses not belonging to the country - Seq id %	Host species
MOG/15/2017	Deren, Dundgovi	cattle	15/01/2018	**O/ME-SA/Ind-2001/e**	Zabaikalskiy/3/RUS/2016 (98.7)	cattle
MOG/2/2018	Gurvansaikhan, Dundgovi	camel	03/01/2018		Zabaikalskiy/3/RUS/2016 (98.3)	
MOG/7/2018	Ongon, Sukhbaatar	cattle	03/02/2018	**O/SEA/Mya-98**	TAI/22/2015 (97.6)	water buffalo
MOG/8/2018	Naran, Sukhbaatar	cattle	06/02/2018	**O/ME-SA/PanAsia**	VIT/42/2011 (98.4)	pig
MOG/9/2018	Sainshand, Dornogovi	sheep	19/02/2018	**O/ME-SA/Ind-2001/e**	Zabaikalskiy/3/RUS/2016 (98.6)	cattle
MOG/10/2018	Ongon, Sukhbaatar	cattle	22/02/2018	**O/ME-SA/PanAsia**	VIT/5/2011 (99.2)	
MOG/11/2018	Tsenhermandal, Khentii	sheep	22/02/2018	**O/ME-SA/Ind-2001/e**	Zabaikalskiy/3/RUS/2016 (98.3 -98.9)	
MOG/12/2018	Chuluunkhoroot, Dornod	cattle	23/02/2018			
MOG/13/2018	Bayandun, Dornod	cattle	23/02/2018			
MOG/15/2018	Kherlen, Khentii	cattle	23/02/2018			
MOG/16/2018	Togttsetsii, Umnugovi	cattle	03/03/2018			
MOG/17/2018	Manlai, Omnogovi	cattle	03/03/2018	**O/ME-SA/PanAsia**	/	/
MOG/18/2018	Sumber, Govisumber	cattle	09/01/2018	**O/ME-SA/Ind-2001/e**	Zabaikalskiy/3/RUS/2016 (98.6 99.1)	cattle
MOG/19/2018	Ongon, Sukhbaatar	sheep	09/04/2018			

Map 3: location of where the FMDV positive samples reported in Table 3 were collected in Mongolia. (Source – Google Maps)



SEACFMD [14]

To date, no FMD outbreaks were reported for the current month in the countries of the South East Asia FMD Campaign.

The number of on-going events in the different reporting countries of this region is as listed in Table 4. Location of the circulating serotypes in the single countries is represented in Maps 4 and 5.

Table 4: FMD outbreaks ongoing and notified during 2018 in the countries of the Southeast Asia Region (Source – SEAFMD Campaign)

Countries	N° of ongoing outbreaks prior to 2018	Jan '18	Feb '18	Mar '18	Apr '18	May '18	Jun '18	Jul '18	Aug '18	Sep '18	N° of current ongoing outbreaks
Cambodia	114	8	3	6	3	14	5	0	1	0	**154**
Laos	8	0	0	12	14	22	0	0	0	0	**56**
Myanmar	3	0	0	0	0	3	0	0	0	0	**6**
Malaysia	54	0	1	1	2	2	0	0	0	0	**60**
Thailand	236	13	7	5	3	3	1	0	0	0	**268**
Viet Nam	15	9	0	0	0	0	0	0	0	0	**24**
Totals	**430**	**30**	**11**	**24**	**22**	**44**	**6**	**0**	**1**	**0**	**568**

Map 4: location of the on-going FMD outbreaks reported during September 2018 due to serotype A in the countries reported in Table 4. (Source – SEAFMD Campaign)

Map 5: location of the on-going FMD outbreaks reported during September 2018 due to serotype O in the countries reported in Table 4. (Source – SEAFMD Campaign)

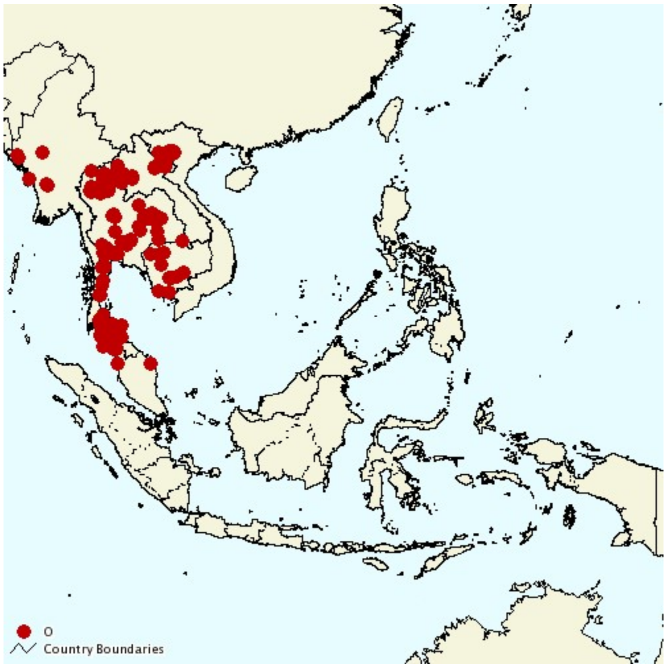
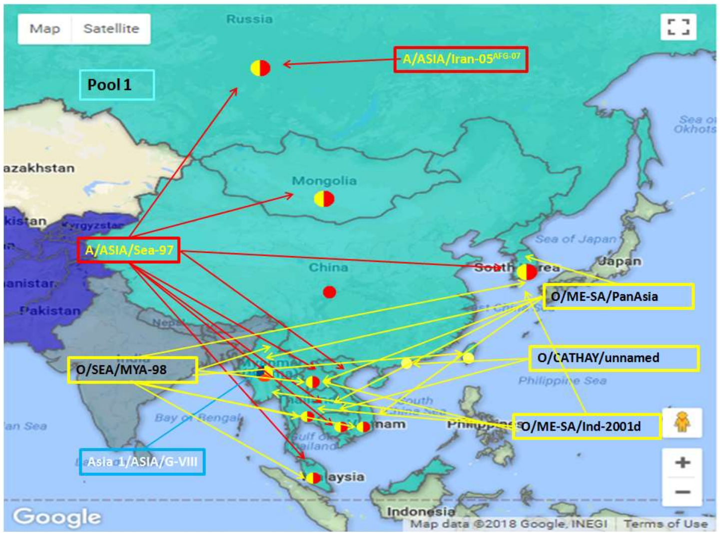


Table 5: Summary of the history of FMD Pool 1 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2013 -2017 see Map 6 below. (Source – Wahis, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE between 2012 – 2017 **(1st semester 2017)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
Cambodia	PENDING/2013-2017 O, A/2016, NOT SAMPLED/2017	Dec 2016/ A & O	**See text**
China	Data up to 1st semester 2016 2013 & 2015/A, 2012-2013, 2016/O, 2012 -2014/NOT TYPED	Sep 2018/O, May 2017/A	**See text**
China, Hong Kong, SAR	O	July 2018/O	**See text**
Democratic People's Republic of Korea	Data up to 2016 O/2016 2012-2013/DISEASE ABSENT 2014 & 2015/ NO DATA REPORTED	May 2014/not confirmed, July 2014/O	Follow-up needed
Lao People's Democratic Republic	O/2016-20117, A /2015 2012/DISEASE PRESENT WITH QUANTITATIVE DATA BUT WITH AN UNKNOWN NUMBER OF OUTBREAKS	Jan 2017/O Mar 2015/A,	**See text**
Malaysia	A/2016, 2012 –2017/O, 2013 & 2017/NOT TYPED	May 2018/O, August 2016/A	**See text**
Mongolia	2014 & 2015, 2017/O, 2013, 2016/A	April 2018/O, Sept 2016/A	**See text**

Myanmar	2012-2017/O, 2015-2017/A & NOT TYPED	May 2018/O, April 2017/Asia 1, July 2016/ not typed, Oct 2015/A	**See text**
Republic of Korea	Data up to 2016 2014 -2016/O, 2012-2013/DISEASE ABSENT	April 2018/A, Feb 2017/O	**See text**
Russian Federation	2016/ASIA 1, 2013 – 2016/A, 2012, 2014 & 2017**/O	Feb 2018/O, Oct 2016/Asia 1, Jan 2016/ A	Follow-up needed
Taiwan Province of China	Data up to 2016 2016/NO DISEASE PRESENT A/2015, 2012-2013/O	Jun 2015/A	Follow-up needed
Thailand	O, A NOT SAMPLED & NOT TYPED	Feb 2017 /A, Jan 2017/O June – July 2016/not typed	**See text**
Viet Nam	Data up to 2016 O, NOT SAMPLED, NOT TYPED 2013-2016/A	November 2017/A, Jan 2018/O and not typed	**See text**

Map 6: FMD distribution between 2013 – 2017 by serotype and topotype in South East Asia – red boxes and circles refer to serotype A genotypes, yellow to serotype O genotypes and white script refers to new introduction of viral lineage in pool or country of the pool during 2017.
(Source – Google Fusion Maps, WRLFMD).



Conjectured circulating FMD viral lineages in Pool 1 [1, 17]:

- Serotype O: O/SEA/Mya-98, O/CATHAY, O/ME-SA/PanAsia, O/ME-SA/Ind-2001d (new detection in Myanmar and Thailand during 2016)
- Serotype A: A/ASIA/Sea-97 and Iran-05^{SIS10} sublineage , only in the Russian Federation
- Serotype Asia-1 – reappearance of this serotype in 2016 in Russia and in 2017 in Myanmar – previous detection in the region was in 2006 in Vietnam and in China (People's Rep. of).

B. POOL 2 – South Asia

India[3]

The ICAR-Directorate of Foot and Mouth Disease, Mukteshwar, India detected FMDV serotype O among the 8 cattle and 4 buffalo samples examined using antigen and/or RNA detection diagnostic methods.

The laboratory also conducted serological testing of 200 samples collected during epidemiological studies. All diagnostic kits used are those developed by ICAR-PDFMD.

The laboratory conducts field investigations of FMD outbreaks and provides expert advice to the Government and to the National and Local authorities. The institution has on-going research studies and collaborations with international organisations.

The sublineages circulating in the country are represented by O/ME-SA/2001d and O/ME-SA/2001e as described in the latest ICAR-DFMD Annual Report of 2016-17.

Nepal [4]

The National Foot and Mouth Disease and TADS Laboratory has again confirmed for the reporting month the circulation of FMDV serotype O.

Last reported topotypes in the country by the WRLFMD are Asia 1/ASIA/unnamed that was previously never reported in the country and O/ME-SA/2001 d; both lineages were detected in samples collected in 2017.

Table 6: Summary of the history of FMD Pool 2 between 2012– 2018. For geographic distribution of circulating FMDVs between 2013 -2017, see Map 7 below. (Source – WAHIS, EuFMD Global Monthly Report)

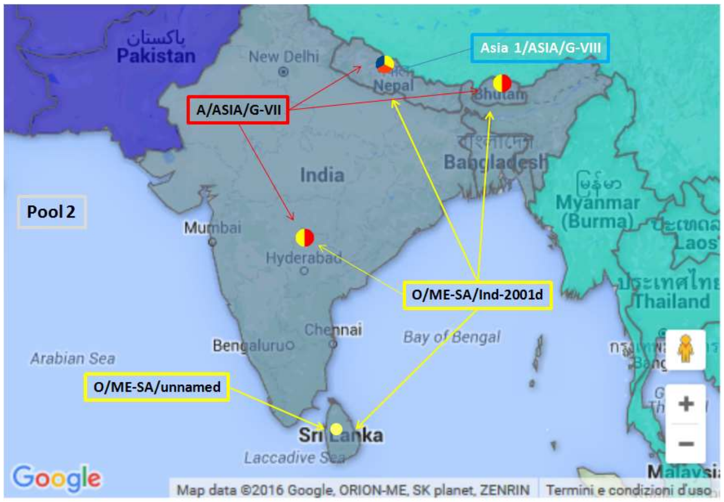
COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE between 2012 – 2017 **(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
Bangladesh	A, AISA 1 & O/2016 -2017, DISEASE PRESENT BUT WITHOUT QUANTITATIVE DATA	Dec 2016/A, ASIA 1 and O	Follow-up needed
Bhutan	2017/ A, 2013-2017/O, NOT TYPED or NOT REPORTED 2013 & 2014/NOT SAMPLED	Apr 2018/O, Sep 2017/A	Follow-up needed
India	O, NOT SAMPLED 2012-2015/A 2012-2014/Asia 1	Sep 2018/O, Apr 2015/A Asia 1	**See text**
Mauritius	2016/O	Sep 2016/0	Follow-up needed
Nepal	O, 2017/A 2012-2103, 2017/Asia 1	Sep 2018/O, Mar 2018/Asia 1, April 2017/A	**See text**
Sri Lanka	Data up to 2016 2012 – 2016/O	May 2018/O	Follow-up needed

Map 7: FMD distribution between 2013 – 2017 by serotype and topotype in South Asia - red boxes and circles refer to serotype A genotypes, yellow to serotype O genotypes and white script refers to new introduction of viral lineage in pool or country of the pool during 2017.
(Source – Google Fusion Maps, WRLFMD)

Conjectured circulating FMDV lineages in Pool 2 [1, 17]:

- O/ME-SA/Ind-2001 predominates outbreaks of this serotype detected also in Mauritius during 2016 (**not reported in Map**).

  The O/ME-SA/Ind-2011 lineage that emerged during 2011 has not been detected during 2012-17.
- A/ASIA/G-VII (genotype 18)
- Asia-1 (lineage C subdivided into Eastern and Western clusters) – not reported in map – reappearance in 2017 in Nepal.



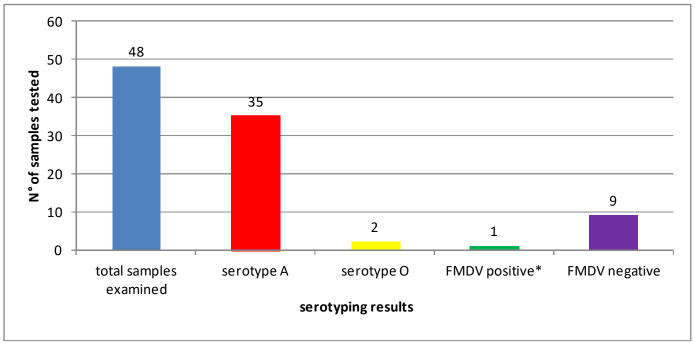
C. POOL 3 – West Eurasia & Middle East

Afghanistan [5]

The Central Veterinary Research and Development Laboratory (CVDRL), Afghanistan detected FMDV serotypes A and O among the 48 samples examined. A summary of the results is represented in Graph 1.

A/ASIA/Iran-05 and O/ME-SA/PanAsia-2 are the most recent lineages detected in samples collected in 2018 that belong to the serotypes reported for the current month.

Graph 1: summary of the serotyping results of the samples examined by the CVDRL, Afghanistan in August 2018.



* samples FMDV positive but not typed as A, Asia 1 and O.

Israel [1]

A FMD outbreak was reported on September 5th 2018 on a cattle and goat farm at Mughar, Kineret, Hazafon were only cattle clinically presented the infection. The diagnosis was confirmed on September 9th 2018 by the Kimron Veterinary Institute, Foot and Mouth Disease Laboratory (National laboratory) using real-time PCR and cell culture isolation on cattle samples.

An epidemiological investigation is ongoing to identify source of infection and the containment measures adopted are as following: movement control inside the country, quarantine, zoning, vaccination permitted (if a vaccine is available) while no treatment is being provided to affected animals even if these have not been suppressed. Other measures that will be adopted are: surveillance outside and within containment and/or protection zone.

A summary of the animals involved and location of outbreak are reported in Table 7 and Map 8.

Latest circulating topotypes belonging to FMDV serotype O reported by the WRLFMD are represented by O/EA-3 and O/ME-SA/PanAsia2 detected in samples respectively collected during 2017 and 2018.

Table 7: summary of the animals involved in the FMD outbreak that occurred on September 5th 2018 on a cattle and goat farm at Mughar, Kineret, Hazafon. (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	200	10	0	0	0	5.00%	0.00%	0.00%	0.00%
Goats	40	0	0	0	0	0.00%	0.00%	-	0.00%

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

Map 8: location of the FMD outbreak of September 5th 2018 on a cattle and goat farm at Mughar, Kineret, Hazafon (Source – WAHIS)

Pakistan [7]

The FMD control project in Pakistan is currently operating only in Punjab and information relative to other areas of the country is provided on a voluntarily basis.

For the present month, of the two suspect FMD outbreaks which respectively occurred in Gujrat and Rawalpind, Punjub only in the later case was the episode confirmed as due to serotype O (Map 9).

Latest circulating topotype belonging to FMDV serotype O reported by the WRLFMD is represented by O/ME-SA/PanAsia2 detected in samples collected during 2017.

Emergency and preventive vaccinations campaigns are conducted in Punjub with the respective administration during the month of September 2018 of 350 and 1,920,525 doses. A summary of the doses administered in the different districts of Punjub is reported in Table 8.

Relative to activities conducted for the capacity building of field veterinary staff for the control of FMD, three training events were held at Arifwala, Pakpattan and Vehari with the participation of 60 Veterinarians and 233 Veterinary Assistants.

Map 9: location of the FMD outbreaks reported in Punjub, Pakistan during September 2018. (Source – Google Fusion Maps, Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator)

Table 8: summary of the FMD outbreaks reported in Pakistan during September 2018. (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator)

District	No. of Households	N° of animals administered 6 monthly Dose		
		Cattles	Buffaloes	Total
Sahiwal	15,872	70,653	101,890	**172,543**
Pakpattan	53,852	231,341	303,318	**534,659**
Sheikhupura	55,926	283,453	392,516	**675,969**
Vehari	48,296	236,802	299,277	**536,079**
Cholistan	51	1,275	0	**1,275**
Punjab (total)	**173,997**	**823,524**	**1,097,001**	**1,920,525**

Table 9: Summary of the history of FMD Pool 3 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2012 -2016, see Map 10 below. (Source – Wahis, EuFMD Global Monthly Report)

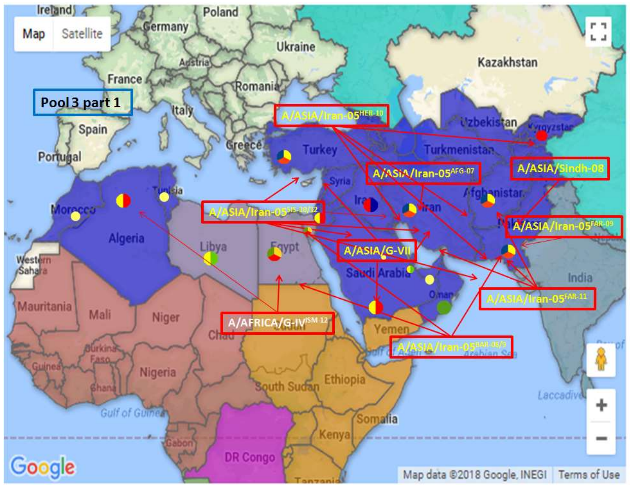
COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 – 2017 **(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
Afghanistan	2013-2017/O, A, Asia 1, NOT TYPED 2012/SEROTYPE NOT REPORTED	Sep 2018/ A & O, July 2018/ Asia 1	**See Text**
Algeria	Data available up to 1st semester 2015 20177A, 2014 -2016/O	Aug 2018/O Apr 2017/A	Follow –up needed
Armenia	2015 -2016/A , 2012-2014, 2017/DISEASE ABSENT	Dec 2015/A	Follow –up needed
Azerbaijan	DISEASE ABSENT	2007/0	Follow –up needed
Bahrain	DISEASE ABSENT/2016, 2017, 2012, 2014 &2015 /O	Mar 2015/O	Follow –up needed
Egypt	2012, 2014, 2016, 2017/SAT 2 2012 – 2017/O, A	April 2017/O, Nov 2016/A May-Jun 2016/Sat 2, Aug 2016/typing pending	Follow –up needed
Georgia	DISEASE ABSENT	2001/ASIA 1	Follow –up needed
Iran (Islamic Republic of)	2012-2017/A, Asia 1 & O	Feb 2018/A, Asia 1& O,	Follow –up needed
Iraq	2015-2017/O, 2012-2016/A 2015/ SEROTYPE NOT REPORTED	Dec 2013/A, ASIA 1	Follow –up needed
Israel	2012-2015, 2017**/O 2017**/A	Sep 2018/O, June2017/A	**See text**
Jordan	2017/O 2012-2016/DISEASE ABSENT	Mar 2017/O	Follow –up needed
Kazakhstan	2014-2017/ DISEASE ABSENT, 2012/O, 2012 –2013/A	Jun 2013/ A & Aug 2012/O	Follow –up needed
Kuwait	2013 – 2014, 2017/ DISEASE ABSENT 2012, 2016/O	April 2016/O	Follow –up needed
Kyrgyzstan	2015 -2017/ DISEASE ABSENT, 2012-2014/O, A	Aug 2014/not typed & Apr 2013 /O, A,	Follow –up needed
Lebanon	2012- 2017**/DISEASE ABSENT	2010/not typed	Follow –up needed
Libya	2015-2017/NO DATA REPORTED	Oct 2013/O	Follow –up needed

	2012-2014/O		
Morocco	2012-2014, 2017**/DISEASE ABSENT, O/2015	Oct 2015/O	Follow –up needed
Oman	2012-2017/O	May 2015/SAT 2	Follow –up needed
Pakistan	2013-2017/O 2013-2014/A & ASIA 1 2012/ NO DATA REPORTED	Sep2018/ A & O, May 2018/ Asia 1	**See text**
Palestine	O, 2012-2013/SAT 2	July 2018/Untyped, Dec 2017/O, Mar 2013/Sat 2	Follow –up needed
Qatar	2012-2017/O 2016-2017/A	Dec 2013/O	Follow –up needed
Saudi Arabia	2012-2014, 2016-2017**/O 2015-2016/A	Oct 2016/A & April 2016/O	Follow –up needed
Syrian Arab Republic	DISEASE ABSENT	2002/ A & O	Follow –up needed
Tajikistan	2014-2017**/DISEASE ABSENT 2012- 2013/NOT TYPED	Nov 2012/ not typed & Nov 2011/Asia 1,	Follow –up needed
Tunisia	2017/A, 2015-16/ DISEASE ABSENT, 2014/O	April 2017/A, Oct 2014/O	Follow –up needed
Turkey	A & O, NOT TYPED 2012-2015/Asia 1	Oct 2015/ A May, 2014-2015/ Asia 1 and O	Follow –up needed
Turkmenistan	2013-2017**/DISEASE ABSENT, 2012/NO DATA REPORTED	Not available	Follow –up needed
United Arab Emirates	2013-2014, 2016-2017/O 2012, 2015/DISEASE ABSENT	Sep 2016/O	Follow –up needed
Uzbekistan	2014, 2016-2017/DISEASE ABSENT 2012, 2013 & 2015/NO DATA REPORTED	Not available	Follow –up needed

Map 10: FMD distribution between 2013 – 2017 by serotype and topotype for West Eurasia and Middle East– red boxes and circles refer to serotype A genotypes, yellow to serotype O genotypes, green to serotype SAT 2 genotypes and white script to new introduction of viral lineage in pool or country of the pool during 2017.
(source – Google Fusion Maps, WRLFMD).
(Note: Kazakhstan is not included in map as declared by OIE as FMD free, divided in zones with and without vaccination)

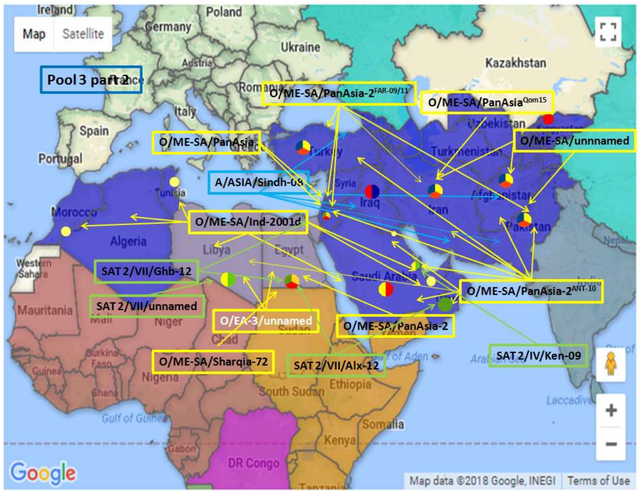
Conjectured circulating FMDV serotype A and Asia 1 lineages in Pool 3 [1, 17]:

- A/ASIA/Iran-05 (from AFG-07, HER 10, SIS-10-13, FAR 11 and BAR-08 sub-lineages)
- A/Asia/G-VII (recent incursion from South Asia)
- A/ASIA/Sea-97
- A/ASIA/Sindh-08
- A/AFRICA/G-IV
- Asia-1 (Sindh-08 lineage).



Conjectured circulating FMDV serotype O and SAT 2 lineages in Pool 3 **(cont'd)**

- O/ME-SA/PanAsia-2 (predominantly from ANT-10 and FAR-09 /11 sub-lineages)
- O/ME-SA/Ind-2001 (recent incursions per 2013/14 from the Indian sub-continent)
- New detection during 2016 of O/ME-SA/Sharqia-72 in Egypt and of O/ME-SA/PanAsia-2^{QOM-15} in Iran
- O/EA-3/unnamed in Egypt, Libya, Israel and Palestine
- SAT 2/IV/Ken-09
- SAT 2/VII/Alx-12 and Ghb-12 sublineages



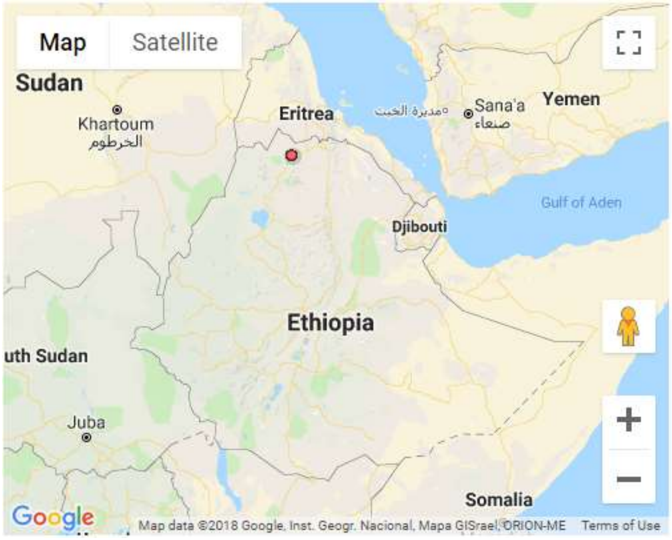
D. POOL 4 – Eastern Africa

Ethiopia [7]

The National Animal Health Diagnostic and Investigation Center (NAHDIC) reported a suspect FMD outbreak in the Tigray Region (Map 11) that had been notified on clinical basis by the regional veterinary offices.

A /AFRICA/G-IV, A/AFRICA/G-I, O/EA-3 and SAT 2/VII/Lib-12 are the most recent lineages reported as circulating in the country by the WRLFMD which were detected in samples during 2017 and 2018.

Map 11: location of the FMD suspect outbreak reported by NAHDIC during September 2018. (Source – Google Fusion Maps and NAHDIC)



Kenya [2, 8]

The FMDNRL, Embakasi, Kenya detected, during September 2018, FMDV A and O among the cattle samples collected from outbreaks while A/AFRICA/G-I, O/EA-2, SAT 1/I and 1 SAT 2/IV were the lineages detected by the WRLFMD among the twenty one bovine samples collected between January 2017 and June 2018.

A summary of the genotyping results and location of were the positive samples were collected are reported in Table 10 and Map 12.

Table 10: genotyping results of the FMDV positive bovine samples collected in Kenya between January 2017 and June 2018. (source – WRLFMD)

Sample Identification	Location origin of sample	Date of collection	Genotype	Most Closely Related Viruses not belonging to the country - Seq id %	Host species
KEN/9/2017	Kasarani, Nairobi	29/05/2017	A/AFRICA/G-I	TAN/18/2013 (95.7)	cattle
KEN/14/2017	Sotik, Bomet	21/09/2017		TAN/66/2012 (94.5)	
KEN/17/2017	Runyenjes, Embu	08/11/2017		TAN/18/2013 (94.9)	
KEN/11/2017	Ruiru, Kiambu	12/07/2017	O/EA-2	TAN-CVL-2011-0039 (94.6)	
KEN/15/2017	Elgeyo-Marakwet	17/10/2017		UGA/1/2004 (91.8)	
KEN/4/2018	Lanet, Nakuru	19/02/2018		TAN/2/2004 (92.1)	
KEN/19/2017	Rongai, Nakuru	25/11/2017	SAT 2/IV	TAN/9/2004 (88.6)	
KEN/8/2017	Subukia, Nakuru	16/03/2017	SAT 1/I	T155/71 (88.9)	

Map 12: location of where the FMDV positive samples reported in Table 10 were collected in Kenya. (Source – Google Maps)

South Sudan [2]

FMDV genome was detected in the seven of the 29 bovine samples collected in the country between April and June 2017 without giving positive results in the cell/culture antigen ELISA serotyping techniques.
This shipment is the first to be carried out by the country to the WRLFMD as there are no reports available relative to circulating strains in the country.

Sudan [2]

The (VMSD) tests conducted on field isolates detected in samples collected in 2017 and 2018 belonging to A/AFRICA/G-IV (A/SUD/9/2018 and A/SUD/9/2018), O/EA-3 (O/SUD/3/2017 and O/SUD/15/2017) and SAT2/VII/ALx-12 (SAT 2/SUD/14/2017) lineages provided the following matching results with the vaccine strains employed:

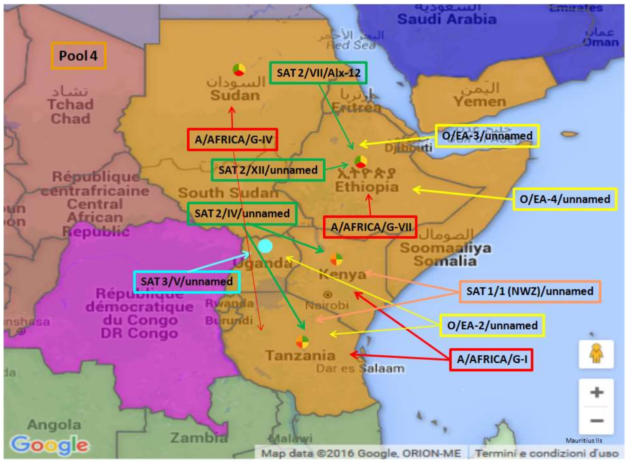
- For field isolates belonging to serotype A, only A/ERI/98 provided good matching results with one of the field viruses, while A IRN/2005, A/TUR/20/2006 and A22 IRQ/24/64 gave negative results.
- For field isolates belonging to serotype O, good matching results with at least one of the field viruses were provided by O 3039 and O TUR 5/09, but not by O Manisa.
- For the field isolate belonging to serotype SAT 2, SAT 2 ERI and SAT 2 ZIM vaccines strains provided good matching results.

Table 11: Summary of the history of FMD Pool 4 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2013 -2017, see Map 13 below. (Source – WAHIS, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 – 2016 **(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE #see pg. 1	Comment
Burundi	DISEASE PRESENT	Aug 2013 / not available	Typing required
Comoros	NO DATA AVAILABLE	2010	Follow –up needed
Democratic Republic of Congo	2012 – 2017**/A, O & SAT 1	June 2017/not typed	Follow –up needed
Djibouti	DISEASE ABSENT	Not available	Follow –up needed
Egypt	2012, 2014, 2016, 2017/SAT 2 2012 – 2017/O & A	May-Jun 2016/ O & Sat 2, March 2016/A, Aug 2016/typing pending	Follow –up needed
Eritrea	2014, 2016-2017/ DISEASE PRESENT 2015/ NO DATA REPORTED 2013/ DISEASE ABSENT, 2012/O	Nov 2016/not reported, Jan 2012/O	Follow –up needed
Ethiopia	O, 2015-2017/SAT 1 2012 & 2017/SAT 2, 2012, 2017/A	April 2018/O & SAT 2 Feb 2018/SAT 1, Jan 2018/A	**See text**
Kenya	A, O, SAT1 & SAT2	Aug 2018/O & A, May 2018/ SAT 1, Nov 2017/SAT 2	**See text**
Libya	2015-2017/NO DATA REPORTED 2012-2014/O	Oct 2013/ O, Sat 2/Apr 2012	Follow-up needed
Rwanda	2012-2013, 2017/A, O, SAT1 & SAT 2 2015-2016/NO DATA AVAILABLE	Nov 2012/not typed	Typing required
Somalia	2012-13, 2015-2017/DISEASE PRESENT, 2014/PENDING	June 2016/not reported	Follow –up needed
Sudan	2012-2014, 2017/O, 2015-2016/A, SAT 1 2013/SAT 2	Mar 2018/A Dec 2016/ not sampled, June 2017/O & SAT 2	**See text**
South Sudan	2015 - 2017/DISEASE PRESENT 2014/A, O, SAT 1, SAT 2 & SAT 3 2012-2013 & 2016 NO DATA REPORTED	2011	**See text**
United Republic of Tanzania	2012-2017/A, O, SAT 1 & SAT 2	Oct 2016/SAT 1, Aug 2016/O & SAT 2, Jun 2016/ A	Follow –up needed
Uganda	2016/DISEASE PRESENT, 2012, 2015, 2017/ SAT 1, 2012, 2014, 2015, 2017/O	May 2017/O Nov 2014/SAT1, Jan 2015/A and SAT 3, July 2015/ SAT 2 and untyped	Follow –up needed

Yemen	2013 – 2017/ DISEASE PRESENT BUT WITHOUT QUANTITATIVE DATA, 2012/O	2009/O	Follow –up needed

Map 13: FMD distribution between 2013 – 2017, by serotype and topotype for East Africa - red boxes and circles refers to serotype A genotypes, yellow refers to serotype O genotypes, green refers to serotype SAT 2 genotypes and light blue refers to SAT 3 genotypes.
(source – Google Fusion Maps, WRLFMD).



East Africa is known to be endemic for FMD, but available data is at present limited.
Conjectured circulating FMDV lineages in Pool 4 [1, 17]:

- O (topotypes EA-2 (Tanzania, DR Congo & Uganda), EA-3 and EA-4 (Ethiopia)
- A/AFRICA (genotypes I (Kenya, Tanzania, D.R. Congo), IV (Sudan, Eritrea, not reported in map) VII (Ethiopia)
- SAT 1 (topotypes I (Kenya, Tanzania), IX (Ethiopia))
- SAT 2 (topotypes IV (Kenya, Tanzania), VII (Sudan, Egypt, Ethiopia), XIII (Ethiopia, Sudan))
- SAT 3 (only detected in African buffalo in the south of the QENP, Uganda in 1970 & 1997 and recently in 2013)

E. POOL 5 – West / Central Africa

Cameroon [9]

The Laboratoire National Vétérinaire (LANAVET), Garoua Cameroon detected FMDV in 24 (9.1%) among the 264 bovine samples examined by panFMDV PCR. The laboratory also conducted NSP ELISA on 184 bovine serum samples with all of them resulting positve.

The last report by the WRLFMD of circulating viral lineages in the country was in 2014 with the detection of A/AFRICA/G-IV and SAT2/VII/Lib-12.

The laboratory continues its collaborative research projects with the Ohio State University and Plum Island, USA.

Guinea Bissau [1]

The Senegalese Institute for Agricultural Research (ISRA) confirmed on August 30th 2018, four FMD outbreaks due to serotype O using reverse transcription - polymerase chain reaction (RT-PCR). The outbreaks occurred on cattle farms at Mansôa and Farim, Oio, during August 2018. Previous detection of this serotype in the country was in 2016 Source of the outbreak is unknown while containment measures applied are vaccination if available with not treatment to the affected animals.

A summary of the animals involved and location of outbreaks are reported in Table 12 and Map 14. Of note are the high apparent morbidity and mortality rate registered in the affected population.

Table 12: summary of the animals involved in the FMD outbreaks that occurred on cattle farms in Oio, during August 2018. (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Species	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	1,473	1,176	123	0	10	Cattle	79.84%	8.35%	10.46%	9.03%

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

Map 14: location of the FMD outbreaks that occurred on cattle farms at Oio, during August 2018. (Source – WAHIS)

Guinea [2, 10]

Samples collected in the country during July 2018, and submitted on behalf of the country to the WRLFMD by ANSES, Paris, France, were identified as O/EA-3 with most closely related sequence of field viruses represented respectively by ALG/1/2018 with a sequence identity (seq id) of 99.4% and NIG/17/2016 with a seq id of 97.6%.
There are no previous reports of circulating lineages by the WRLFMD for the reporting country.

Nigeria [11]

The National Veterinary Research Institute (NVRI) Vom, Nigeria detected FMDV serotype O, using antigen ELISA, in two epithelial tissues from Plateau State and one epithelia and one swab from Kaduna State, all collected from cattle. Location of sample collection is represented in Map 15.
The most recent circulating lineages pertaining to the serotype detected for the current month are represented by O/WA and O/EA-3 detected in samples collected in 2016.
The laboratory has on-going projects with CODA-CERVA, Belgium and ANSES, France.

Map 15: location of where the FMDV positive samples were collected during September 2018. (Source –NVRI, Nigeria, Google Fusion Maps)

Senegal [12]

The LNERV, Senegal reported the occurrence in the country of three FMD outbreaks and the detection of FMDV serotype O and a suspect of serotype SAT 1.

The laboratory is preparing a shipment of samples tot eh WRLFMD for genotyping.

There are no previous reports of circulating strains by the WRLFMD for the reporting country.

Sierra Leone [1]

Two clinical FMD outbreaks for which serotyping is still pending were notified during September 2018 in cattle of villages of Kambia and Kono.

The clinical signs which the affected animals were presenting were typical of FMD with scialorrea, peeling of the epithelial tissue in the mouth, ulceration and sores of the tongue and the buccal cavity, loss of appetite, reduction of milk production, inflammation of the coronary band of the feet and death among the young animals.

The source of infection is attributed to illegal movement of animals, animals in transit and contact of infected animals at grazing/watering points. The control measures adopted are movement control inside the control, vaccination if a suitable one is available and no treatment of the affected animals.

A summary of the animals and location of the outbreaks are reported in Table 13 and Map 16.

Table 13: summary of the animals involved in the FMD notified during September 2018 in cattle of villages of Kambia and Kono. (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	6,000	1,200	40	0	0	20.00%	0.67%	3.33%	0.67%

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

Map 16: location of the FMD outbreaks notified during September 2018 in cattle of villages of Kambia and Kono. (Source – WAHIS)

Table 14: Summary of the history of FMD Pool 5 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2012 -2016, see Map 17 below. (Source – WAHIS, EuFMD Global Monthly Report)

Country	FMD history FMDV serotypes, reported to OIE in 2012 – 2017 **(1st semester)	Last outbreak reported/serotype #see pg. 1	Comment (Genotyping would be useful for this region)
Benin	2017/NO DATA REPORTED 2012-2016/A, O, SAT 1, SAT 2	Jun 2014/O, A, SAT 1, SAT 2	Follow –up needed
Burkina Faso	DISEASE PRESENT	Dec 2016/ not available	Follow –up needed
Cameroon	**DISEASE PRESENT	Sep 2018/untyped, Nov 2014/O, SAT 2, May 2014/SAT 1, Apr 2014/ A	**See text**
Cabo Verde	DISEASE ABSENT	Not available	Follow –up needed
Central African Republic	DISEASE PRESENT BUT WITHOUT QUANTITATIVE DATA	Not available	Follow –up needed
Chad	2016 - 2017/DISEASE PRESENT 2014-15/ DISEASE ABSENT 2012 – 2013/ DISEASE PRESENT	Aug 2016/Not reported	Follow –up needed
Democratic Republic of the Congo	2012 – 2017**/A, O & SAT 1	Mar 2018/untyped Dec 2016/A, O & Sat 1	Follow –up needed
Congo	NO DATA AVAILABLE	Jun 2013/not typed	Typing required

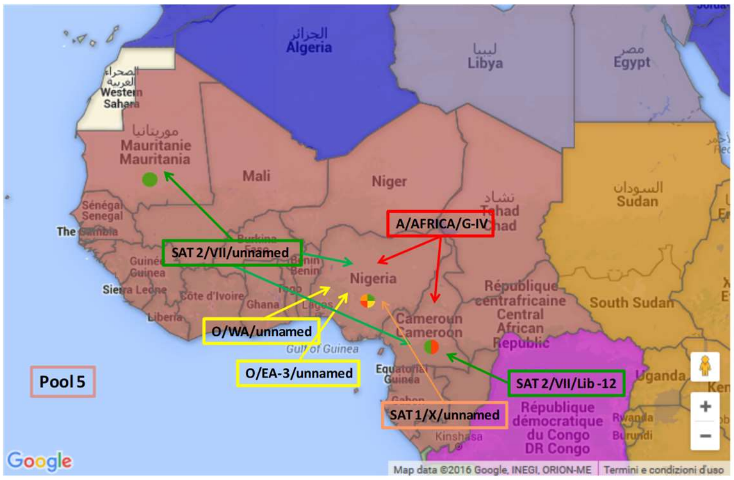
Côte d'Ivoire	2013-2017/DISEASE PRESENT, 2012/A,	Jul 2016/not reported	Follow –up needed
Equatorial Guinea	2014 – 2017/ NO DATA AVAILABLE 2012 – 2013/DISEASE SUSPECTED	Not available	Follow –up needed
Gabon	2017/NO DATA AVAILABLE 2012, 2014-16/DISEASE ABSENT 2013/NO DATA AVAILABLE	Not available	Follow –up needed
Gambia	NO DATA AVAILABLE	July 2018/untyped 2012/O	Follow –up needed
Ghana	2012 – 2017/DISEASE PRESENT	July 2018/untyped June 2017/O, Dec 2016/ SAT 2 2014/not available	Follow –up needed
Guinea-Bissau	2014-2017**/DISEASE PRESENT 2012-2013/DISEASE ABSENT	Aug 2018/O Dec 2016/SAT1 & SAT 2	**See text**
Guinea	2012-2013, 2015-2017 DISEASE ABSENT 2014/ DISEASE PRESENT	2014/not available	Follow –up needed
Liberia	NO DATA AVAILABLE	Not available	Follow –up needed
Mali	2017/ NO DATA AVAILABLE 2016/DISEASE ABSENT 2015/A, SAT 1 2014-2015/SAT 2 2012/ NO DATA AVAILABLE	Oct 2016/not reported	Follow –up needed
Mauritania	2017/ NO DATA AVAILABLE 2016/DISEASE SUSPECTED, 2014-2015**/SAT 2, 2012-2013/NO REPORTED OUTBREAKS	Dec 2014/SAT 2	Follow –up needed
Niger	2017/ DISEASE SUSPECTED 2016/DISEASE PRESENT BUT WITH NO QUALITATIVE DATA, 2015/O 2012 – 2014/NOT SAMPLED	2014/not sampled, May 2015/O	Follow –up needed
Nigeria	2015-2017/DISEASE PRESENT 2012-2014/O	Sep 2018/O &Sat 2 Sept 2016/ SAT 1, Nov 2015/A	**See text**
Sao Tome Principe	2013-2017/NO DATA AVAILABLE 2012/DISEASE ABSENT	Not available	Follow –up needed
Senegal	2017/ DISEASE SUSPECTED 2015-2016/DISEASE PRESENT 2012, 2014/NOT SAMPLED 2013/NO DATA AVAILABLE	Sep 2018/O, Feb 2015/ A, 2014/ SAT 2	**See text**
Sierra Leone	2017/NO DATA AVAILABLE 2012 – 2016/DISEASE ABSENT	Sep 2018/serotyping pending, Oct 1958	Follow –up needed

Togo	O & SAT 1	2012/O	Follow –up needed

Map 17: FMD distribution between 2013 – 2017 by serotype and topotypes for West Africa. Red boxes and circles refer to serotype A genotypes, yellow refers to serotype O genotypes, orange boxes to serotype SAT 1 genotypes, green refers to serotype SAT 2serotypes and white script in map refers to new introduction of viral lineage in pool or country of the pool during 2017. (Source – Google Fusion Maps, WRLFMD).

Conjectured circulating FMDV lineages in Pool 5 [17]:

- Serotype O (topotypes WA, EA-3 (Nigeria))
- Serotype A (topotypes AFRICA IV & VI)
- Serotype SAT 1 - detection of a new viral lineage, SAT 1/X/unnamed in Nigeria
- Serotype SAT 2 (topotype VII/Lib-12 (Mauritania), and unnamed genotypes)



F. *POOL 6 – Southern Africa*

Malawi [5]

A FMD outbreak, further to those reported at the beginning of the month caused by serotype SAT 2 was reported during August 2018 in cattle of villages in Lilongwe.

The outbreak occurred in a naive population kept by animal trader who buys from different sources and mixes his flock. For this source of infection is attributed to legal and illegal movement of animals, animals in transit and contact with infected animals at grazing/watering points.

The control measures adopted are movement control inside the country, vaccination in response to the outbreak, screening, traceability, official disposal of carcasses, by-products and waste, surveillance outside containment and/or protection zone, surveillance within containment and/or protection zone, quarantine, disinfection, process to inactivate the pathogenic agent in products or by-products, ante and post-mortem inspections and no treatment of affected animals and movement control inside the country.

Ring vaccination has been conducted in Lilongwe covering 29059 out of 29787 cattle while a booster vaccination is scheduled for 4 weeks after the primer one.

A summary of the animals involved in the outbreak and location of this are respectively represented in Table 15 and Map 18.

Table 15: summary of the cattle involved in the FMD outbreak due to SAT 2 that occurred on August 29th 2018 in cattle at Lilongwe. (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	3,000	64	0	0	0	2.13%	0.00%	0.00%	0.00%

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

Map 18: location of the cluster of FMD outbreak due to SAT 2 that occurred on August 29th 2018 in cattle at Lilongwe. (Source –WAHIS-OIE)

South Africa [14]

The ARC Onderstepoort Veterinary Institute detected the presence of FMDV serotype SAT 2 in three of the eight samples examined using PCR which were also submitted for sequencing.

The laboratory examined 2,559 serological tests for FMDVs SAT-1, SAT-2, and SAT-3, using the ELISA and 161 tests in NSP ELISA.

Zimbabwe [1]

Fifty FMD outbreaks that occurred in cattle in different areas of the country were reported between July and September 2018 caused by FMDV serotypes SAT 1 and SAT2 and also with some of these outbreaks with serotyping pending. The episodes were located in Mashonaland East, West and Central, Midlands and Masvingo.

Laboratory diagnosis was carried out by the Botswana vaccine Institute (Regional Reference Laboratory) using liquid-phase blocking ELISA and virus isolation.

The source of the episodes is attributed to the illegal movement of animals, introduction of new live animals and contact with infected animals at grazing/watering points.

As FMD infection continues to slowly spread in the affected districts, these areas were placed under quarantine with veterinary check-points that also controlled by police personnel placed at strategic areas to prevent cattle movement. Inspections and community education campaigns are currently on-going and all illegally moved cattle are being destroyed to discourage farmers from illegally moving their cattle.

An intensive surveillances ongoing and implementation of control measures remain in force in the North-East of the country. Vaccinations are currently on-going in the infected districts with 127,265 cattle vaccinated in Mashonaland Central and 500 cattle in Mashonaland East.

Other control measures in place are as following: movement control inside the country, vaccination in response to the outbreaks, surveillance outside and within containment and/or protection zone, traceability, quarantine, control of wildlife reservoirs, ante and post-mortem inspection, official destruction of animals products, zoning, while no treatment is being provided to the affected animals.

Summary of the animals involved and location of the outbreaks are represented in Table 0 and Map 0.

Table 16: summary of the cattle involved in the FMD outbreaks reported between July and September 2018 in different areas of Zimbabwe. (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	64,417	4,071	0	0	0	6.32%	0.00%	0.00%	0.00%

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

Map 19: location of the FMD outbreaks reported between July and September 2018 in different areas of Zimbabwe. (Source –WAHIS-OIE)

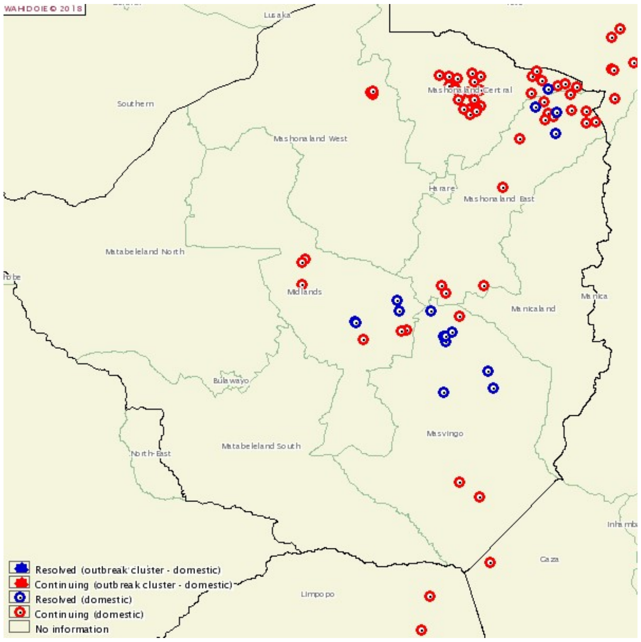
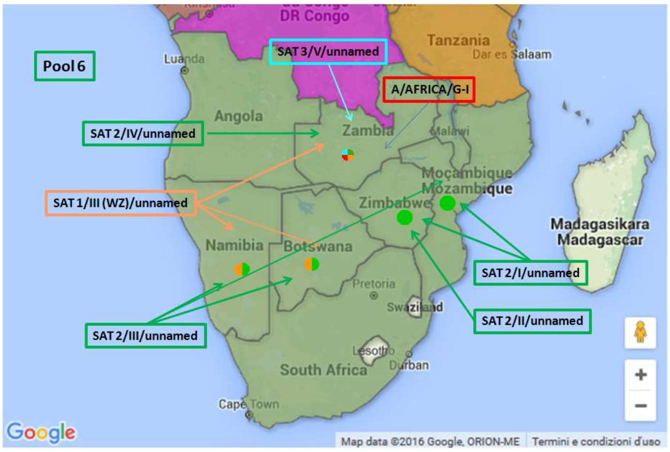


Table 17: Summary of the history of FMD Pool 6, 2013 – 2018, for geographic distribution see Map 20 below. (Source – WAHIS, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 – 2017 **(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE #see pg. 1	Comment
Angola	2013-2017/NO DATA AVAILABLE 2015-2016/ DISEASE PRESENT 2013-2014/DISEASE ABSENT 2012/DISEASE SUSPECTED BUT NOT CONFIRMED	April 2016/SAT 2, July 2015/ SAT 2	Follow –up needed
Botswana	2012-2017/SAT 2 2014-2015/SAT 1	July 2018/SAT 2, June 2015/SAT 1	Follow –up needed
Democratic Republic of the Congo	2012 – 2017**/A, O & SAT 1	Dec 2016/A, O & Sat 1	Follow –up needed
Malawi	2016 – 2017/SAT 2 2013-2015/ NO DATA AVAILABLE 2012/NO OUTBREAKS REPORTED	Aug 2018/SAT 2 June 2016/SAT 1	**See text**
Mozambique	2016 – 2017/SAT 2 2012 -2015/DISEASE ABSENT	June 2018/ Typing pending, Oct 2017/SAT 2,	Follow –up needed

		May 2015/ SAT 1	
Namibia	2017/NO DATA AVAILABLE 2014-2016**/SAT 2 22012-2014/SAT 1	Sep 2017/SAT 2, Aug 2017/typing pending, May 2015/SAT 1	Follow –up needed
South Africa	2012-2015, 2017/SAT 2 2013, 2017/SAT 1 2015-16/SAT 3	Sep 2018/SAT 2, Oct 2017/SAT 1, Dec 2015/SAT 3	**See text**
Zambia	2016 – 2017/NOT TYPED 2016/SAT 3, 2013-2014/ NO DATA AVAILABLE 2012/SAT 1 & SAT 2	April 2018/ A &O, May 2017/SAT 3, Mar 2017/SAT 2, Jan 2013/SAT 1	Follow –up needed
Zimbabwe	2012-2017/SAT 2 2014-2015/SAT 1 2013/SAT 3	Sep2018/typing pending, SAT 1 & SAT 2, Jun 2013/SAT 3	**See text**

Map 20: FMD distribution by serotype and topotype for Southern Africa, 2013 – 2017 - red refers to serotype A, orange refers to SAT 1, green refers to serotype SAT 2. (source – Google Fusion Maps, WRLFMD).



Swaziland and Lesotho are free from FMD without vaccination. There is a zone in both Botswana and Namibia, which has been FMD free without vaccination, since 2010 and 1997 respectively.

Conjectured circulating FMDV lineages in pool 6 [1, 17]:

- Serotype SAT 1 (topotypes I, II and III) – new detection of SAT 1/III (WZ)/unnamed in Botswana during 2016
- Serotype SAT 2 (topotypes I, II, III and IV) - new detection of SAT 2/III/unnamed in Namibia
- Serotype SAT 3 (?) (topotypes I, II and III) – new detection of SAT 3/V/unnamed in Zambia during 2016

G. POOL 7 – South America

Columbia [1]

Following the episodes of last year, FMD was again notified in the country caused by the same serotype O, with an outbreak that started on September 19th 2018 on a cattle farm situated at El Cerrito, Segunda Chorrera, Sogamoso, Boyacá which is in the central part of the country (Map 21). A summary of the animals involved is reported in Table 18.

Diagnosis was confirmed on September 29th 2018 by the National Veterinary Diagnosis Laboratory using PCR and virus isolation.

The source of the outbreak is unknown and for this an epidemiological investigation is ongoing.

Vaccination is being administered on the affected farm and the area, where this is localised, has high vaccination coverage. The outbreak is within the containment zone, which was recognized by the OIE on December 11th 2017.

Control measures put in force are movement control inside the country, surveillance outside containment and/or protection zone, surveillance within containment and/or protection zone, traceability, quarantine, disinfection, vaccination permitted (if a vaccine exists) with no of treatment of affected animals. Further measures that will be applied are official destruction of animal products, official disposal of carcasses, by-products and waste and stamping out.

Table 18: summary of the cattle involved in the FMD outbreak that started on September 19th 2018 on a cattle farm situated at Boyacá, Columbia. (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	19	1	0	19	0	5.26%	0.00%	0.00%	100.00%

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

Map 21: location of the FMD outbreak that started on September 19th 2018 on a cattle farm situated at Boyacá, Columbia. (Source –WAHIS-OIE)

Rest of Latin America [1, 12, 17]

The OIE FMD status of the countries in South America as reported in October 2018 is presented in Map 22.

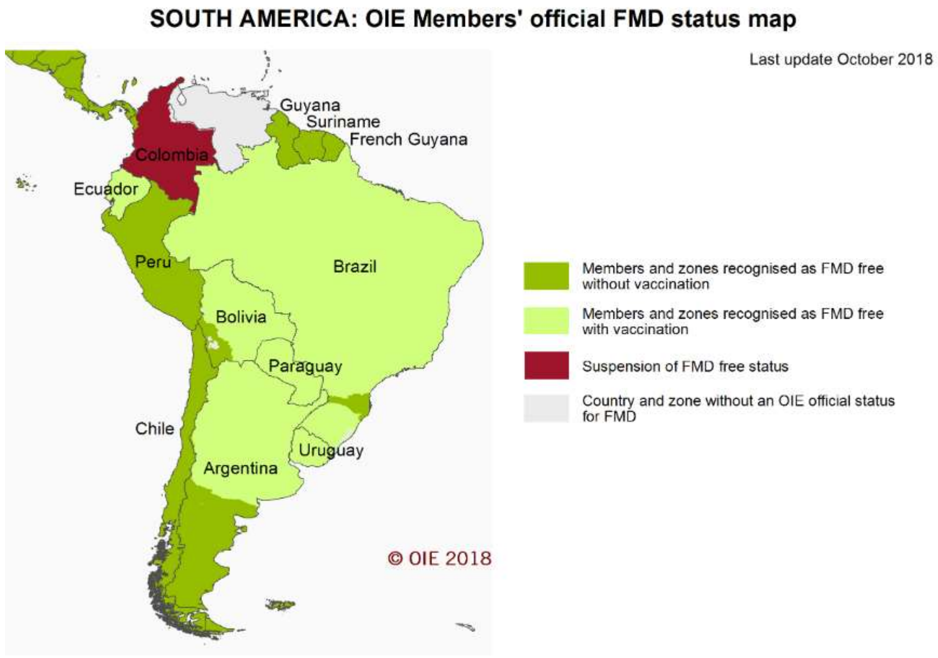
Most South American countries are FMD free with vaccination (Uruguay) or without vaccination (Chile, Guyana) or with free zones with vaccination (Argentina, Bolivia, Brazil, Peru and continental Ecuador) or without vaccination (Argentina, Bolivia, Brazil, Colombia, Peru) as described by the OIE maps (see: http://www.oie.int/en/animal-health-in-the-world/official-disease-status/fmd/en-fmd-carte/).

Small areas of the continent may still be considered as endemic but clinical cases are rare (Map 22). In fact, before the outbreak which occurred in Columbia, PANAFTOSA reported data for historical FMD outbreaks that occurred in Venezuela in 2013 caused by serotype A during the OIE/FAO FMD Laboratory Meeting held in November 2016. The FMD history relative to the Region for 2012 –2017 is reported in Table 19.

Table 19: Summary of the history of FMD Pool 16 between 2012 – 2018, for geographic distribution see Map 22. (Source – WAHIS, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 2016**(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE #see pg. 1	Comment
Colombia	DISEASE ABSENT	July 2018/O	Follow –up needed
Venezuela (Bolivarian Republic of)	DISEASE ABSENT**	2011/O, 2013/A	National situation needs verification

Map 22: FMD status for South America [1] (Source – OIE)

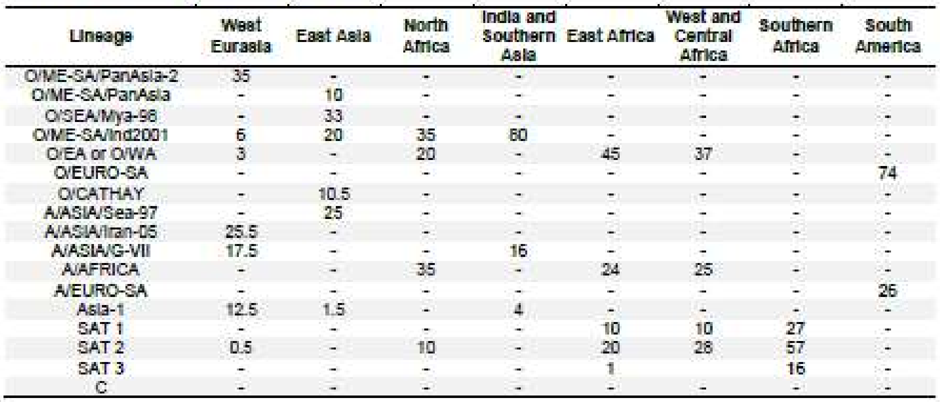


IV. OTHER NEWS:

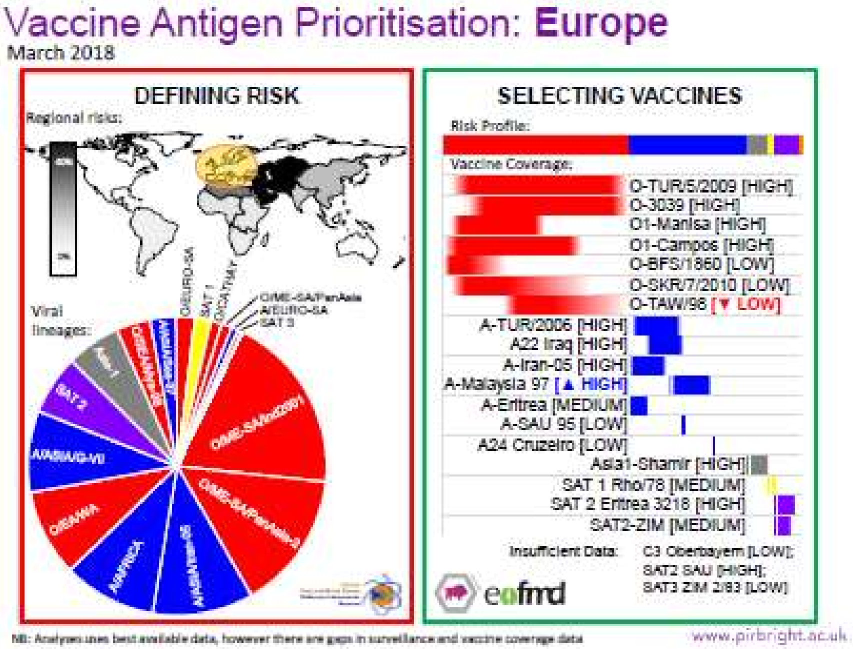
[2]The 3rd WRLFMD Quarterly Report for the period July – October 2018 contains a new format for recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of Table 23 is available within the report.

Table 23: Recommendations from WRLFMD® on FMD virus strains to be included in FMDV antigen banks (for Europe).

This report showcases a new format for 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	60	-	-	-	-
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

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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.

V. REFERENCES - Superscripts

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6. Progressive Control of Foot and Mouth Disease in Pakistan - *Dr. Muhammad Afzal*, Project Coordinator.
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