JUNE 2017 MONTHLY REPORT FOOT-AND-MOUTH DISEASE SITUATION

European

Food and Agriculture Organization of the United Nations

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

June 2017

Guest Editor:
Dr. Donald King – WRLFMD, Pirbright, UK

#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.

Global Foot-and-Mouth Disease Situation

June 2017

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Guest Editor's comments:

I am pleased to be asked to write a few words to introduce this month's EuFMD update that describes new FMD outbreaks and changing patterns of FMD virus distribution. A common theme of "dynamic" FMD viral movements highlighted in previous reports has continued over the recent months. These encompass examples of unpredictable and long-distance (trans-regional) transmission of a number of different FMDV lineages (most notably the O/ME-SA/Ind-2001d lineage in North Africa, the Gulf States of the Middle East, Southeast and East Asia and Mauritius, but also involving the spread of other FMDV lineages into new geographical areas such as A/ASIA/G-VII, A/AFRICA/G-IV, O/EA-3, O/ME-SA/PanAsia and SAT 2/VII). During the past three months (since my last update), the WRLFMD has continued to monitor reports of FMD outbreaks in different endemic countries. New FMD cases in May in northern Israel (Hazafon) represent further onward spread of the A/ASIA/G-VII lineage (previously found in Iran, Turkey, Saudi Arabia and Armenia). In response to the earlier reports of poor performance of vaccine strains derived from the A/ASIA/Iran-05 strain against this lineage, WRLFMD (in partnership with the FMD Reference Laboratories in Lelystad (The Netherlands) and Geelong (Australia) has undertaken vaccine potency trials for alternative candidate vaccines; where preliminary data indicates that the A-May-97 vaccine may provide protection in cattle, in contrast to the A22 vaccine that does not appear to induce



Delegates of the 2-day workshop of EU National Reference Laboratories for FMD held in May 2017 (Surrey, UK)

a protective response (these data will be presented in more detail shortly). New FMD cases in Myanmar (due serotype Asia-1) are also epidemiologically important events; since these are the first cases due to this serotype in the country since 2005, and sequence data indicates that the causative virus is most closely related to viruses from Bangladesh. These data highlight the continued threats posed by all of the FMD lineages in the Indian sub-continent (similar patterns in southeast Asia recently reported for O/ME-SA/Ind-2001d). New outbreaks in Columbia (serotype O) represent the first clinical FMD cases anywhere in the South American continent since 2013 (in Venezuela). The emergence and circulation of novel strains within established endemic settings, and outbreaks in new countries inevitably heightens the risk of exotic incursions in FMD-free countries via global trade and movement of animals and animal products. An update on these recent events, and their potential impacts upon Europe were widely discussed at the annual NRL Workshop of EU Member States held in East Horsley, Surrey, UK in May 2017 (see https://www.eurl-fmd.org/annual-fmd-referencelaboratories-workshops for further details).

This EuFMD monthy updates provides a vital source of information to help define the global patterns of FMD. When considering the global burden of FMD, one of the greatest challenges is to define the the most-likely distribution of FMD in countries where the disease is only rarely (or never) reported! In response to these obvious gaps, the OIE/FAO FMD Laboratory Network has prepared conjectured status maps for different high priority FMD virus lineages – presented in the Annual Report of the Network (see http://www.foot-and-mouth.org/sites/foot/files/user-files/research-paper/pdf/07-

<u>17/FMD%20Laboratory%20Network%20Report%202016.pdf</u>. We anticipate that these maps will be reviewed on an annual basis to reflect new laboratory and field data (as well as non-official reports of FMD cases).

Don King, Pirbright, July 2017

I. GENERAL OVERVIEW

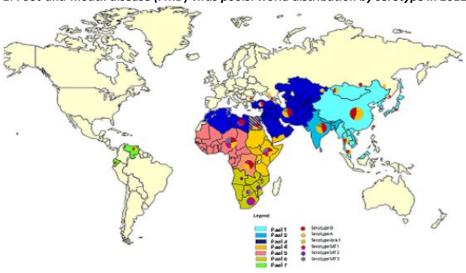
Pools represent independently circulating and evolving foot-and-mouth disease virus (FMDV) genotypes; within the pools, cycles of emergence and spread occur that usually affect multiple countries in the region. In the absence of specific reports, it should be assumed that the serotypes indicated below 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 2011 – 2016

POOL	REGION/COUNTRIES – colour pools as in Map	SEROTYPES
1	SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA Cambodia, China (People's Rep. of), China (Hong Kong, SAR), China (Taiwan Province), Korea (DPR), Korea (Rep. of), Laos PDR, Malaysia, Mongolia, Myanmar, Russian Federation, Thailand, Viet Nam	O, A and Asia 1
2	<u>SOUTH ASIA</u> Bangladesh, Bhutan, India, Mauritius, Nepal, Sri Lanka	O, A and Asia 1
3	WEST EURASIA & MIDDLE EAST Afghanistan, Algeria, Armenia, Azerbaijan, Bahrain, Bulgaria, Egypt, Georgia, Iran, 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	O, A and Asia 1
4	<u>EASTERN AFRICA</u> Burundi, Comoros, Congo D. R. , Djibouti, Egypt , Eritrea, Ethiopia, Kenya, Libya , Rwanda, Somalia, Sudan, South Sudan, Tanzania, Uganda, Yemen	O, A, SAT 1, SAT 2 and SAT 3
5	WEST/CENTRAL AFRICA Benin, Burkina Faso, Cameroon, Cape Verde, Central Afr. Rep., Chad, Congo D. R., Congo, Côte d'Ivoire, Equatorial Guinea, Gabon, Gambia, Ghana, Guinea Biss., 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	<u>SOUTH AMERICA</u> Paraguay, Venezuela	O and A

Egypt, Libya and **Congo D. R.** (highlighted in bold) are indicated as being in multiple pools, since they have evidence of FMDV originating from 2 or more pools in the past four years. * ONLY IN NORTH ZAMBIA AS SPILL-OVER FROM POOL 4

MAP 1: Foot-and-mouth disease (FMD) virus pools: world distribution by serotype in 2011-2016



II. HEADLINE NEWS

POOL 1- SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA

Laos 1 – All the FMDVs detected in samples collected from cattle during January 2017 were genotyped as O/SEA/Mya-98 by the WRLFMD.

Mongolia ¹ – FMDVs detected in bovine and sheep samples collected from 2015 to 2017 were respectively genotyped as A/ASIA/SEA-97, O/SEA/Mya-98 and O/ME-SA/PanAsia.

Myanmar ¹ – FMDVs detected in bovine samples collected between January and May 2017 were genotyped as Asia 1/ASIA/G-VIII and O/ME-SA/Ind-2001d.

Thailand ¹ - FMDVs detected in bovine and porcine samples collected from August 2016 to February 2017 were genotyped as A/ASIA/SEA-97 and O/SEA/Mya-98.

POOL 2 - SOUTH ASIA

India ² – The Indian Council of Agricultural Research - Directorate of Foot and Mouth Disease (ICAR-PDFMD), Mukteswar, India reported the detection of FMDV serotype O from the bovine samples tested using antigen and/or RNA detection assays.

POOL 3 - WEST EURASIA & MIDDLE EAST

Afghanistan ³ - During June 2017, FMDV serotypes A and O were detected in the 78 samples examined by the Central Veterinary Diagnostic and Research Laboratory (CVDRL), of Kabul Afghanistan.

Israel ^{1, 4} – FMDV A/ASIA/G-VII was confirmed by the WRLFMD in the bovine samples collected during the outbreak that occurred on the 1st of May 2017 at Aramsha, Acco, Hazafon.

A new FMD outbreak due to serotype O was registered in cattle at Ein Saala, Hadera, Haifa on the 29th of May 2017 which was reported as already resolved on the 13th of June 2017.

Pakistan ^{5, 6} – The Progressive Control of Foot and Mouth Disease Project UTF/PAK/139/PAK reported 15 FMD outbreaks occurring in some of the territories of the country. FMDV Asia 1 and O were the serotypes responsible for the present outbreaks. As the above-mentioned Project was completed, reporting from this country is currently on voluntary basis.

During the Progressive Control of Foot and Mouth Disease Project GCP/PAK/123/USA – Development of Technical Framework for Progressive Control of Foot and Mouth Disease in Pakistan, conducted from October 2015 to March 2017, 2,669 FMD outbreaks were detected.

Palestinian Auton. Territories ^{1,4} – FMDV O/EA-3 was the lineage detected in the sheep sample collected during the FMD outbreak, which occurred on 1st May 2017 at Hebron, Yatta, West Bank.

Two new FMD outbreaks for which serotyping is pending respectively occurred on the 29th of May at Hebron, Alberig, Dora, and on the 5th of June 2017 at West Bank, Salem, Nablus, West Bank involving small ruminant farms.

POOL 4 - EASTERN AFRICA

Ethiopia ^{1,7} – FMDV O/EA-4 was the only lineage detected in the 54 bovine samples collected in the country during 2016 and 2017.

Vaccine matching strain differentiation (VMSD) tests identified only one vaccine strain having good matching results with the two field isolates employed that respectively belonged to FMDV O/EA-3 and O/EA-4 genotypes.

The National Animal Health Diagnostic and Investigation Center (NAHDIC) detected FMDV serotype A in the bovine samples collected from an outbreak.

Kenya ⁸ - FMDV serotypes O, SAT 1 and SAT 2 were detected in the five bovine samples examined by the FMD National Reference Laboratory, Embakasi.

POOL 5 - WEST/CENTRAL AFRICA

No FMD outbreaks were reported for this region during June 2017.

POOL 6 - SOUTHERN AFRICA

Zimbabwe ¹ – A FMD outbreak due to serotype SAT 2 occurred on the 17th of May 2017 in cattle of the village of Nemangwe, Gokwe South, Midlands.

POOL 7 - SOUTH AMERICA

Columbia 4

A FMD outbreak due to serotype O occurred at La Marota, Curipao, Tame, Arauca, Columbia on the 11th of June 2017 involving beef cattle. Previous FMD episodes in the country occurred in 2009.

Rest of Latin America ^{4, 9, 15} - Last registered circulation of FMD in Latin America previous to the above-mentioned event was announced during the OIE/FAO FMD Laboratory Meeting held in November 2016, where PANAFTOSA reported sequence data for historical FMD outbreaks that occurred in Venezuela in 2013.

COUNTER

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

III. DETAILED POOL ANALYSIS

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

Laos 1

FMDVs detected in two samples collected from cattle during January 2017 were both genotyped as O/SEA/Mya-98 with most closely related sequence of field virus not pertaining to the country represented by that detected in Thailand in cattle during 2016 (TAI/50/2016) presented a high sequence identity (seq id) of 99.5%.

Reports by the WRLFMD of the circulation of the present genotype go back to 2007, while other genotypes belonging to the same serotype which were previously detected in the country are O/ME-SA/PanAsia, since 2006 and O/ME-SA/Ind-2001d, since 2015.

VMSD tests for O/SEA/Mya-98 were conducted on field isolate LAO/1/2013 where good matching results were obtained for vaccine strain O TAW/98 but not for O 3039, O Manisa and O/TUR/5/09. Location of field isolates is represented in Map 2.

Map 2: location of the field isolates collected in January 2017 in Laos and submitted for genotyping.



Mongolia 1

FMDV serotypes A and O were detected in ten of the sixteen samples collected between March 2015 and April 2017, of which one was from a sheep and the remaining from cattle.

Genotyping of the VP1 of the detected viruses identified the following lineages: A/ASIA/SEA-97 and O/SEA/Mya-98 and O/ME-SA/PanAsia. All the genotypes detected in the present batch of samples were already circulating in the country.

The most recent VMSD tests available were carried out on two of the most recently detected genotypes obtaining the following results:

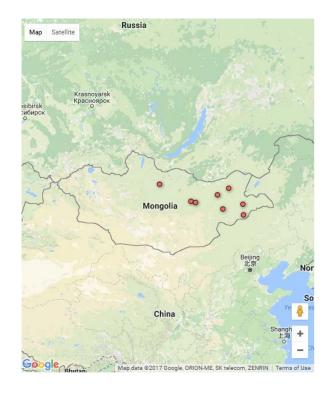
- For A/ASIA/SEA-97 conducted on field isolates A/MOG/11/2013 and A/MOG/13/2013 good matching results were obtained with vaccine strains A Iran05, A 22IRQ and A TUR/06.
- For O/SEA/Mya-98 conducted on field isolates O/MOG/2/2015 and O/MOG/5/2015, good matching results were obtained with vaccine strains O 3039 and O/TUR/5/2009 but not for O Manisa.

A summary of the genotyping results is reported in Table 2 and location of where the samples were collected is represented in Map 3.

Table 2: summary of genotyping results of FMDV isolates collected in Mongolia between March 2015 and April 2017.

Sample Identification	Location origin of sample	Date of collection	Host species	Genotype	Most Closely Related Viruses not belonging to the country (Seq id %)	Host species											
MOG/1/2016	Ulaanbaatar, Tuv, Baynjargalan	29/08/2016	cattle	A/ASIA/Sea-97	MYA/2/2015 (98.4)	cattle											
MOG/2/2016	Ulaanbaatar, Tuv, Bayan	20/09/2016	sheep	A/ A3IA/ 364-37	MYA/2/2015 (98.4)	cattle											
MOG/5/2015	Ulaanbaatar, Khovd, Bulgan	03/03/2015	cattle	O/SEA/Mya-98	MAY/2/2014 (99.4)	cattle											
MOG/6/2015	Ulaanbaatar, Sukhbaatar, Uulbayan	12/05/2015			VIT/13/2013 (98.1)	cattle											
MOG/1/2017	Ulaanbaatar, Sukhbaatar, Erdenetsagaan	28/01/2017	- cattle O/Me-SA/PanAsia -	,	,												
MOG/2/2017	Ulaanbaatar, Sukhbaatar, Erdenetsagaan	28/01/2017			l									l	O/Ma SA/DayAsia	,	/
MOG/3/2017	Ulaanbaatar, Dornod, Matad	31/01/2017		O/ Ivie-SA/ PanAsia	VIT/16/2011 (99.7)	water buffalo											
MOG/10/2017	Ulaanbaatar, Khentii, Batnorov	23/03/2017			/	/											
MOG/11/2017	Ulaanbaatar, Khentii, Batnorov	23/03/2017]					VIT/16/2011 (99.7)						
MOG/12/2017	Ulaanbaatar, Dornod, Tsagaan- Ovoo	03/04/2017			VIT/16/2011 (99.8)	water buffalo											

Map 3: location of the field isolates collected in Mongolia March 2015 and April 2017 and submitted for genotyping.



Myanmar ¹

FMDVs ASIA 1 and O were detected in four of the five bovine samples collected between January and May 2017. The VP1 of the detected viruses was genotyped as Asia 1/ASIA/G-VIII and as O/ME-SA/Ind-2001d. Of note is that the last detection of Asia 1 serotype in Pool 1 was in 2009 in China (People's Rep. of).

For Asia 1/ASIA/G-VIII, the most closely related sequence of a field virus not pertaining to the country is represented by that detected in cattle of Bangladesh (BAN GA Sr-187 2013) during 2013, with a seq id of 97.6%. For the viruses belonging to the O/ME-SA/Ind-2001d lineage, the most closely related sequence of a field isolates not pertaining to the country are those represented by the one detected in cattle of the Russian Federation (Zabaikalskiy/3/RUS/2016), with a seq id major then 99.4% and in cattle of Nepal (MYA/19/2017), with a seq id of 98.7%. Location of samples is reprorted in Map 4.

Map 4: location of the field isolates collected in Myanmar between January and May 2017 and submitted for genotyping. Yellow dot – FMDV Asia 1 Green dots – FMDV O



Thailand ¹

FMDVs were detected in all of the samples (one porcine and 27 bovine samples) collected between August 2016 and February 2017 and were genotyped as A/ASIA/SEA-97 and O/SEA/Mya-98.

A summary of the genotyping results of the FMDVs detected is reported in Table 3 and location of the samples collected is represented in Map 5.

Map 5: location of the field isolates collected in Thailand between August 2016 and February 2017 and submitted for genotyping. Yellow dots – A/ASIA/SEA-97 Green dots – O/SEA/Mya-98 Pink dots – both lineages



 Table 3: summary of genotyping results of FMDV isolates collected in Thailand between January and May 2017.

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
TAI/52/2016	Pathom		04/11/2016		VIT/62/2013 - 97.3	cattle
TAI/53/2016	Chiang Rai		08/11/2016		,	,
TAI/54/2016	Saraburi		11/11/2016		/	/
TAI/57/2016	Kanchanaburi		29/11/2016			
TAI/58/2016	Nakhon Ratchasima	cattle	30/11/2016	A/ASIA/SEA-97	Amur/2/RUS/2013 - 96.3	cattle
TAI/60/2016	Surin	Cattle	30/11/2016	A/ASIA/SEA-9/	VIT/58/2013 - 96.7	
TAI/2/2017	Nakhon Phanom		11/01/2017			
TAI/3/2017	Saraburi		13/01/2017			
TAI/4/2017	Nakhon		19/01/2017		/	/
TAI/4/2017	Ratchasima		19/01/2017			
TAI/5/2017	Songkhla		03/02/2017			
TAI/38/2016	Lamphun		03/08/2016			
TAI/39/2016	Sukhothai		03/08/2016			
TAI/40/2016	Chiang Mai		09/08/2016			
TAI/41/2016	Lamphun		09/08/2016			
TAI/42/2016	Chiang Rai		09/08/2016			
TAI/43/2016	Chiang Mai		09/08/2016			
TAI/44/2016	Lamphun		09/08/2016			
TAI/45/2016	Chiang Rai		15/08/2016			
TAI/46/2016	Chiang Mai	cattle	22/08/2016			
TAI/47/2016	Khon Kaen	Cattle	26/08/2016	O/SEA/Mya-98	/	/
TAI/48/2016	Phatthalung		29/08/2016			
TAI/49/2016	Phatthalung		01/09/2016			
TAI/50/2016	Sukhothai		02/09/2016			
TAI/51/2016	Lamphang		02/09/2016			
TAI/55/2016	Surin		28/11/2016			
TAI/56/2016	Nakhon		29/11/2016			
1A1/30/2016	Ratchasima		23/11/2010			
TAI/59/2016	Chaiyaphum		30/11/2016			
TAI/1/2017	Ratchaburi	swine	10/01/2017			

Table 4: Summary of the history of FMD Pool 1, 2012 – 2017, for geographic distribution see Map 6 below.

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 Cambodia O, A/2016, NOT SAMPLED, (ASIA /2016)		Follow-up needed
China (People's Rep. of)	Data up to 1 st semester 2015 2013 & 2015/A, 2012-2013/O, 2012 -2014/NOT TYPED	May 2017/A and O	Follow-up needed
China (Hong Kong, SAR)	China (Hong Kong, SAR)		Follow-up needed
China (Taiwan Province)	2016/NO DISEASE PRESENT A/2015, 2012-2013/O	Jun 2015/A	Follow-up needed

Korea (DPR)	O/2016 2012-2013/DISEASE ABSENT 2014 & 2015/ NO DATA REPORTED	May 2014/not confirmed, July 2014/O	Follow-up needed
Korea (Rep. of)	Data up to 1 st semester 2015 2014 -2015/O, 2012-2013/DISEASE ABSENT	Feb 2017/O & A	Follow-up needed
Laos PDR	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	Malaysia A/2016, 2012 –2016/O, 2013 & 2015/NOT TYPED		Follow-up needed
Mongolia	Disease Absent /2016**, 2014 & 2015/O, 2013/A & NOT TYPED	April 2017/O, Sept 2017/A,	See text
Myanmar	2012-2016/O, 2015/A & NOT TYPED	April 2017/Asia 1 & O, July 2016/ not typed, Oct 2015/A	See text
Russian Federation	2013 – 2016**/A, 2012, 2014 & 2015/O	Dec 2016/O, Oct 2016/Asia 1, Jan 2016/ A	Follow-up needed
Thailand	O, A NOT SAMPLED & NOT TYPED	Feb 2017 /A, Jan 2017/O June – July 2016/not typed	See text
Vietnam	O, NOT SAMPLED, NOT TYPED 2013-2016/A		Follow-up needed

Map 6: FMD distribution by serotype and topotype in South East Asia, 2012 – 2016 – white script in map refers to new introduction of viral lineage in pool or country of the pool during 2016.

Conjectured circulating FMD viral lineages in Pool 1 per 2016 $^{1,\,15}$:

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



B. POOL 2 - South Asia

India 2

The ICAR-PDFMD, Mukteswar, India reported that for the month of June 2017, FMDV serotype O was detected from nine bovine samples tested using antigen and/or RNA detection assays. Two isolates positive for this serotype were also submitted to genotyping. A total of 4,600 serum samples were tested for FMDV antibodies. The FMD diagnostic kits used for these analyses were those developed at ICAR-DFMD, Mukteswar.

The personnel of ICAR-PDFMD continue to be involved in the field investigations of FMD outbreaks and in providing expert advice to the Government and to the National and Local authorities. The institution is continuing its research studies and collaborations with international organisations.

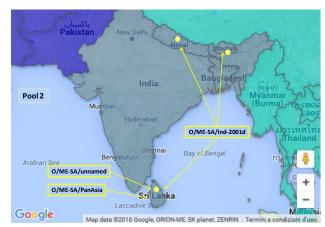
Table 5: Summary of the history of FMD Pool 2, 2012 – 2017, for geographic distribution see Map 7 below.

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	May 2017/Untyped, June 2016/O	Follow-up needed
India	NO DATA AVAILABLE/2016, O, A, NOT SAMPLED 2012-2014/Asia 1 2013/NOT TYPED	Jun 2017/O, Apr 2015/A Asia 1	See text
Mauritius	DISEASE ABSENT	Sep 2016/0	Follow-up needed
Nepal	O, 2012-2103/Asia 1	May 2017/O	Follow-up needed
Sri Lanka	2015 -16/NO DATA REPORTED, 2012 – 2014/O	2016/0	Follow-up needed

Map 7: FMD distribution by serotype and topotype in South Asia, 2012 – 2016 (EuFMD).

Conjectured circulating FMDV lineages in Pool 2 per 2016 ^{1, 15}:

- O/ME-SA/Ind-2001d predominates (the O/ME-SA/Ind-2011 lineage that emerged during 2011 has not been recognized during 2012-15), outbreaks of this serotype detected in Mauritius during 2016 (not reported in Map)
- O/ME-SA/PanAsia-2 (last detected in 2011 in Sri Lanka)
- A/ASIA/G-VII (genotype 18)
- Asia-1 (lineage C subdivided into Eastern and Western clusters)



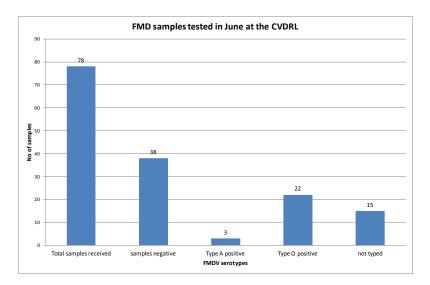
C. POOL 3 - West Eurasia & Middle East

Afghanistan³

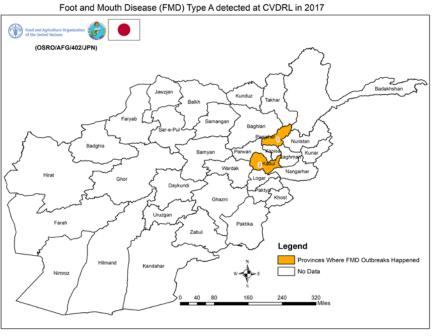
FMDV serotypes A and O were detected by the CVDRL of Kabul, Afghanistan in the 78 bovine samples, collected during June 2017 from the different provinces of the country. The relative distribution of the serotypes among the samples is reported in Graph 1.

Provinces in which FMDV serotypes were detected up to the present month of 2017 are presented in Maps 8 and 9. The laboratory is involved in providing expert advice to Government services national/local authorities and is also conducting collaborations with international organizations.

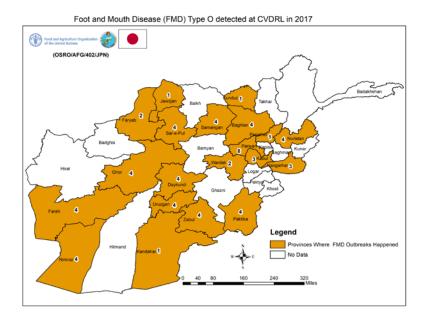
Graph 1: relative distribution of the FMDV serotypes among the samples 78 samples collected during June 2017 from the different provinces of Afghanistan.



Map 8: location of samples positive for FMDV serotype A that were detected at CVDRL, Afghanistan during 2017.



Map 9: location of samples positive for FMDV serotype O that were detected at CVDRL, Afghanistan during 2017.



Israel 1,4

The presence of the FMDV A/ASIA/G-VII lineage was confirmed by the WRLFMD in the bovine samples collected in the outbreaks involving two free ranging beef herds that occurred on the 1st of May 2017 at Aramsha, Acco, Hazafon. The most closely related field virus to the field strains isolated in Israel is represented by ARM/2/2015 with a seq id above 97.8%.

VMSD tests carried out on a FMDV field isolate, O/ISR/1/2017, belonging to viral lineage O/EA-3 that was responsible of the outbreaks that occurred in the country during February 2017, identified with the exception of O Manisa, vaccine strains O 3039 and O TUR/5/09 has those having good matching results.

Following the outbreaks due to serotype O that occurred in February 2017, a new FMD event was registered on the 29th of May 2017 in cattle at Ein Saala, Hadera, Haifa. The event was reported as resolved on the 13th of June 2017. The Kimron Veterinary Institute, Foot and Mouth Disease Laboratory employing real-time PCR confirmed diagnosis on the same day of the notification of the outbreak.

The affected animals belonged to a free-ranging beef herd which had had undergone vaccination 6 months ago. The only adult cow showing clinical signs in which ulcers were observed was an unvaccinated animal. No mortality was registered.

Source of outbreak is unknown while the sanitary control measures employed for the control of the spread of the virus are the following: movement control inside the country, vaccination in response to the outbreak, screening, quarantine and zoning.

A summary of the animals involved in the outbreak and location of this event are reported in Table 6 and Map 10.

Table 6: summary of the animals involved in the FMD outbreak of the 25th of May 2017 at Ein Saala, Hadera, Haifa, Israel.

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	127	8	0	0	0	6.30%	0.00%	0.00%	0.00%

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

Map 10: location of the FMD outbreak of the 25th of May 2017 at Ein Saala, Hadera, Haifa, Israel.



Pakistan 5,6

The Progressive Control of Foot and Mouth Disease Project UTF/PAK/139/PAK reported 15 FMD outbreaks occurring in some of the territories of the country during the reporting month. FMDV Asia 1 and 0 were the serotypes responsible for the outbreaks. The location and number of outbreaks in the different provinces of the country per FMDV serotypes responsible for these events is reported in Table 7 and Map 11.

Ring vaccination was carried out with the administration of 300 doses in Azad Kashmir.

Map 11: location of the FMD outbreaks reported in Pakistan during June 2017.



Table 7: summary of the FMD outbreaks reported in Pakistan during June 2017.

Location o	of outbreaks	Number of	Number of outbreaks due to FMD Virus Serotype(s)			
Province	District	outbreaks	' O'	'Asia-1'	Un-Typed	
Azad Kashmir	Mirpur	13	12		1	
Duniah	Sahiwal	1		1		
Punjab	Sheikhupura	1		1		
Т	otal	15	12	2	1	

During the Progressive Control of Foot and Mouth Disease Project GCP/PAK/123/USA – Development of Technical Framework for Progressive Control of Foot and Mouth Disease in Pakistan, conducted from October 2015 to March 2017, a total of FMD 2,669 outbreaks were reported.

Samples from each outbreak were submitted to the diagnostic laboratories and the distribution of the various circulating serotypes was as following: serotype O (42.4 %), A (9.6 %) and Asia-1 (16.9 %). Outbreaks due to mixed infections, with two or more serotypes, were also detected (3.4 %) while 27.7 % of the outbreaks were found negative by the ELISA test.

Palestinian Auton. Territories 1,4

The field virus detected in the sheep sample collected during the FMD outbreak, which occurred on 1st May 2017 at Hebron, Yatta, West Bank was genotyped as a FMDV O/EA-3 with the closest related field virus not pertaining to the country represented by ISR/8/2017, isolated in cattle in Israel, with a seq id of 99.5%,.

Further to the outbreaks registered in May 2017, the country has again experienced two other outbreaks involving small ruminant farms that occurred on the 29th of May at Hebron, Alberig, Dora, and on the 5th of June 2017 at West Bank, Salem, Nablus, West Bank. While serotyping is pending, the Central Veterinary Laboratory confirmed the diagnosis employing real-time PCR, respectively on the 31st of May and on the 6th of June 2017. Source of infection is unknown and the control measures set up for the containment of the spread of the infection are as following: movement control inside the country, vaccination in response to the outbreaks, surveillance within and outside containment and/or protection zone, screening, traceability, quarantine, zoning and disinfection.

Table 9. summary of the animals involved in the EMD outbreaks of the 20th of May at Hebren. Alberia, Dara, and

A summary of the animals involved and location of the outbreaks are represented in Table 8 and Map 12.

Table 8: summary of the animals involved in the FMD outbreaks of the 29th of May at Hebron, Alberig, Dora, and on the 5th of June 2017 at West Bank, Salem, Nablus, West Bank, Palestinian Auton. Territories.

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Species	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Sheep / goats	120	36	0	0	0	Sheep / goats	30.00%	0.00%	0.00%	0.00%

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

Map 12: location of the FMD outbreaks of the 29th of May at Hebron, Alberig, Dora, and on the 5th of June 2017 at West Bank, Salem, Nablus, West Bank, Palestinian Auton. Territories.



Table 9: Summary of the history of FMD Pool 3, 2012 – 2017, for geographic distribution see Map 13 below.

	FMD HISTORY		
COUNTRY	FMDV serotypes, reported to OIE in 2012 – 2016 **(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
	2013-2016**/O, A, Asia 1, NOT TYPED	June 2017/A & O May	
Afghanistan	2012/SEROTYPE NOT REPORTED	June 2017/A, & O, May 2017/ Asia 1	See text
	Data available up to 1st semester	2017/ Asia 1	
Algeria	2015	Apr 2017/A, Apr 2015/O	Follow –up needed
Algeria	2013 2014 -2015/O	Apr 2017/A, Apr 2013/0	Tollow up liceaea
	2015 -2016**/A ,		
Armenia	2012-2014/DISEASE ABSENT	Dec 2015/A	Follow –up needed
Azerbaijan	DISEASE ABSENT	2007/0	Follow –up needed
-	DISEASE ABSENT/2016,	-	-
Bahrain	2012, 2014 &2015 /0	Mar 2015/O	Follow –up needed
		May-Jun 2016/ O & Sat 2,	
Egypt	2012, 2014, 2016**/SAT 2	March 2016/A, Aug	Follow –up needed
071	2012 – 2016**/O, A	2016/typing pending	
Georgia	DISEASE ABSENT	2001/ASIA 1	Follow –up needed
	2012-2016/A,	Feb 2017/A & O,	
Iran	Asia 1 & O	2013/Asia 1	Follow –up needed
	2015-16/O, 2012-2016/A		
Iraq	2015/ SEROTYPE NOT REPORTED,	Dec 2013/A, ASIA 1	Follow –up needed
	2012-13		·
Israel	2012-2015**/0	May 2017/A & O	See text
Jordan	DISEASE ABSENT	Mar 2017/O, 2006/A	Follow –up needed
WI-I+	2014-2016**/ DISEASE ABSENT,	L 2012 / A & A 2012 / O	Fallani na na adad
Kazakhstan	2012/O,2012 –2013/A	Jun 2013/ A & Aug 2012/O	Follow –up needed
	0/2016		
Kuwait	2013 – 2014/ DISEASE ABSENT,	April 2016/O	Follow –up needed
	2012/0		
Kyrgyzstan	2015 -16/ DISEASE ABSENT,	Aug 2014/not typed & Apr	Follow –up needed
Kyigyzstaii	2012-2014/O, A	2013 /O, A,	Tollow –up lieeded
Lebanon	DISEASE ABSENT/2016**,	2010/not typed	Follow –up needed
Lebanon	2015/ NO DATA REPORTED		•
Libya	NO DATA REPORTED	Oct 2013/O	Follow –up needed
Morocco	2012-14,2016**/DISEASE ABSENT,	Oct 2015/O	Follow –up needed
141010000	0/2015	000 2013/ 0	Tollow up liceaea
Oman	2016/ NO DATA REPORTED,	May 2015/SAT 2	Follow –up needed
	2012-2015/0	•	Tonon up necueu
Pakistan	2012 & 2015-16/ NO DATA REPORTED	Jun 2017/ Asia 1 & O,	See text
	2013-2014/A, ASIA 1 & O	May 2017/ A	000 10
	Ο,	Jun 2017/serotying pending	
Palestine	2012-2013/SAT 2	May 2017/O,	See text
	·	Mar 2013/Sat 2	
Qatar	NO DATA AVAILABLE/2016	Dec 2013/O	Follow –up needed
-	2012-2015/0	<u> </u>	•
Saudi Arabia	2012-2014, 2016**/O	Oct 2016/A & April 2016/O	See text
	A/2015	, ,	Follow –up needed
Syrian Arab	DISEASE ABSENT**	2002/ A & O	Follow –up needed
Republic		-	'

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	See text
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

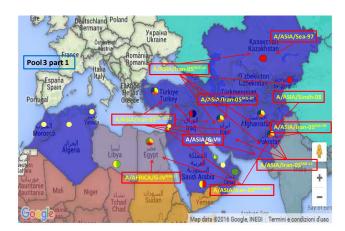
Map 13: FMD distribution by serotype and topotype for West Eurasia and Middle East, 2012 – 2016 (EuFMD) - white script in map refers to new introduction of viral lineage in pool or country of the pool during 2016.

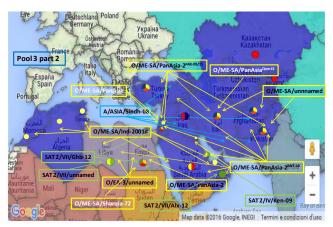
Conjectured circulating FMDV serotype A lineages in Pool 3 per 2016 ^{1, 15}:

- A/ASIA/Iran-05 (from AFG-07, HER 10, SIS-10/12, FAR-09/11 and BAR-08 sublineages)
- A/Asia/G-VII (recent incursion from South Asia - detected also in Iran in 2016)
- 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 and Lybia
- SAT 2/IV/Ken-09
- SAT 2/VII/Alx-12 and Ghb-12 sublineages





D. POOL 4 – Eastern Africa

Ethiopia 1,7

The National Animal Health Diagnostic and Investigation Center (NAHDIC) detected FMDV serotype A in the bovine samples collected from an outbreak.

Furthermore, 1,250 caprine and ovine sera were tested for FMD certification and 149 (11.92%) were found positive for FMDV antibodies.

The NAHDIC personnel was also involved in the preparation of a FMD control strategy design and control based on the Progressive Control Pathway strategy.

Futher to the above activities, FMDV O/EA-4 lineage was detected in 14 of the 54 bovine samples collected in the country between March 2016 and April 2017. The lineages clustered within two major groups and were all related to other field viruses pertaining to the country which were isolated during 2016. Location of where samples positive for FMDV were collected is presented in Map 14.

Vaccine matching strain differentiation (VMSD) tests conducted on two field isolates (O/ETH/11/206 and O/EHT/2/2017) that respectively belonged to genotypes O/EA-3 and O/EA-4on identified only O Tur 5/09, among the other vaccine strains used, i.e. O 3039 and O Manisa, as having good matching results.

Map 14: location of the FMDV positive samples collected in Ethiopia between March 2016 and April 2017 and submitted for genotyping.



Kenya⁸

FMDV serotypes O, SAT 1 and SAT 2 were detected in the three of the four bovine samples examined by the FMD National Reference Laboratory, Embakasi. The laboratory has ongoing collaborations with Sandia National Laboratories, USA.

Samples last forwarded by the country to the WRLFMD for genotyping was in 2013. The genotypes detected in relation to the serotypes reported this month were A/AFRICA/G-I and SAT 2/IV/unnamed from samples respectively collected in 2013 and 2012.

Table 10: Summary of the history of FMD Pool 4, 2012 – 2017, for geographic distribution see Map 15 below.

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
Congo d. R.	2012 – 2016**/A, O, SAT 1	Jun 2013/not typed	Typing required
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	Nov 2016/not reported,	Follow –up needed

	2015/ NO DATA REPORTED	Jan 2012/O		
	2013/ DISEASE ABSENT,	ŕ		
	2012/0			
Ethionia	O, 2015-16/SAT 1	Jun 2017/A, March 2017/O &	See text	
Ethiopia	2012 & 2105/SAT 2, 2012/A	SAT 1, May 2016/SAT 2	See text	
Kenya	2012 – 2016 /NOT TYPED,	Jun 2017/ O, SAT 1 & SAT 2,	See text	
Kenya	A, O, SAT1, SAT2	Jan 2016/ A		
Libya	NO DATA REPORTED	Oct 2013/ O, Sat 2/Apr 2012	Follow-up needed	
Rwanda	2015-16/NO DATA AVAILABLE	Nov 2012/not typed	Typing required	
Nwanaa	2012-2013/A, O, SAT1, SAT 2	1404 2012/110t typeu	Typing required	
	2012-13, 2015-16/DISEASE			
Somalia	PRESENT,	June 2016/not reported	Follow –up needed	
	2014/PENDING			
	2015-16 -16/A, SAT 1 & NOT Dec 2016/ not sampled, Oct			
Sudan	SAMPLED,	2016/O, Dec 2013/A,	Follow –up needed	
	2012-2014/O & NOT TYPED	Jan 2014/SAT 2	тополь ар постои	
	2013/SAT 2,	, ,		
	2015/DISEASE PRESENT			
	2014/A, O SAT 1, SAT 2, SAT 3	2011		
South Sudan	2012-2013 & 2016 NO DATA	2011	Follow –up needed	
	REPORTED			
		Oct 2016/SAT 1,		
Tanzania	2012-2016/A, O, SAT 1, SAT 2	Aug 2016/O & SAT 2,	Follow –up needed	
	, , , ,	Jun 2016/ A	·	
	2016/NO DATA REPORTED			
	2013-16/NOT TYPED or NOT	May 2014/O Nov 2014/SAT1,		
Uganda	SAMPLED,	Jan 2015/A and SAT 3, July	Follow –up needed	
	2012, 2015/ SAT 1,2012,	2015/ SAT 2 and untyped		
	2014-15/0			
	2015-16/NO DATA REPORTED			
Yemen	2013 – 2014/ DISEASE	2009/O	Fallow was ad	
remen	PRESENT BUT WITHOUT	2009/0	Follow –up needed	
	QUANTITATIVE DATA, 2012/O			

Map 15: FMD distribution by serotype and topotype for East Africa. 2011 – 2015 (EUFMD)

East Africa is known to be endemic for FMD, but available data is at present limited.

Conjectured circulating FMDV lineages in Pool 4 per 2015 2 $^{1,\,15}$:

- O (topotypes EA-2 (Kenya, Tanzania, DR Congo & Uganda), EA-3 (Egypt, Ethiopia, Eritrea, Kenya & Sudan) and EA-4 (Ethiopia, Kenya, Uganda).
- A/AFRICA (genotypes I (Kenya, Tanzania, D.R. Congo), IV (Sudan, Eritrea & Egypt) and VII (Ethiopia & Egypt))
- A/ASIA/Iran-05 BAR-08 sub-lineage (Egypt)
- 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 10, Ghana 11, Nigeria 12 and Senegal 13

The Laboratoire National Vétérinaire (LANAVET), Garoua, Cameroon, the ACCRA Veterinary Laboratory, Ghana and the Laboratoire National de l'Elevage et de Recherches Vétérinaires of Senegal reported that there were no communications or diagnostic confirmation of FMD outbreaks in the respective countries while the National Veterinary Research Institute Vom, Nigeria received a FMD suspect sample that is yet to be examined. The latter laboratory was also involved in outbreak investigations and in giving advice to the local farmers. OIE twining programme is still ongoing with between the laboratory and the CODA CERVA, Belgium.

Table 11: Summary of the history of FMD Pool 5, 2012 – 2017, for geographic distribution see Map 16 below.

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 2017/untyped, Nov 2014/O, SAT 2, May 2014/SAT 1, Apr 2014/ A	See text
Cape Verde	DISEASE ABSENT	Not available	Follow –up needed
Central Afr. Rep.	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
Congo D. R.	2012 – 2016/A, O, SAT 1	Dec 2016/A, O & Sat 1	Typing required
Congo R.	NO DATA AVAILABLE	Jun 2013/not typed	Typing required
Cote D'Ívoire	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	2012/0	Follow –up needed

		T	7	
	2016/NO DATA AVAILABLE	Dec 2016/ O & SAT 2		
Ghana	2012 – 2015/DISEASE	2014/not available	See text	
	PRESENT	2014/1100 available		
	2015-16**/DISEASE			
Guinea Biss.	SUSPECTED	Oct 2016/O	Follow –up needed	
Guinea Biss.	2014/ DISEASE PRESENT	Dec 2016/SAT1 &SAT 2	Follow –up fleeded	
	2012-2013/DISEASE ABSENT			
	2012-2013, 2015-16**/			
Guinea	DISEASE ABSENT	2014/not available	Follow –up needed	
	2014/ DISEASE PRESENT			
Liberia	NO DATA AVAILABLE	Not available	Follow –up needed	
	2013, 2016/DISEASE			
	PRESENT			
Mali	2015/A, SAT 1	Oct 2016/not reported	Follow –up needed	
	2014-2015/SAT 2			
	2012/ NO DATA AVAILABLE			
	2016/DISEASE SUSPECTED,			
NAi-	2014-2015**/SAT 2,	Doc 2014/SAT 2	Follow up pooded	
Mauritania	2012-2013/NO REPORTED	Dec 2014/SAT 2	Follow –up needed	
	OUTBREAKS			
	2016**/DISEASE PRESENT			
Nimon	BUT WITH NO QUALITATIVE	2014/not sampled, May	Fallow was and d	
Niger	DATA, 2015/O	2015/O	Follow –up needed	
	2012 – 2014/NOT SAMPLED			
	201E 16/DISEASE DRESENT	Feb 2017/not typed		
Nigeria	2015-16/DISEASE PRESENT	Sept 2016/ O & SAT 1 Nov	See text	
	2012-2014/0	2015/A, Sept 2014/ SAT 2		
Sao Tomo	2013-16/NO DATA			
Sao Tome	AVAILABLE 2012/DISEASE	Not available	Follow –up needed	
Principe	ABSENT			
	2015-16/DISEASE PRESENT	Fob 2015 / A and O 2014 /		
Senegal	2012, 2014/NOT SAMPLED	Feb 2015/ A and O, 2014/	See text	
	2013/NO DATA AVAILABLE	SAT 2		
Sierra Leone	DISEASE ABSENT**	Oct 1958	Follow –up needed	
Togo	O, SAT 1	2012/0	Follow –up needed	

Map 16: FMD distribution by serotype and topotypes for West Africa, 2012 – 2015 (EuFMD) - white script in map refers to new introduction of viral lineage in pool or country of the pool during 2016.

Conjectured circulating FMDV lineages in Pool 5 per 2016 ^{1, 15}:

- 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

Republic of South Africa 14

All of the 35 suspect samples examined in PCR by the ARC- Onderstepoort Veterinary Institute resulted negative. The laboratory also examined 3,588 serum samples using liquid-phase blocking ELISA for the detection of FMDV serotypes SAT 1, SAT 2 and SAT 3 and 472 sera using FMD NSP ELISA. The ARC-Onderstepoort Veterinary Institute is continuing its collaboration with international organisations on research projects.

Zimbabwe ¹

A FMD outbreak due to serotype SAT 2 occurred on the 17th of May 2017 in cattle of the village of Nemangwe, Gokwe South, Midlands. Fourteen cases were reported in the cattle herd that was at a dip tank, of Gokwe South. Illegal cattle movement and contact with infected animals at grazing and watering points are thought to be responsible for the spread of infection. Weekly inspections are being conducted in the infected and neighbouring areas. No other cases were reported from other outbreak areas. Roadblocks remain in place to control movement of cattle and also to distribute awareness material on the control of FMD.

A summary of the animals involved in the outbreak and location of this are respectively reported in Table 12 and Map 17.

Control measures adopted for the control of the spread of the disease consist in movement control inside the country, traceability, quarantine and surveillance outside containment and/or protection zone. Vaccination in response to the outbreaks was carried out in 1000 animals of the infected and neighbouring farms with a 28-day booster.

Table 12: summary of the animals involved in the FMD outbreak of the 17th of May 2017 in cattle of the village of Nemangwe, Gokwe South, Midlands.

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	3,571	14	0	0	0	0.39%	0.00%	0.00%	0.00%

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

Map 17: location of the FMD outbreak of the 17th of May 2017 in cattle of the village of Nemangwe, Gokwe South, Midlands.

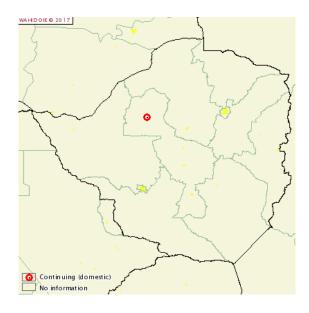


Table 13: Summary of the history of FMD Pool 6, 2012 – 2017, for geographic distribution see Map 18 below.

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	Jun 2015/typing pending July 2015/SAT 2, June 2015/SAT 1	Follow –up needed
Congo D. R.	2012 – 2016/A, O, SAT 1	Dec 2016/A, O & Sat 1	Typing required
Malawi	2012/NO OUTBREAKS REPORTED 2013-2015/ NO DATA AVAILABLE	Oct 2011, Sep 2015/serotyping pending	Follow –up needed
Mozambique	2016**/ NO DATA AVAILABLE 2012 -2015/DISEASE ABSENT	Dec 2016/SAT 2, Sep 2016/ Typing pending, May 2015/ SAT 1	Follow –up needed
Namibia	2014-2016**/SAT 22012-2014/SAT 1	May 2015/SAT 1, Jun 2015/SAT 2, July/typing pending	Follow –up needed
South Africa	2015-16**/SAT 3 2012-2015/SAT 2 2013/SAT 1	Feb 2017/SAT 2 Dec 2015/SAT 3, Aug 2013/SAT 1	See text
2016/SAT 3 & NOT TYPEC Zambia 2013-2014/ NO DATA AVAILABLE 2012/SAT 1, SAT 2		Mar 2017/SAT 2, Jan 2013/SAT 1, Feb 2015/A, Mar 2016/SAT 3	Follow –up needed
Zimbabwe	2012-2016/SAT 2 2014-15SAT 1	May 2017/SAT 2, Aug 2015/ SAT 1, Jun 2013/SAT 3	See text

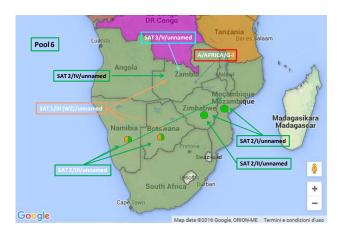
2013/SAT 3	

Map 18: FMD distribution by serotype and topotype for Southern Africa, 2012 – 2015 (EuFMD)

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 per 2015 ^{1, 15}:

- 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 4

After four years of absence of the detection of FMDV in the region, an outbreak that involved beef cattle occurred at La Marota, Curipao, Tame, Arauca, Columbia due to serotype O was notified on the 11th of June 2017. FMD free status with vaccination was suspended for the country.

On the 29th of June 2017 the outbreak was however already reported as resolved. The National Veterinary Diagnostic Laboratory confirmed the FMDV diagnosis on the 23rd of June 2017 using antigen detection ELISA and PCR. Previous FMD episodes in the country occurred in 2009 due to the serotype O.

An investigation is ongoing to identify the origin of the outbreak while the control measures adopted are as following, surveillance within and outside containment and/or protection zone, quarantine, disinfection and vaccination if available for the serotype responsible of the outbreak. Other measures to be adopted are movement control inside the country, traceability, official destruction of animal products and carcasses, by-products and waste, stamping out and zoning.

A summary of the animals involved and location of the outbreak is respectively represented in Table 14 and Map 19.

Table 14: summary of the animals involved in the FMD outbreak of the 11th of June 2017 in cattle at La Marota, Curipao, Tame, Arauca, Columbia.

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	136	7	0	136	0	5.15%	0.00%	0.00%	100.00%

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

Map 19: location of the FMD outbreak of the of the 11th of June 2017 in cattle at La Marota, Curipao, Tame, Arauca, Columbia.



Rest of Latin America 4, 9, 15

The OIE FMD status of the countries in South America as reported in June 2017 is presented in Map 15. Most South American countries are FMD free with vaccination (Uruguay) or without vaccination (Chile, Guyana) or with free zones with vaccination (Argentina, Bolivia, Brazil, Colombia, 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 15). In fact, further to the outbreak reported in Columbia, during the OIE/FAO FMD Laboratory Meeting held in November 2016, PANAFTOSA reported data for historical FMD outbreaks that occurred in Venezuela in 2013. The FMD history relative to the Region for 2012 –2017 is reported in Table 20.

Table 15: Summary of the history of FMD Pool 16, 2012 – 2017, for geographic distribution see Map 20 below.

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 2016**(1st semester)	LAST OUTBREAK REPORTED/SEROTYPE #see pg. 1	Comment	
Columbia	DISEASE ABSENT	June 2017/O	Follow –up needed	
Paraguay	DISEASE ABSENT	Dec 2011/O	Follow –up needed	
Venezuela	DISEASE ABSENT**	2011/O, 2013/ A	National situation needs verification	

Map 20: FMD status for South America 4



IV. OTHER NEWS:

¹The 2nd WRLFMD Quarterly Report for the period April – June 2017 the table below (Table 21) that contains a list of recommended FMDV strains for antigen banks of FMD-Free countries. The discussion of this table is within the report.

The WRLFMD is at present working to adopt a risk-based approach for identifying circulating FMDV lineages and relate these to priority vaccines for use in Europe and other FMD-free settings.

Table 21: Recommendations from WRLFMD® on FMD virus strains to be included in FMDV antigen banks (for FMD-free countries).

Note: Virus strains are NOT listed in order of importance

RECOMMENDATIONS FROM WRLFMD® ON FMD VIRUS STRAINS TO BE INCLUDED IN FMDV ANTIGEN BANKS (FOR FMD-FREE COUNTRIES)

June 2017:

Note: Virus strains are <u>NOT</u> listed in order of importance

	A/ASIA/G-VII(G-18)*
	O Manisa
	O PanAsia-2 (or equivalent)
High	Asia 1 Shamir
_	A Iran-05 (or A TUR 06)
Priority	A22 Iraq
	A24 Cruzeiro
	O BFS or Campos
	SAT 2 Saudi Arabia (or equivalent i.e. SAT 2 Eritrea)
	A Eritrea-98
	SAT 2 Zimbabwe
Medium	SAT 1 South Africa
	A Malaysia 97 (or Thal equivalent such as A/Sakolnakom/97)
Priority	A Argentina 2001
	O Taiwan 97 (pig-adapted strain or Philippine
	equivalent)
	A Iran '96
	A Iran '99
	A Iran 87 or A Saudi Arabia 23/86 (or equivalent)
Low	A15 Bangkok related strain
Driority	A87 Argentina related strain
Priority	C Noville
	SAT 2 Kenya
	SAT 1 Kenya
	SAT 3 Zimbabwe

Note: Discussions are currently underway to adopt a risk-based approach for different FMD viral lineages to identify priority vaccines for use in Europe and other FMD-free settings.

V. REFERENCES - Superscripts

- 1. World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD), www.wrlfmd.org.
- 2. Project Directorate on Foot and Mouth Disease (PD-FMD), Indian Council of Agricultural Research, Mukteswar, India *Dr. S. Saravanan*.
- 3. Central Veterinary Diagnostic and Research Laboratory (CVDRL), of Kabul Afghanistan Dr. Nazem Shirazi.
- 4. WAHID Interface OIE World Animal Health Information Database http://web.oie.int/wahis/public.php?page=home
- 5. Progressive Control of Foot and Mouth Disease in Pakistan, *Dr. Manzoor Hussain*, National Project Director and *Dr. Muhammad Afzal*, Project Coordinator.
- 6. Development of National Control Program for Foot and Mouth Disease in Pakistan TCP/PAK/3503, FAO Rome, Italy.

[&]quot;Recent In vitro data from WRLFMD for serotype A viruses from Saudi Arabia and Iran highlights an apparent gap in vaccines supplied by international manufacturers for this viral lineage.

- 7. National animal health diagnostic and investigation center (NAHDIC), Ethiopia Dr. Daniel Gizaw.
- 8. National FMD Reference Laboratory, Embakasi, Kenya Dr. Abraham Sangula, Dr. Kenneth Ketter.
- 9. 44a Reunión Ordinaria de la Comisión Sudamericana para la Lucha contra la Fiebre Aftosa 6 8 March 2017, Rio de Janeiro, Brasil.
- 10. Laboratoire National Vétérinaire (LANAVET) Garoua, Cameroon Dr. Simon Dickmu Jumbo.
- 11. ACCRA Veterinary Laboratory, Ghana Dr. Joseph Adongo Awuni.
- 12. FMD Research Centre, Virology Research Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria *Dr. Ularamu Hussaini*.
- 13. Laboratoire National de l'Elevage et de Recherches Vétérinaires (LNERV, Senegal) *Miss Mariame Diop and Dr. Moustapha Lô.*
- 14. ARC -Onderstepoort Veterinary Institute, Republic of South Africa Ms E. Kirkbride, Dr F. Maree, Dr L. E. Heath.
- 15. OIE/FAO FMD Reference Laboratory Network, Annual Report 2016