APRIL

2018

MONTHLY REPORT
FOOT-AND-MOUTH DISEASE SITUATION

Food and Agriculture
Organization of the
United Nations

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

April 2018

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#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.

April 2018

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As in every month, in April, EuFMD brings us this comprehensive picture of the FMD situation worldwide. Except for pool 7 in South America, every single geographical pool experienced several outbreaks mostly of serotypes A and O but also of Asia-1 and SAT-2. While in most outbreaks the affected species were cattle, pigs and sheep, in Israel, in addition to free ranging cattle for beef production, mountain gazelle were infected. Gazelles are known to be very susceptible to the disease and often suffer high mortality even in adult animals due to separation of hoof that prevent them from movement, which leads to starvation and death. In several countries, gazelles were blamed to be the main factor for FMD spread, whereas scientific evidence shows the opposite.

In the present report, outbreaks were notified mostly from endemic countries that are not necessarily important exporter of animal products, however, the impact on livelihoods and food security cannot be overlooked, particularly of smallholder livestock owners. It is important to remember that the impact of the disease among smallholders is not only through reduced milk production and through corporal performance but also in the crop sector as in many countries cattle and buffalos are being used as draft animals. This can have a huge impact on thousands of families' income and daily food consumption.

This month's report, like previous ones, reminds us that we still have a long journey to go toward adequate control of the disease in endemic countries. The Food and Agriculture Organization of the United Nations (FAO) together with OIE and EUFMD has been dedicating significant amount of resources and efforts working with countries to reach a sustainable approach to control the disease by using the Progressive Control Pathway (PCP), a tool that is supported by the Global Strategy for the Control of FMD. The Global strategy advocates for regional coordination that aims at information sharing between countries to improve early detection and rapid response. Nevertheless, this essential approach requires from countries to keep their commitment for transparency and timely reporting to OIE. This is an opportunity to emphasize once again the importance of timely and accurate information sharing to improve our understanding on the disease dynamic and hence improve our possibilities to control its spread through adequate and effective vaccination. I therefore, would like also to congratulate the countries not only for their efforts to control the disease, often with very limited resources, but also for reporting the OIE and sending adequate samples to reference laboratories for further genetic analysis. Finally, I would like to thank EUFMD for inviting me as a guest editor and felicitate them for this comprehensive report.

ERAN RAIZMAN
Senior Animal Health Officer
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I. GENERAL OVERVIEW

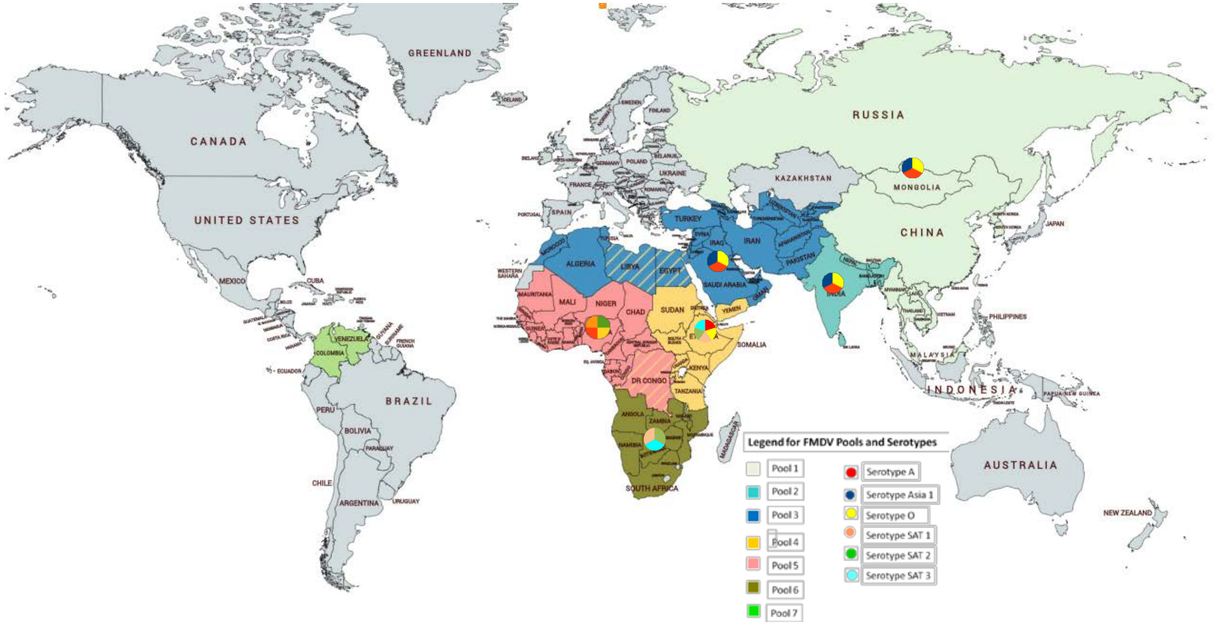
Pools represent independently circulating and evolving foot-and-mouth disease virus (FMDV) *genotypes; within the pools, cycles of emergence and spread occur that usually affect multiple countries in the region. In the absence of specific reports, it should be assumed that the serotypes indicated below 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] – Further to the FMD outbreak, caused by serotype O, reported in February 2018 at Henan, another three episodes were notified in March and April 2018 affecting cattle and in pigs respectively at Gansu, Xinjiang and Guangxi.

China (Hong Kong, SAR) [2] – FMDV O CATHAY was detected in samples collected in October and November 2017, in a pig slaughterhouse of Sheung Shui.
The vaccine strains tested in the FMD vaccine matching strain differentiation (VMSD) assay did not give good matching results with the field viruses detected in the samples mentioned previously.

Republic of Korea [1, 2] – In April 1st 2018, FMDV serotype A caused an outbreak on another big pig herd at Gyeonggi-Do that was also reported as resolved.
FMDV A/ASIA/Sea 97 was detected in the samples collected in March 2018 in pigs.

Vietnam [2] – FMDV serotypes A and O were detected in the pig, cattle and buffalo samples collected between June 2016 and January 2018.

POOL 2 - SOUTH ASIA

India [3] –FMDV O continues to be the only serotype detected as since May 2015 in the samples examined by the Indian Council of Agricultural Research - Directorate of Foot and Mouth Disease (ICAR-PDFMD).

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan [4] **–** The Central Veterinary Research and Development Laboratory (CVDRL), Afghanistan reported for April 2018 the circulation of FMDV serotypes Asia 1 and O.

Iran [2] **–** FMDV serotypes A, ASIA 1 and O are the serotypes detected in sheep and cattle samples collected during the first two months of 2018. Genotyping of these strains was carried out.

Israel [1] – Following the FMD outbreak caused by serotype O which occurred on April 4th 2018 in free ranging cattle at Hazafon, further outbreaks were registered in three other farms of the same species, as well as, in mountain gazelle with some animals found dead.

Pakistan [5] – FMDV circulating serotypes for the current month in Punjab are A, Asia1 and O.

POOL 4 - EASTERN AFRICA

Democratic Republic of Congo [1] **–** Five FMD outbreaks were reported during April 2018 to have occurred on cattle farms during May and June 2017.

Ethiopia [2, 6] – The National Animal Health Diagnostic and Investigation Center (NAHDIC), Ethiopia reported for April 2018 the detection of FMDV serotypes O and SAT 2 in the cattle samples collected from outbreaks.
In addition, genotyping was carried out for FMDV serotypes A, O and SAT 2 detected in the bovine samples collected between June 2017 and February 2018.

Kenya [7] – The FMD National Reference Laboratory, Embakasi, Kenya detected FMDV serotypes O and SAT 1 during the reporting month in the cattle samples collected from outbreaks.

POOL 5 - WEST/CENTRAL AFRICA

Cameroon [8] **–** The Laboratoire National Vétérinaire (LANAVET) - Garoua, Cameroon reported FMDV in the samples tested during the reporting month.

Nigeria [9] - The FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria reported the presence of FMDV in samples examined during April 2018.

POOL 6 - SOUTHERN AFRICA

Zambia [1, 2] **–** FMDV serotype O was detected in the samples collected from FMD outbreaks of March and April 2018.

POOL 7 - SOUTH AMERICA [2, 10, 11]

No FMD notifications were notified for this pool during the reporting month.
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 occurring in Venezuela in 2013.

COUNTER

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

III. DETAILED POOL ANALYSIS

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

China [1]

FMDV serotype O was responsible for the outbreaks that were respectively notified on March 22nd and April 11th and 12th 2018 in two cattle farms at Gansu, Xinjiang and at a pig slaughterhouse of Guangxi.

The Lanzhou National Reference Laboratory for Foot and Mouth Disease (OIE Reference Laboratory), using reverse transcription - polymerase chain reaction (RT-PCR) and gene sequencing, confirmed FMDV between April 11th and 14th 2018.

Clinical forms were observed in both species present in the outbreaks, as reported in the summary table of the animals involved in the outbreak (Table 2). Location of the outbreaks is represented in Map 2.

While for the outbreaks reported at the slaughterhouse, the source of infection is unknown, for the episodes, which occurred on the cattle farms, the source was attributed to the legal movement of animals. In this case, infected cattle were transported from Linxia county to Hami city, of the neighbouring province of Xinjiang Uygur Autonomous Region.

The control measures adopted are movement control inside the country, screening, traceability, quarantine, official destruction of animal products, official disposal of carcasses, by-products and waste, stamping out, disinfection, vaccine permitted if a suitable one is available, while no treatment is being administered to the affected animals.

Table 2: summary of the animals involved in the FMD outbreaks that were respectively notified on March 22nd and April 11th and 12th 2018 on two cattle farms at Gansu, Xinjiang and at a pig slaughterhouse of Guangxi. (Source – WAHIS)

Location	Date of outbreak	Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Linxia, Gansu	22/03/2018	Cattle	35	2	0	35	0	5.71%	0.00%	0.00%	100.00%
Yizhou District, Xinjiang	12/04/2018	Cattle	41	6	0	41	0	14.63%	0.00%	0.00%	100.00%
Cenxi City, Guangxi	11/04/2018	Swine	51	15	0	51	0	29.41%	0.00%	0.00%	100.00%

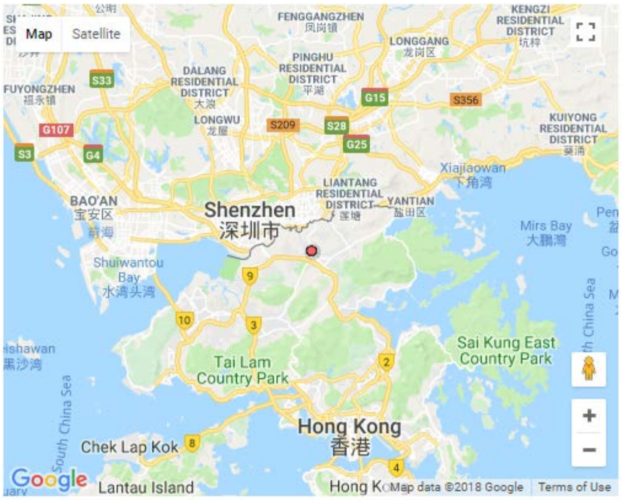
Map 2: location of the FMD outbreaks that were respectively notified on March 22nd and April 11th and 12th 2018 on two cattle farms (yellow dots) at Gansu, Xinjiang and at a pig slaughterhouse (green dot) of Guangxi. (Source – WAHIS, Google Fusion Maps)

China (Hong Kong, SAR) [2]

FMDV O CATHAY was detected in four pig samples collected in October and November 2017 at an abattoir of Sheung Shui (Map 3). These genotyped viruses presented a close sequence identity (SI) only to strains that were previously circulating in the country with the most closely related field virus, detected in a pig in September 2017, having a 100% S.I.

FMDV O CATHAY is the only genotype circulating in the country since 2011.

None of the vaccine strains used, O 3039, O Manisa and O TUR 5/09, gave good matching results in the VMSD assay with the field viruses O/HKN/8, 11 and 12/2017 detected in the samples mentioned in the previous paragraph.



Map 3: location of the abattoir at Sheung Shui where FMDV O CATHAY was detected in four pig samples collected in October and November 2017 (Source – WRLFMD, Google Fusion Maps)

Republic of Korea [1, 2]

FMDV serotype A was responsible for an outbreak on April 1st 2018, in a large pig herd at Gyeonggi-Do that was reported as resolved on April 30th. A summary of the animals involved and location of the outbreak are represented in Table 3and Map 4.

The Animal and Plant Quarantine Agency (OIE Reference Laboratory) confirmed the diagnosis on April 4th using real-time reverse transcriptase/polymerase chain reaction.

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

The control measures applied are the following: movement control inside the country, vaccination in response to the outbreak, surveillance outside containment and/or protection zone, surveillance within and outside containment and/or protection zone, screening, traceability, quarantine, official destruction of animal products, official disposal of carcasses, by-products and waste, stamping out, control of wildlife reservoirs, zoning, disinfection, and no treatment of affected animals.

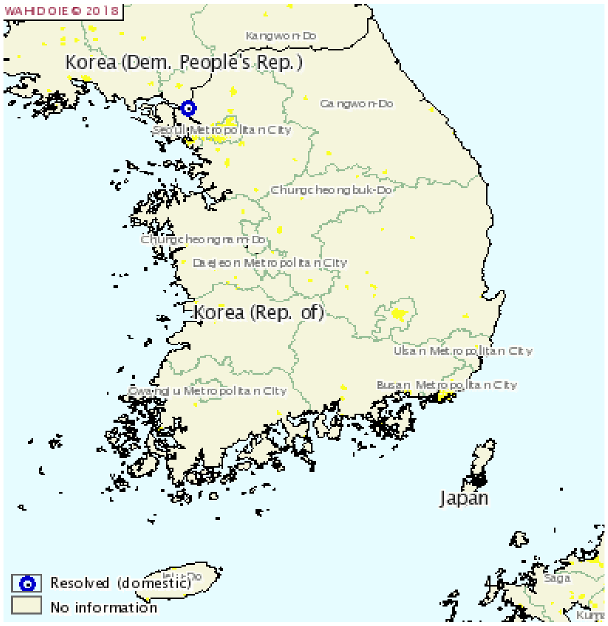
Of the four pig samples collected in March 2018 that were forwarded to the WRLFMD, only one was FMDV positive that was genotyped as A/ASIA/Sea 97. The most closely related field virus not belonging to the country is represented by an isolate detected in pigs in China in 2013 with a SI of 95.7%.

During the previous year, the country also experienced the circulation of lineage 0/ME-SA/Ind-2001d.

Table 3: summary of the animals involved in the FMD outbreak that took place in a large pig herd at Gyeonggi-Do on April 1st 2018. (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*
Swine	3,000	45	0	3000	0	1.50%	0.00%	0.00%	100.00%

Map 4: location of the FMD outbreak that took place in a large pig herd at Gyeonggi-Do on April 1st 2018. (Source – WAHIS)



Russian Federation [12]

No FMD related activities were reported by the All-Russian Research Institute for Animal Health (FGBI-ARRIAH) (OIE Reference Laboratory) except for the serological examination of 579 samples for post vaccination monitoring purposes.

The laboratory is also studying the immunological properties of FMDV serotype A.

Other current activities carried out are the provision of materials to the Federal Service for Veterinary and Phytosanitary Surveillance of the Ministry of Agriculture of the Russian Federation and advice to the veterinary services of the Russian Federation Subjects.

SEAFMD [13]

No FMD outbreaks were reported in the area for April 2018 and on-going outbreaks in the different reporting countries are as those listed in Table 4.

Although FMDV Asia 1 is reported as still circulating in Viet Nam, further confirmation of this is required as last detection reports of the serotype in the country are those relative 2007 as also confirmed by the latest batch of samples, collected between 2016 and 2018 and tested by the WRLFMD (see below).

Distribution of the serotypes in the single countries is represented in Maps 5, 6 and 7.

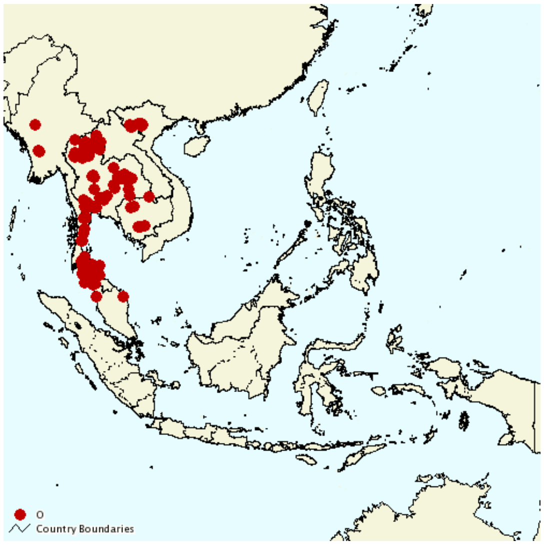
Table 4: number of FMD outbreaks reported up to April 2018 in the countries of the Southeast Asia Region for (Source – SEAFMD Campaign)

Country	Ongoing prior outbreaks	jan-18	feb-18	mar-18	Total per country
Cambodia	114	0	0	0	**114**
Laos	8	0	0	0	**8**
Malaysia	54	0	1	1	**56**
Myanmar	3	0	0	0	**3**
Thailand	236	13	7	0	**256**
Viet Nam	15	9	0	0	**24**
Total per month	**430**	**22**	**8**	**1**	**461**

Map 5: location of the ongoing FMD outbreaks occurring during April 2018 due to serotype A in the countries reported in Table 5. (Source – SEAFMD Campaign)

Map 6: location of the ongoing FMD outbreaks last reported in 2007 in Vietnam due to serotype Asia 1. (Source – SEAFMD Campaign)

Map 7: location of the ongoing FMD outbreaks occurring during April 2018 due to serotype O in the countries reported in Table 6. (Source – SEAFMD Campaign)



Vietnam [2]

FMDV serotypes A and O were detected in the pig, cattle and buffalo samples collected between June 2016 and January 2018. A summary of the distribution of the serotypes in the various species is reported in Table 5.

In the pig samples, only FDMV serotype O was isolated.

A/ASIA/Sea-97, O/ME-SA/Ind-2001d and O/CATHAY are the most recent lineages, relative to the serotypes diagnosed in the above batch of samples that were detected in this country.

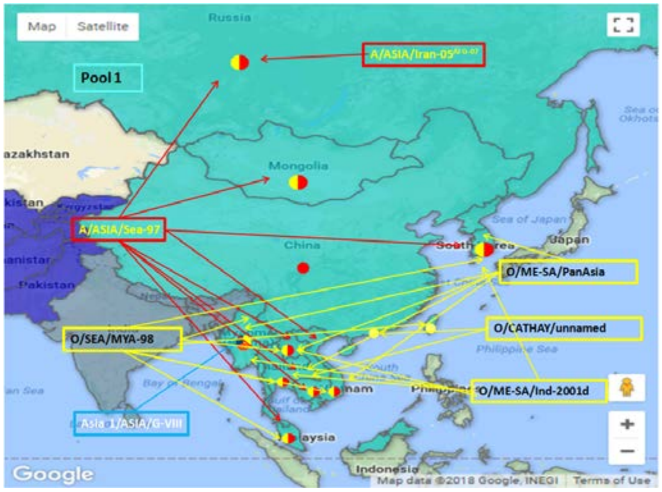
Table 5: summary of the serotyping results of the pig, cattle and buffalo samples collected between June 2016 and January 2018 in Vietnam (Source – WRLFMD)

	N° Serotypes (% of positives)				
Sample species	**A**	**O**	**FMDV genome detected**	**Virus detected without serotyping**	**Total samples**
buffalo	3 (23.08)	2 (10)	0	0	**5**
cattle	10 (76.92)	11 (55)	3	0	**24**
pigs	0 (0)	7 (35)	3	1	**11**
Total serotypes	**13 (39.39)**	**20 (60.61)**	**6**	**1**	**40**

Table 6: Summary of the history of FMD Pool 1 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2013 -2017 see Map 8 below. (Source – Wahis, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE between 2012 – 2016 **(1st semester 2016)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
Cambodia	PENDING/2013-2016 O, A/2016, NOT SAMPLED, (ASIA /2016)	Dec 2016/ A & O	**See text**
China	Data up to 1st semester 2015 2013 & 2015/A, 2012-2013/O, 2012 -2014/NOT TYPED	April 2018/O, May 2017/A	**See text**
China, Hong Kong, SAR	O	Nov 2017/O	**See text**
Democratic People's Republic of Korea	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	Data up to 1st semester 2015) A, O/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 –2016/O, 2013 & 2015/NOT TYPED	August 2016/A & O	**See text**
Mongolia	Disease Absent /2016**,	March2018/O, Sept 2016/A	**See text**

	2014 & 2015/O, 2013/A & NOT TYPED		
Myanmar	2012-2016/O, 2015/A & NOT TYPED	Dec 2017/O, April 2017/Asia 1, July 2016/ not typed, Oct 2015/A	**See text**
Republic of Korea	Data up to 1st semester 2015 2014 -2015/O, 2012-2013/DISEASE ABSENT	April 2018/A, Feb 2017/O	**See text**
Russian Federation	2013 – 2016**/A, 2012, 2014 & 2015/O	Feb 2018/O, Oct 2016/Asia 1, Jan 2016/ A	**See text**
Taiwan Province of China	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	O, NOT SAMPLED, NOT TYPED 2013-2016/A	November 2017/A, Jan 2018/O and not typed	**See text**



Map 8: 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, 10]:

- 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 [5]

FMDV O is still the serotype that is exclusively detected by ICAR-PDFMD in the samples examined this month, as from May 2015. The virus was detected using antigen and/or RNA detection among the eight bovine samples tested. Seven FMDV serotype O isolates were submitted for genotyping and ten other isolates belonging to the same serotype were subjected to vaccine matching tests. Serological testing was conducted on 1,880 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.

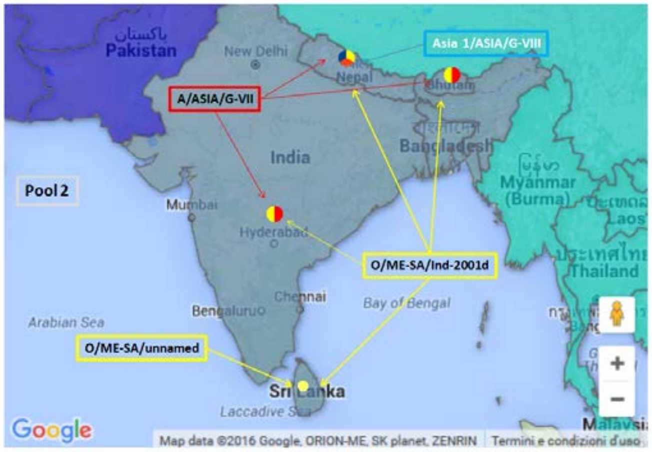
Table 7: Summary of the history of FMD Pool 2 between 2012– 2018. For geographic distribution of circulating FMDVs between 2013 -2017, see Map 9 below. (Source – WAHIS, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE between 2012 – 2016 **(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
Bangladesh	NO DATA AVAILABLE/2016, DISEASE PRESENT BUT WITHOUT QUANTITATIVE DATA	Dec 2016/A, ASIA 1 and O	Follow-up needed
Bhutan	2013-2016/O, NOT TYPED or NOT REPORTED 2013 & 2014/NOT SAMPLED	Sep 2017/untyped, July 2017/O, April 2017/A	Follow-up needed
India	NO DATA AVAILABLE/2016, O, A, NOT SAMPLED 2012-2014/Asia 1 2013/NOT TYPED	April 2018/O, Apr 2015/A Asia 1	**See text**
Mauritius	DISEASE ABSENT	Sep 2016/0	Follow-up needed
Nepal	O, 2012-2103/Asia 1	Mar 2018/O & Asia 1, April 2017/A	Follow-up needed
Sri Lanka	2015 -16/NO DATA REPORTED, 2012 – 2014/O	Sep 2017/O	Follow-up needed

Map 9: 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, 10]:

- O/ME-SA/Ind-2001d predominates (the O/ME-SA/Ind-2011 lineage that emerged during 2011 has not been detected during 2012-17), outbreaks of this serotype detected also in Mauritius during 2016 (**not reported in Map**)
- 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 – <u>West Eurasia & Middle East</u>

Afghanistan [4]

The CVDRL, Afghanistan reported for April 2018 the circulation of FMDV serotypes Asia 1 (n =1 sample) and O (n=4 samples). During the previous year, A/ASIA/Iran-$^{05FAR-11,\ 13}$ and O/ME-SA PanAsia-2^{ANT-10} were the lineages that were detected in the country for the serotypes reported for this month.

The laboratory has also forwarded a set of field samples to the WRLFMD that are currently being processed.

Iran [2]

FMDV serotypes A, ASIA 1 and O are the serotypes detected in 24 of the 25 sheep (n=1) and cattle (n=24) samples collected during the first two months of 2018. The genotyping results of these viruses are reported in Table 8, while locations are represented in Map 10.

Table 8: genotyping results of samples collected in various areas of Iran in January and February 2018 in sheep and cattle. (Source – WRLFMD)

Sample Identification	Location origin of sample	Host species	Date of collection	Genotype	Most Closely Related Viruses not belonging to the country - Seq id %	Host species
IRN/4/2018a	Mirjaveh, Sistan & Bluchestan	cattle	14/01/2018	**A/ASIA/Iran-05**$^{SIS-13}$	AFG/6/2017 (>96.1)	cattle
IRN/4/2018b	Mirjaveh, Sistan & Bluchestan		14/01/2018			
IRN/2/2018	Kerman		06/01/2018			
IRN/3/2018	Esfahan		09/01/2018		PAK/3/2016 (98.3)	
IRN/6/2018	Rafsanjan, Kerman		20/01/2018	**A/ASIA/Iran-05**$^{SIS-13}$	AFG/6/2017 (97.0)	
IRN/9/2018	Nazarabad, Alborz		24/01/2018	**A/ASIA/G-VII**	ARM/2/2015 (97.9)	
IRN/10/2018	Abyek, Qazvin		25/01/2018	**A/ASIA/Iran-05**$^{SIS-13}$	PAK/3/2016 (97.6)	
IRN/18/2018	Oskou, West Azerbaijan		01/02/2018		PAK/3/2016 (98.3)	
IRN/23/2018	BirJand, South Khorasan		12/02/2018		AFG/6/2017 (96.5)	
IRN/25/2018	Bokan, East Azerbaijan		23/02/2018	**A/ASIA/G-VII**	ARM/2/2015 (97.9)	
IRN/7/2018	Heris, West Azerbaijan	cattle	21/01/2018	**Asia 1/ASIA/Sindh-08**	PAK/35/2014 (97.3)	water buffalo
IRN/14/2018	Garmsar, Semnan		29/01/2018		PAK/27/2016 (96.7)	cattle
IRN/17/2018	Nazarabad, Alborz		01/02/2018		PAK/35/2014 (97.3)	water buffalo
IRN/19/2018	Jafariyeh, Qom		04/02/2018		PAK/27/2016 (96.7)	cattle
IRN/1/2018	Mashad, Razavi	cattle	03/01/2018	**O/ME-SA/PanAsia-2**$^{ANT-10}$	PAK/7/2016 (98.3)	cattle
IRN/8/2018	Kashan, Esfahan	sheep	22/01/2018	**O/ME-SA/PanAsia-2**$^{QOM-15}$	/	
IRN/11/2018	Savojbelagh, Alborz	cattle	26/01/2018			
IRN/12/2018	Lenjan, Esfahan		28/01/2018		KUW/2/2016 (98.7)	cattle
IRN/13/2018	Ahar, West Azerbaijan		28/01/2018		/	
IRN/15/2018	Qom, Qom		31/01/2018			
IRN/16/2018	Rey, Tehran		31/01/2018			
IRN/20/2018	Jafariyeh, Qom		05/02/2018			
IRN/21/2018	Qom, Qom		10/02/2018			
IRN/22/2018	Rey, Tehran		12/02/2018			
IRN/24/2018	Qom, Qom		14/02/2018			

Map 10: location of the genotyped FMDV samples collected in various areas of Iran in January and February 2018 in sheep and in cattle samples in Iran. (Source – WRLFMD, Google Fusion Maps)

Israel [1]

Further to the FMD serotype O outbreak of April 4th 2018, in free ranging cattle at Hazafon, that had presented clinical signs in all age categories, new episodes of the disease were registered on April 26th 2018 in a dairy farm unit and in two free ranging beef herds present the same area.

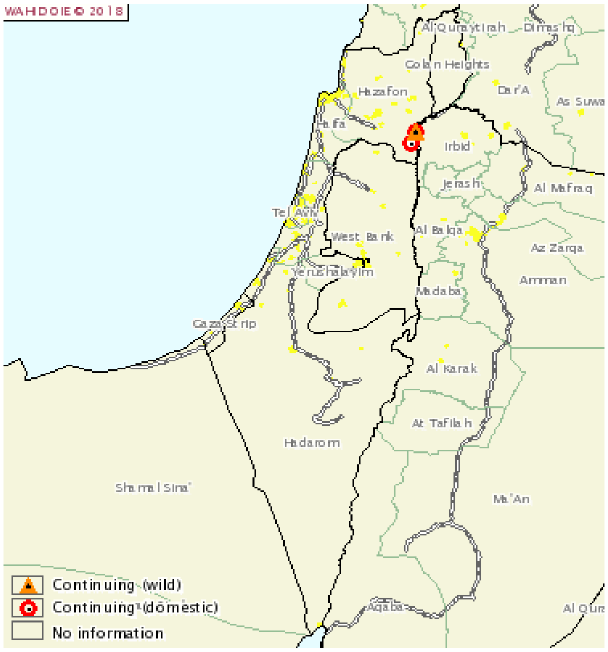
Apart from domestic species, the infection was also observed on April 26th 2018 in mountain gazelles (Gazella gazelle) of the national park at Nahal Tavor, Yizreel, Hazafon.

FMD was confirmed in these animals by the Kimron Veterinary Institute, Foot and mouth disease Laboratory (National laboratory) by cell culture isolation on April 29th 2018.

The number of animals involved in these events is unknown as also the source of infection, and for this, an epidemiological investigation is ongoing. The number of animals present and affected on the different farms is not reported while the location of the outbreaks is shown in Map 11.

Sanitary measures in place for the containment of infection are movement control inside the country, vaccination in response to the outbreaks, surveillance outside containment and/or protection zone, surveillance within containment and/or protection zone, quarantine, zoning, while no treatment is being administered to the affected animals.

Map 11: location of the FMD outbreaks that occurred on April 24th and 26th 2018 at Hazafon. (Source – WAHIS)



Pakistan [5]

At current, the FMD control project in Pakistan is operated only in Punjab and information relative to other areas of the country is provided on a voluntarily basis.

For the reporting month, 34 FMD outbreaks due to serotypes A, Asia 1 and O were detected in different districts of Punjub. A summary of the distribution of the outbreaks relative to locations and serotypes are represented in Table 9 and Map 12.

Punjab is also continuing its emergency and preventive vaccinations with the respective administration of 2,175 and 1,880,025 76,425 doses. A summary of the doses administered in the different districts of Punjab are reported in Table 10.

Table 9: summary of the FMD outbreaks reported in Pakistan during April 2018. (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator)

Province	District	Number Outbreaks	N° of Outbreaks (%) due to FMD Virus Serotype(s)			
			'O'	'A'	'Asia-1'	Un-Typed
Punjab	Jhelum	4	4	--	--	--
	Rawalpindi	1	1	--	--	--
	Rahim Yar Khan	2	1	1	--	--
	Sargodha	3	1	2	--	--
	Mianwali	2	0	2	--	--
	Chiniot	1	1	--	--	--
	Chakwal	6	6	--	--	--
	Faisalabad	1	0	1	--	--
	Jhang	3	2	--	--	1
	Kasur	1	0	1	--	--
	Lahore	3	1	1	--	1
	Muzaffargarh	6	0	4	2	--
	Shaikhupura	1	1	--	--	--
Total (%)		**34**	**18 (52.9)**	**12 (35.3)**	**2 (5.9)**	**2 (5.9)**

Map 12: location of the FMD outbreaks reported in Punjub, Pakistan during April 2018. (Source – Google Fusion Maps, Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator)

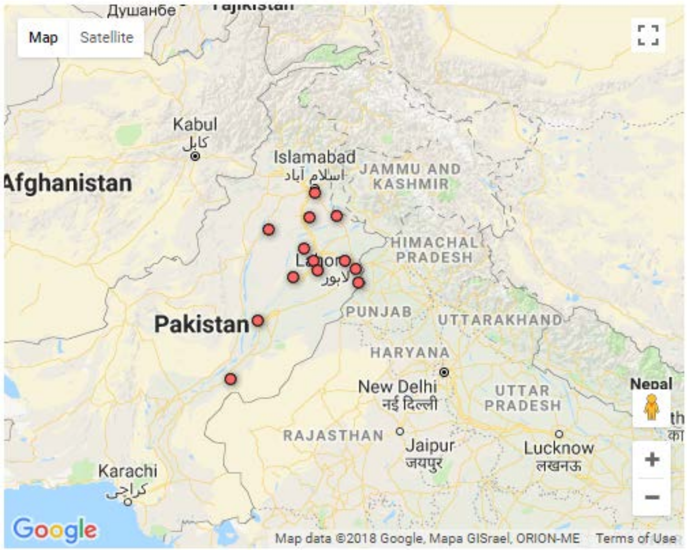


Table 10: summary of the preventive vaccination activities conducted in the province of Punjab, Pakistan during April 2018. (Source – Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Muhammad Afzal*, Project Coordinator)

District	No. of Households	Animals Vaccinated (6 Monthly Dose)		
		Cattles	Buffaloes	Total
Okara	73,856	178,835	246,544	425,379
Sahiwal	1,986	13,897	13,249	27,146
Vehari	53,944	379,727	289,836	669,563
Pakpattan	24,624	103,838	133,976	237,814
Bahawalnagar	52,280	222,096	298,027	520,123
Punjab	**206,690**	**898,393**	**981,632**	**1,880,025**

Table 11: Summary of the history of FMD Pool 3 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2012 -2016, see Map 13 below. (Source – Wahis, EuFMD Global Monthly Report)

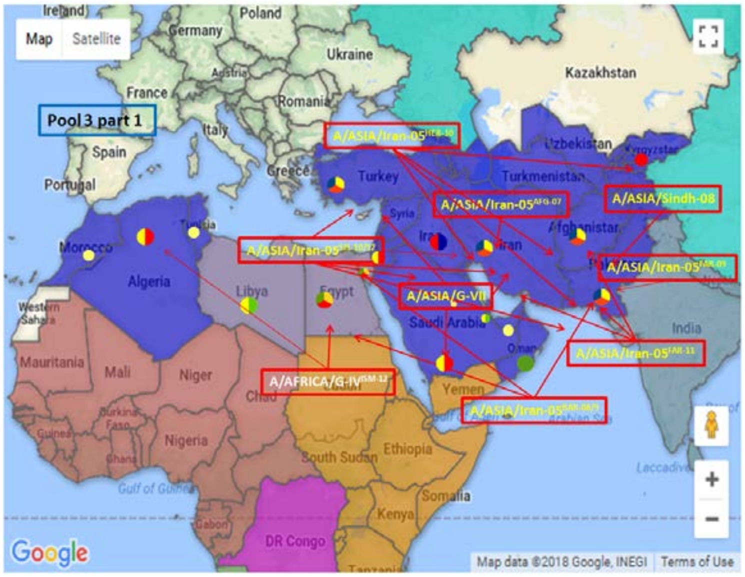
COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 – 2016 **(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
Afghanistan	2013-2016**/O, A, Asia 1, NOT TYPED 2012/SEROTYPE NOT REPORTED	Mar 2018/A, April 2018/Asia 1 & O,	**See Text**
Algeria	Data available up to 1st semester 2015 2014 -2015/O	Apr 2017/A, Apr 2015/O	Follow –up needed
Armenia	2015 -2016**/A , 2012-2014/DISEASE ABSENT	Dec 2015/A	Follow –up needed
Azerbaijan	DISEASE ABSENT	2007/0	Follow –up needed
Bahrain	DISEASE ABSENT/2016, 2012, 2014 &2015 /O	Mar 2015/O	Follow –up needed
Egypt	2012, 2014, 2016**/SAT 2 2012 – 2016**/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)	2012-2016/A, Asia 1 & O	Feb 2018/A, Asia 1& O,	**See text**
Iraq	2015-16/O, 2012-2016/A 2015/ SEROTYPE NOT REPORTED, 2012-13	Dec 2013/A, ASIA 1	Follow –up needed
Israel	2012-2015**/O	April 2018/O, June2017/A	**See text**
Jordan	DISEASE ABSENT	Mar 2017/O, 2006/A	Follow –up needed
Kazakhstan	2014-2016**/ DISEASE ABSENT, 2012/O,2012 –2013/A	Jun 2013/ A & Aug 2012/O	Follow –up needed
Kuwait	O/2016 2013 – 2014/ DISEASE ABSENT, 2012/O	April 2016/O	Follow –up needed
Kyrgyzstan	2015 -16/ DISEASE ABSENT, 2012-2014/O, A	Aug 2014/not typed & Apr 2013 /O, A,	Follow –up needed
Lebanon	DISEASE ABSENT/2016**, 2015/ NO DATA REPORTED	2010/not typed	Follow –up needed
Libya	NO DATA REPORTED	Oct 2013/O	Follow –up needed
Morocco	2012-14,2016**/DISEASE ABSENT, O/2015	Oct 2015/O	Follow –up needed
Oman	2016/ NO DATA REPORTED, 2012-2015/O	May 2015/SAT 2	Follow –up needed
Pakistan	2012 & 2015-16/ NO DATA REPORTED 2013-2014/A, ASIA 1 & O	April 2018/ A, Asia 1 & O	**See text**
Palestine	O, 2012-2013/SAT 2	Dec 2017/O, untyped Mar 2013/Sat 2	Follow –up needed
Qatar	NO DATA AVAILABLE/2016 2012-2015/O	Dec 2013/O	Follow –up needed
Saudi Arabia	2012-2014, 2016**/O	Oct 2016/A & April 2016/O	Follow –up needed

	A/2015		
Syrian Arab Republic	DISEASE ABSENT**	2002/ A & O	Follow –up needed
Tajikistan	2016/ NO DATA REPORTED 2014-2015**/DISEASE ABSENT 2012- 2013/NOT TYPED	Nov 2012/ not typed & Nov 2011/Asia 1,	Follow –up needed
Tunisia	2015-16**/ DISEASE ABSENT, 2014/O	April 2017/A, Oct 2014/O	Follow –up needed
Turkey	A & O, NOT TYPED Asia 1/2012-15	Oct 2015/ A May, 2014-2015/ Asia 1 and O	Follow –up needed
Turkmenistan	2013-2016**/DISEASE ABSENT, 2012/NO DATA REPORTED	Not available	Follow –up needed
United Arab Emirates	O/2016 2012, 2015/DISEASE ABSENT 2013-2014/O	Sep 2016/O	Follow –up needed
Uzbekistan	2012,2013 & 2015/NO DATA REPORTED 2014/DISEASE ABSENT	Not available	Follow –up needed

Map 13: 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)

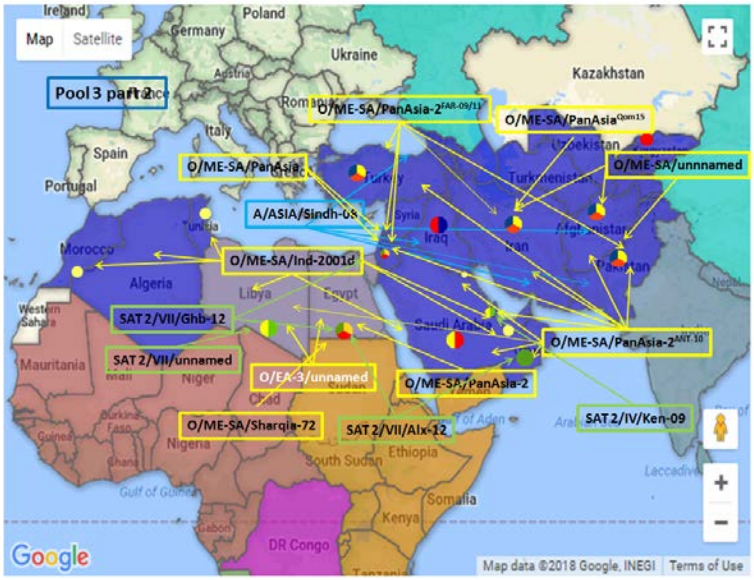
Conjectured circulating FMDV serotype A and Asia 1 lineages in Pool 3 [1, 10]:

- 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-2QOM-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*

Democratic Republic of Congo [1]

A series of FMD outbreaks, affecting cattle farms in Uvira, Sud-Kivu for which serotyping was not carried out were reported during April 2018 as having occurred during the previous May and June 2017. While the disease was already present in Sud-Kivu, this is the first occurrence in Uvira.

Although all age categories and sexes were clinically involved, the young age category and those of exotic breed were the mostly affected animals. The outbreaks were caused by the introduction of new live animals and the illegal movement of animals.

Control measures in place are movement control inside the country, surveillance within and outside the containment and/or protection zone, quarantine, zoning, vaccination permitted, if a suitable vaccine exists.

A summary of the animals involved and location of the outbreaks are reported in Table 12 and Map 14.

Map 14: location of the FMD outbreak that occurred during May and June 2017 affecting cattle farms in Uvira, Sud-Kivu. (Source – WAHIS)

Table 12: summary of the animals involved in the FMD that occurred during May and June 2017 affecting cattle farms in Uvira, Sud-Kivu. (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	3,813	428	7	0	0	11.22%	0.18%	1.64%	0.18%

Ethiopia [2, 6]

The National Animal Health Diagnostic and Investigation Center (NAHDIC), Ethiopia reported for April 2018 the detection of FMDV serotypes O and SAT 2, using antigen detection ELISA, in 27 swab and tissue samples collected from four cattle outbreaks.

Of the 28 bovine samples collected in the country between June 2017 and February 2018, FMDV serotype A (n –7 25%), O (n=11-39.3%) and SAT 2 (n= 1-3.6%) were detected by antigen ELISA. The remaining nine samples were either virus negative (n= 2-7.1%) or only PCR positive (n= 7 – 25%). A summary of the genotyping results are reported in Table 13 and location of collection of FMD positive samples is represented on Map 15.

Table 13: genotyping results of samples collected in various areas of Ethiopia between June 2017 and February 2018 in cattle. (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
ETH/8/2017	La'ilay Adiyabo, Northwestern Zone, Tigray	27/06/2017	**A/AFRICA/G-IV**	SUD/3/2006 (91.9)	cattle
ETH/9/2017	La'ilay Adiyabo, Northwestern Zone, Tigray				
ETH/12/2017	Mekele, Western Zone, Tigray	18/11/2017			
ETH/1/2018	Meki, East Shewa Zone, Oromia	05/01/2018	**A/AFRICA/G-I**	TAN/26/2013 cattle(>95.6)	
ETH/2/2018	Meki, East Shewa Zone, Oromia				
ETH/3/2018	Meki, East Shewa Zone, Oromia				
ETH/6/2018	Meki, East Shewa Zone, Oromia				
ETH/10/2017	Este, South Gondar Zone, Amhara	24/10/2017	**O/EA-3**	EGY/9/2016 (98.6)	
ETH/17/2017	Kewet, North Shewa Zone, Amhara	20/12/2017		Ismailia 2/Egy/2016 (98.1)	
ETH/7/2018	Kewet, North Shewa Zone, Amhara	24/01/2018		Ismailia 2/Egy/2016 (98.1)	
ETH/8/2018	Kewet, North Shewa Zone, Amhara	24/01/2018		Ismailia 2/Egy/2016 (98.4)	
ETH/9/2018	Kewet, North Shewa Zone, Amhara			Ismailia 2/Egy/2016 (98.9)	
ETH/10/2018	Kewet, North Shewa Zone, Amhara			Ismailia 2/Egy/2016 (98.1)	
ETH/12/2018	Albeko, South Wollo Zone, Amhara	31/01/2018		Ismailia 2/Egy/2016 (98.3)	
ETH/13/2018	Albeko, South Wollo Zone, Amhara			Ismailia 2/Egy/2016 (98.3)	
ETH/14/2018	Werrababu, South Wollo Zone, Amhara			Ismailia 2/Egy/2016 (97.9)	
ETH/15/2018	Werrababu, South Wollo Zone, Amhara			Ismailia 2/Egy/2016 (98.1)	
ETH/16/2018	Gaweta, Keffa Zone, SNNPR	01/02/2018		EGY/33/2017 (98.6)	
ETH/11/2018	Kafta Humera, Western Zone, Tigray	25/01/2018	**SAT/VII/Lib-12**	CAR/9/2012 (95.5)	

Map 15: location of the genotyped FMDV samples collected in various areas of Ethiopia between June 2017 and February 2018 in cattle. (Source – WRLFMD, Google Fusion Maps)

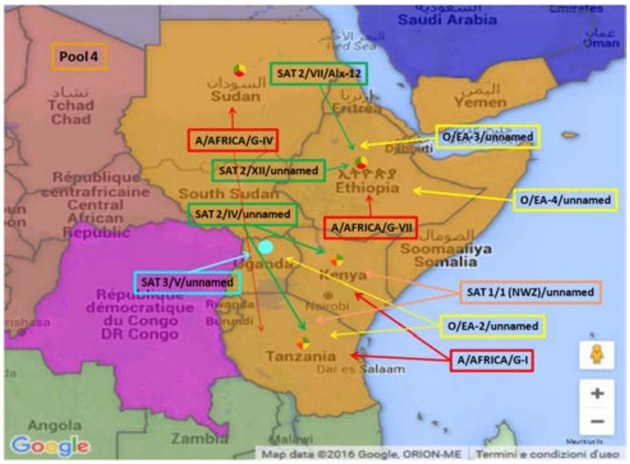
Kenya [7]
The FMD National Reference Laboratory, Embakasi, Kenya detected FMDV serotypes O and SAT 1 during the reporting month in the cattle samples collected from outbreaks where disease investigations were carried out.
Latest lineages detected in the country belonging to the serotypes reported for the current month are O EA-2 and SAT 1/I (NWZ).

Table 14: Summary of the history of FMD Pool 4 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2013 -2017, see Map 16 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 – 2016**/A, O, SAT 1	June 2017/not typed	**See text**
Djibouti	DISEASE ABSENT	Not available	Follow –up needed
Egypt	2012, 2014, 2016**/SAT 2 2012 – 2016**/O, A	May-Jun 2016/ O & Sat 2, March 2016/A, Aug 2016/typing pending	Follow –up needed
Eritrea	2014, 16/ DISEASE PRESENT 2015/ NO DATA REPORTED 2013/ DISEASE ABSENT, 2012/O	Nov 2016/not reported, Jan 2012/O	Follow –up needed
Ethiopia	O, 2015-16/SAT 1 2012 & 2105/SAT 2, 2012/A	April 2018/O & SAT 2 Feb 2018/SAT 1, Jan 2018/A	**See text**
Kenya	2012 – 2016 /NOT TYPED, A, O, SAT1, SAT2	April 2018/O & SAT 1, Nov 2017/A & SAT 2	**See text**
Libya	NO DATA REPORTED	Oct 2013/ O, Sat 2/Apr 2012	Follow-up needed
Rwanda	2015-16/NO DATA AVAILABLE 2012-2013/A, O, SAT1, SAT 2	Nov 2012/not typed	Typing required

Somalia	2012-13, 2015-16/DISEASE PRESENT, 2014/PENDING	June 2016/not reported	Follow –up needed
Sudan	2015-16 -16/A, SAT 1 & NOT SAMPLED, 2012-2014/O & NOT TYPED 2013/SAT 2,	Dec 2016/ not sampled, Oct 2016/O, Dec 2013/A, Jan 2014/SAT 2	Follow –up needed
South Sudan	2015/DISEASE PRESENT 2014/A, O SAT 1, SAT 2, SAT 3 2012-2013 & 2016 NO DATA REPORTED	2011	Follow –up needed
United Republic of Tanzania	2012-2016/A, O, SAT 1, SAT 2	Oct 2016/SAT 1, Aug 2016/O & SAT 2, Jun 2016/ A	Follow –up needed
Uganda	2016/NO DATA REPORTED 2013-16/NOT TYPED or NOT SAMPLED, 2012, 2015/ SAT 1,2012, 2014-15/O	May 2017/O Nov 2014/SAT1, Jan 2015/A and SAT 3, July 2015/ SAT 2 and untyped	Follow –up needed
Yemen	2015-16/NO DATA REPORTED 2013 – 2014/ DISEASE PRESENT BUT WITHOUT QUANTITATIVE DATA, 2012/O	2009/O	Follow –up needed

Map 16: 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, 10]:

- O (topotypes EA-2 (Tanzania, DR Congo & Uganda), EA-3 and EA-4 (Ethiopia)
- A/AFRICA (genotypes I (Kenya, Tanzania, D.R. Congo), VII (Ethiopia)
- SAT 1 (topotypes I (Kenya, Tanzania), IX (Ethiopia))
- SAT 2 (topotypes IV (Kenya, Tanzania), VII (Sudan, Egypt, Ethiopia), XII (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 [8]
LANAVET - Garoua, Cameroon detected FMDV in 13 (13.8%) of the 94 cattle samples tested during reporting month. The laboratory continues its collaborative research projects with the Ohio State University and Plum Island, USA.

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

Nigeria [9]

The FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria reported during April 2018, the presence of FMDV in a bovine sample examined using the lateral flow device test. The sample was collected at Barakin Ladi local government area in Plateau State. For location, see Map 17.

The most recent viral lineages reported by the WRLFMD for the country was in 2016 with the detection of O/WA, O/EA-3 and SAT1/X.

Map 17: location of where the FMDV bovine epithelial tissue was collected. (Source –NVRI, Nigeria, Google Fusion Maps)

Table 15: Summary of the history of FMD Pool 5 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2012 -2016, see Map 18 below. (Source – WAHIS, EuFMD Global Monthly Report)

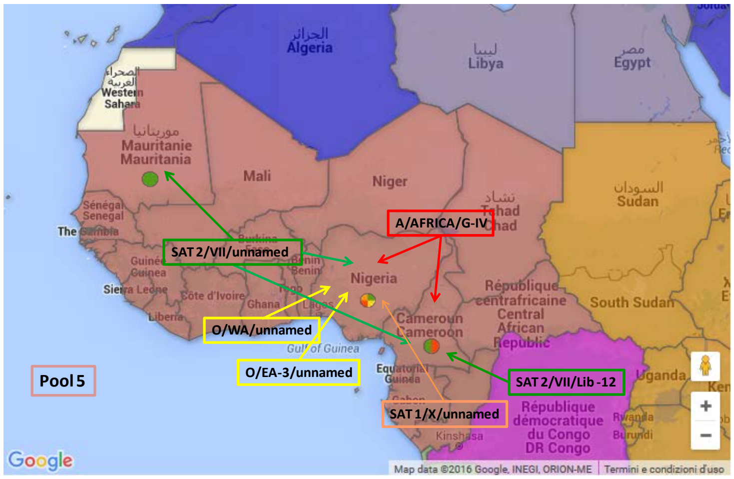
Country	**FMD history FMDV serotypes, reported to OIE in 2012 – 2016 **(1st semester)**	**Last outbreak reported/serotype** #see pg. 1	**Comment** (Genotyping would be useful for this region)
Benin	2016/NO DATA REPORTED A, O, SAT 1, SAT 2/2012-2015	Jun 2014/O, A, SAT 1, SAT 2	Follow –up needed
Burkina Faso	DISEASE PRESENT	Dec 2016/ not available	Follow –up needed
Cameroon	2016/NO DATA REPORTED DISEASE PRESENT	April 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/DISEASE PRESENT 2014-15/ DISEASE ABSENT 2012 – 2013/ DISEASE PRESENT	Aug 2016/Not reported	Follow –up needed

Democratic Republic of the Congo	2012 – 2016/A, O, SAT 1	Dec 2016/A, O & Sat 1	Typing required
Congo	NO DATA AVAILABLE	Jun 2013/not typed	Typing required
Côte d'Ivoire	2013-16/ not sampled or not reported, 2012/A,	Jul 2016/not reported	Follow –up needed
Equatorial Guinea	2014 – 2016/ NO DATA AVAILABLE 2012 – 2013/DISEASE SUSPECTED	Not available	Follow –up needed
Gabon	2012, 2014-16/DISEASE ABSENT 2013/NO DATA AVAILABLE	Not available	Follow –up needed
Gambia	NO DATA AVAILABLE	2012/O	Follow –up needed
Ghana	2016/NO DATA AVAILABLE 2012 – 2015/DISEASE PRESENT	Feb 2017/O, Dec 2016/ SAT 2 2014/not available	Follow –up needed
Guinea-Bissau	2015-16**/DISEASE SUSPECTED 2014/ DISEASE PRESENT 2012-2013/DISEASE ABSENT	Oct 2016/O Dec 2016/SAT1 & SAT 2	Follow –up needed
Guinea	2012-2013, 2015-16**/ DISEASE ABSENT 2014/ DISEASE PRESENT	2014/not available	Follow –up needed
Liberia	NO DATA AVAILABLE	Not available	Follow –up needed
Mali	2013, 2016/DISEASE PRESENT 2015/A, SAT 1 2014-2015/SAT 2 2012/ NO DATA AVAILABLE	Oct 2016/not reported	Follow –up needed
Mauritania	2016/DISEASE SUSPECTED, 2014-2015**/SAT 2, 2012-2013/NO REPORTED OUTBREAKS	Dec 2014/SAT 2	Follow –up needed
Niger	2016**/DISEASE PRESENT BUT WITH NO QUALITATIVE DATA, 2015/O 2012 – 2014/NOT SAMPLED	2014/not sampled, May 2015/O	Follow –up needed
Nigeria	2015-16/DISEASE PRESENT 2012-2014/O	April2018/untyped Mar 2018/ SAT 2 Feb Sept 2016/ O & SAT 1 Nov 2015/A	**See text**
Sao Tome Principe	2013-16/NO DATA AVAILABLE 2012/DISEASE ABSENT	Not available	Follow –up needed
Senegal	2015-16/DISEASE PRESENT 2012, 2014/NOT SAMPLED 2013/NO DATA AVAILABLE	Feb 2015/ A and O, 2014/ SAT 2	Follow –up needed
Sierra Leone	DISEASE ABSENT**	Oct 1958	Follow –up needed
Togo	O, SAT 1	2012/O	Follow –up needed

Map 18: 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 [10]:

- 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*

South Africa [14]

The Agriculture Research Council- Onderstepoort Veterinary Institute examined FMDV suspect samples that resulted PCR negative and 2,865 serum samples using liquid-phase blocking ELISA for the detection of FMDV serotypes SAT 1, SAT 2 and SAT 3 and 330 sera using FMD NSP ELISA.

Zambia [2]

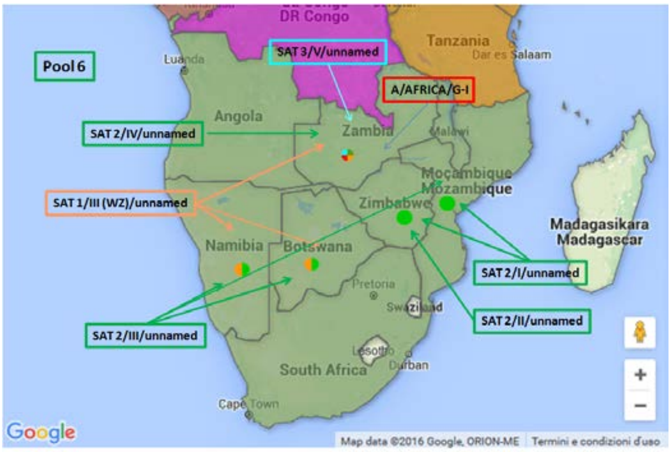
The three cattle samples collected in the country in March and April of this year were all positive for FMDV serotype O. The latest outbreaks that the country has experienced correspond to the time of collection of these samples.
The most recent viral lineage reported by the WRLFMD for the country was in 2017 with the detection of SAT3/II (WZ).

Table 16: Summary of the history of FMD Pool 6, 2013 – 2018, for geographic distribution see Map 19 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
Angola	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	2012-2016**/SAT 2 2014-2015/SAT 1	Sep 2017/SAT 2, June 2015/SAT 1	Follow –up needed
Democratic Republic of the Congo	2012 – 2016/A, O, SAT 1	Dec 2016/A, O & Sat 1	Follow –up needed
Malawi	2012/NO OUTBREAKS REPORTED	June 2016/SAT 1, Oct 2011,	Follow –up needed

	2013-2015/ NO DATA AVAILABLE		
Mozambique	2016**/ NO DATA AVAILABLE 2012 -2015/DISEASE ABSENT	Dec 2017/ Typing pending, Oct 2017/SAT 2, May 2015/ SAT 1	Follow –up needed
Namibia	2014-2016**/SAT 22012-2014/SAT 1	Sep 2017/SAT 2, Aug 2017/typing pending, May 2015/SAT 1	Follow –up needed
South Africa	2015-16**/SAT 3 2012-2015/SAT 2 2013/SAT 1	Oct 2017/SAT 1, May 2017/SAT 2 Dec 2015/SAT 3,	**See text**
Zambia	2016/SAT 3 & NOT TYPEC 2013-2014/ NO DATA AVAILABLE 2012/SAT 1, SAT 2	April 2018/ A, May 2017/SAT 3, Mar 2017/SAT 2, Jan 2013/SAT 1	**See text**
Zimbabwe	2012-2016/SAT 2 2014-15SAT 1 2013/SAT 3	Jan 2018/typing pending, May 2017/SAT 2, Aug 2015/ SAT 1, Jun 2013/SAT 3	Follow –up needed

Map 19: 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, 10]:

- 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

Rest of Latin America [2, 10, 11]

The OIE FMD status of the countries in South America as reported in December 2017 is presented in Map 20.

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/).

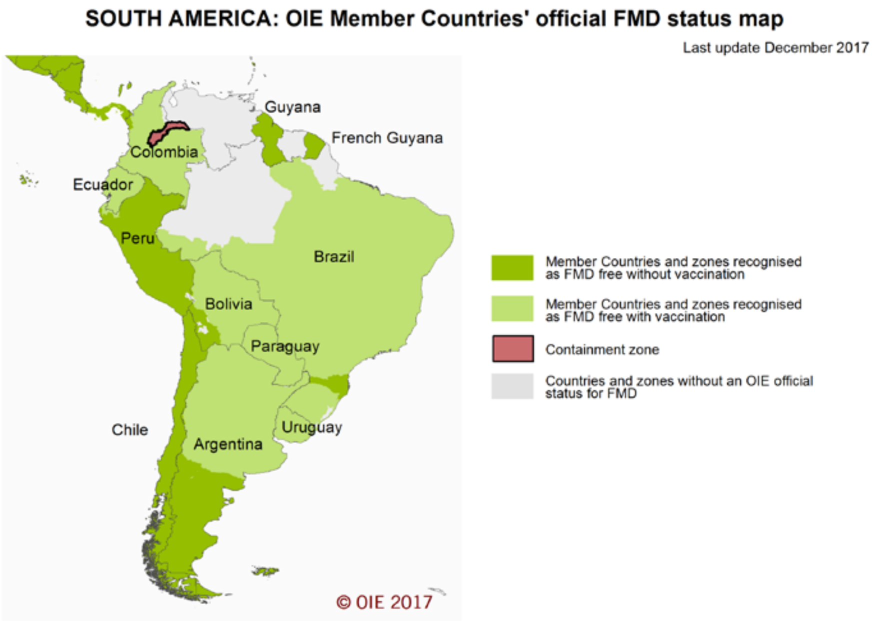
Small areas of the continent may still be considered as endemic but clinical cases are rare (Map 20). In fact, before the outbreak which occurred in Columbia, PANAFTOSA reported data for historical FMD outbreaks that occurred in

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 17.

Table 17: Summary of the history of FMD Pool 16 between 2012 – 2018, for geographic distribution see Map 20 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
Colombia	DISEASE ABSENT	July 2017/O	Follow –up needed
Venezuela (Bolivarian Republic of)	DISEASE ABSENT**	2011/O, 2013/A	National situation needs verification

Map 20: FMD status for South America (Source – OIE)



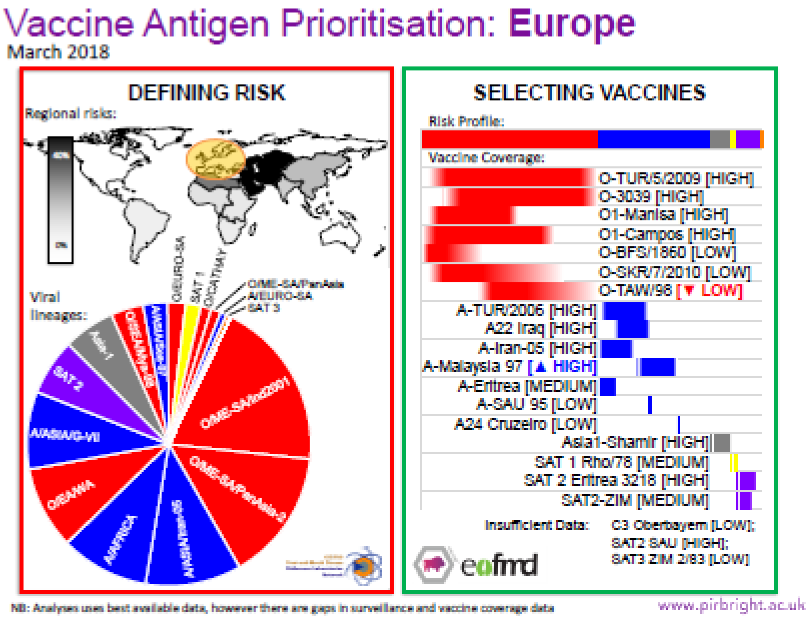
IV. OTHER NEWS:

[2]The 3rd WRLFMD Quarterly Report for the period January – March 2018 contains a new format for recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of this table is within the report. (Table 18)

Table 18: 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	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**
March 2018

NB: Analyses uses best available data, however there are gaps in surveillance and vaccine coverage data
www.pirbright.ac.uk

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

1. WAHID Interface – OIE World Animal Health Information Database http://web.oie.int/wahis/public.php?page=home
2. World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD), www.wrlfmd.org.
3. Project Directorate on Foot and Mouth Disease (PD-FMD), Indian Council of Agricultural Research, Mukteswar, India - *Dr. S. Saravanan*.
4. Central Veterinary Research and Development Laboratory (CVDRL), Aghanistan - *Dr. Ghulam,* Head of Laboratory.

5. Progressive Control of Foot and Mouth Disease in Pakistan, - *Dr. Manzoor Hussain*, National Project Director and *Dr. Muhammad Afzal*, Project Coordinator.
6. National animal health diagnostic and investigation center (NAHDIC), Ethiopia - *Dr. Daniel Gizaw.*
7. National FMD Reference Laboratory, Embakasi, Kenya – Dr. *Eunice Chepkwony Miss. Hellen Mutua.*
8. Laboratoire National Vétérinaire (LANAVET) - Garoua, Cameroon - *Dr. Simon Dickmu Jumbo*.
9. FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria - *Dr. Ularamu Hussaini.*
10. OIE/FAO FMD Reference Laboratory Network, Annual Report 2016.
11. 44a Reunión Ordinaria de la Comisión Sudamericana para la Lucha contra la Fiebre Aftosa - 6 – 8 March 2017, Rio de Janeiro, Brasil.
12. Regional Reference Laboratory for FMD (ARRIAH, Russia) - *Dr. S. Fomina.*
13. South East Asia FMD (SEAFMD) Campaign - http://www.arahis.oie.int/reports.php?site=seafmd.
14. ARC -Onderstepoort Veterinary Institute, Republic of South Africa - *Dr LE Heath/Ms E Kirkbride.*