



November

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2018

MONTHLY REPORT  
FOOT-AND-MOUTH DISEASE SITUATION



Food and Agriculture  
Organization of the  
United Nations



European  
Commission

**eofmd**  
european commission for the  
control of foot-and-mouth disease

November 2018

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

**November 2018**

**Guest Editor:**  
**Fabrizio Rosso (EuFMD)**

**#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.***

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## Guest Editor's comments:

It is a great honour and pleasure to be invited as a Guest Editor of the Global Monthly Report (GMR), especially after some years of work within the EuFMD workplan - aimed at improving the preparedness of Europe against FMD and at reducing the risk of its incursion through improved FMD control in the European neighbourhood.

The Global Monthly Report is a useful tool for providing essential information on the distribution of FMD worldwide and for understanding its evolution within and across the regions.

The regional approach for controlling the disease, regularly promoted in international fora, should in fact commence from the regular **sharing of risk information** related to the occurrence of outbreaks, results of the genotyping and link between the different events reported. Additional information could then be shared between countries to improve the risk assessment and the response capacity. Such an example of a mutual agreement has been established between Turkey, Iran, Russian Federation and Transcaucasus countries in order to enable the availability of more risk information (e.g. outbreaks in border areas, vaccination coverage, vaccination performance and effectiveness) useful to regularly assess the FMD risk within the region. The developed system is regularly updated and will soon be improved in order to capture additional data connected to animal movements, animal and meat market prices.

The ability and possibility to better understand the **change of risk overtime** and foresee the threat of FMD incursion at regional level can definitely increase early detection capacity and rapid response. The FMDV genotype O/EA-3 which occurred in Algeria during 2017 (described in this GMR), has been recognised as similar to the strain identified in West Africa (Guinea, Gambia, Senegal, Mauritania, Cameroon) with a clear epidemiological link between the two areas. A better understanding of such links between and within different regions would improve the possibility to implement better risk based surveillance and control measures.

**Results of surveillance** are also an important source of information. Considering the recent incursions of FMD in North Africa (years 2014/15 – 2017 – 2018), Algeria-Tunisia-Morocco agreed to implement and share the results of a coordinated multi-country risk based surveillance aimed at verifying the silent circulation of the disease in the region. The surveillance that was carried out before the occurrence of outbreaks in Algeria (2018), was able to demonstrate the presence of FMDV circulation among the small ruminant population in Algeria and in some border areas of Morocco (with Algeria), and Tunisia (with Algeria and Libya).

With regards to other aspects of FMD control that require specific attention, considering that vaccination is one of the main tool used for the control of FMD in endemic settings as well as emergency measure, the capacity to **select vaccines** according to risk and assess their **quality and effectiveness** needs to be improved through the development of tools (such as the PRAGMATIST - Prioritisation of Antigen Management with International Surveillance Tool, developed by EuFMD and the WRL to assist risk managers to select which strains are most important to maintain in their vaccine bank) and through activities aimed at supporting the implementation of immunogenicity studies (e.g. studies recently/currently implemented in Georgia, Azerbaijan, Morocco and Tunisia).

Overall, improving national and regional capacity for the management of FMD through the development and delivery of **training programme** for national staff (face-to-face training and e-learning) allows the national veterinary services to gain a more sustainable and long term capacity to investigate outbreaks and collect samples of good quality, to prevent and control FMD, to understand its impact in international trade and identify options to reduce the FMD risk associated with trade.

All the activities and targets mentioned above are currently included in the EuFMD workplan 2015-2019 for improving the FMD control in the European neighbouring areas and assist countries that have embarked in the Progressive Control Pathway.

Fabrizio Rosso

**I. GENERAL OVERVIEW**

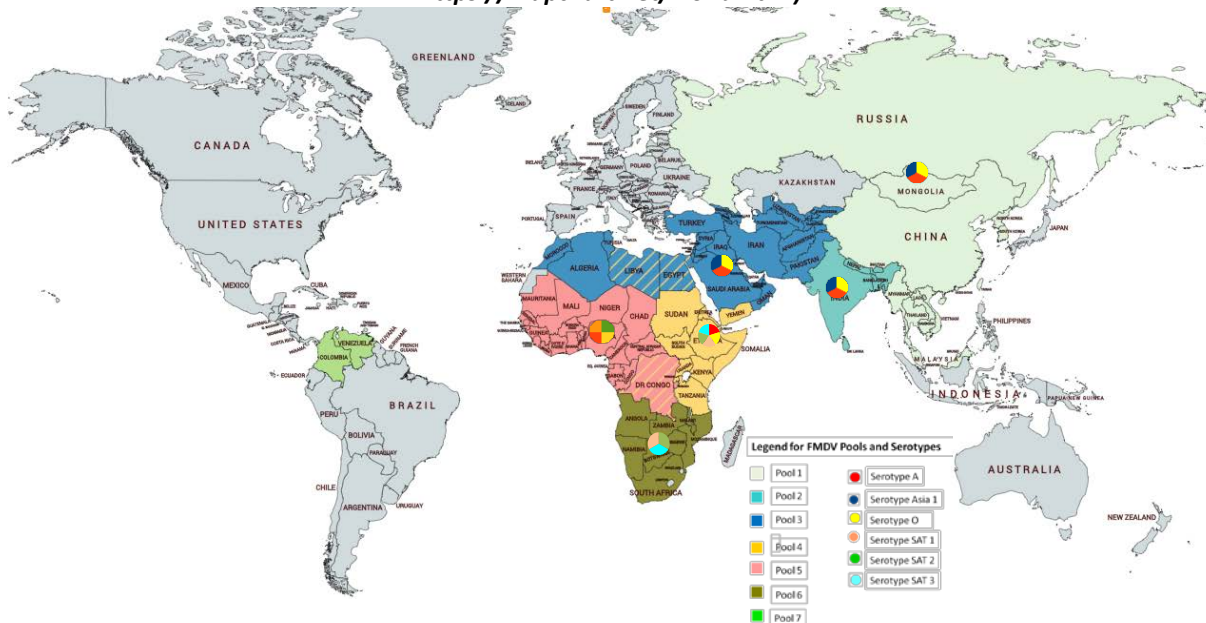
Pools represent independently circulating and evolving foot-and-mouth disease virus (FMDV) genotypes; within the pools, cycles of emergence and spread occur that usually affect multiple countries in the region. In the absence of specific reports, it should be assumed that the serotypes indicated below 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	<b>SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA</b> 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	<b>SOUTH ASIA</b> Bangladesh, Bhutan, India, Mauritius, Nepal, Sri Lanka	A, Asia 1 and O
3	<b>WEST EURASIA &amp; MIDDLE EAST</b> Afghanistan, Algeria, Armenia, Azerbaijan, Bahrain, <b>Egypt</b> , Georgia, Iran (Islamic Republic of), Iraq, Israel, Jordan, Kazakhstan, Kuwait, Kyrgyzstan, Lebanon, <b>Libya</b> , Morocco, Oman, Pakistan, Palestine, Qatar, Saudi Arabia, Syrian Arab Republic, Tajikistan, Tunisia, Turkey, Turkmenistan, United Arab Emirates, Uzbekistan	A, Asia 1 and O
4	<b>EASTERN AFRICA</b> Burundi, Comoros, <b>Democratic Republic of Congo</b> , Djibouti, <b>Egypt</b> , Eritrea, Ethiopia, Kenya, <b>Libya</b> , Rwanda, Somalia, Sudan, South Sudan, United Republic of Tanzania, Uganda, Yemen	O, A, SAT 1, SAT 2 and SAT 3
5	<b>WEST/CENTRAL AFRICA</b> Benin, Burkina Faso, Cameroon, Cabo Verde, Central Afr. Rep., Chad, <b>Democratic Republic of Congo</b> , 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	<b>SOUTHERN AFRICA</b> Angola, Botswana, <b>Congo D. R.</b> , Malawi, Mozambique, Namibia, South Africa, Zambia*, Zimbabwe	{O, A}*, SAT 1, SAT 2 and SAT 3
7	<b>SOUTH AMERICA</b> 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. SUMMARY OF THE NEWS OF THE MONTH

### POOL 1 - SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA

**China**<sup>1</sup> – Further to the FMD outbreak due to serotype O, notified on October 10<sup>th</sup> 2018, on a cattle farm at Bayantuohai Township, Evenk Autonomous Banner, Hulunbeir, Inner Mongolia, another event due to the same serotype was reported in Xinjiang on October 25<sup>th</sup>.

### POOL 2 - SOUTH ASIA

**India**<sup>2</sup> – Since 2015, FMDV O continues to be the only serotype detected in the country as reported by the Project Directorate on Foot and Mouth Disease (PD-FMD), Indian Council of Agricultural Research, Mukteswar, India.

**Nepal**<sup>3</sup> – Even for this country, FMDV O is the serotype detected by the National Foot and Mouth Disease and TADS laboratory for the reporting month.

### POOL 3 - WEST EURASIA & MIDDLE EAST

**Afghanistan**<sup>4</sup> – The Central Veterinary Research and Development Laboratory (CVDRL), Afghanistan reported the detection of FMDV serotype O among the samples examined.

**Israel**<sup>1</sup> – Two outbreaks due to serotype O were reported during November 2018 in free ranging cattle farms at Hazafon, following that notified in September 2018, caused by the same serotype.

### POOL 4 - EASTERN AFRICA

**Ethiopia**<sup>5</sup> - The National Animal Health Diagnostic and Investigation Center (NAHDIC) informed on FMD outbreaks in the regions of North Shoa of Amhara and Oromia.

**Kenya**<sup>6,7</sup> – The National FMD Reference Laboratory, Embakasi, Kenya detected FMDV serotype O in the samples examined.

FMD vaccine matching strain differentiation (VMSD) tests for field viruses belonging to FMDV serotypes A, O and SAT 2 provided good matching results for the latter two serotypes but not with serotype A.

#### **POOL 5 - WEST/CENTRAL AFRICA**

**Cameroon**<sup>8</sup> - The Laboratoire National Vétérinaire (LANAVET), Garoua Cameroon detected FMDV among the 276 bovine samples examined.

**Gambia**<sup>6</sup> – FMDVs detected in samples collected in cattle during 2018 were genotyped as O/EA-3, similar to the lineages isolated in neighbouring countries of West Africa and in Algeria during 2018.

**Mauritania**<sup>6,9</sup> – FMDV VP1 sequences of viruses detected in samples collected during July 2018 and submitted by the FAO/OIE Reference Laboratory, ANSES, France were genotyped as O/EA-3 which as for Gambia were similar to those isolated in the region as well as in Algeria.

**Senegal**<sup>6,10</sup> - The Laboratoire National d'Elevage et de Recherches Vétérinaires (LNRV), Senegal confirmed for the reporting month the detection of FMDV serotype O.

In addition, as reported for Gambia and Mauritania, O/EA-3 was the lineage genotyped from samples collected between May and July 2018.

**Sierra Leone**<sup>6</sup> – FMDV genome was detected in only three of the 34 bovine samples collected during August 2018.

#### **POOL 6 - SOUTHERN AFRICA**

**Malawi**<sup>1</sup> – A FMD outbreak was reported on clinical basis in a cattle population of Northern in October 10<sup>th</sup> 2018.

#### **POOL 7 - SOUTH AMERICA**<sup>1, 11, 12</sup>

**Columbia**<sup>1</sup> – Two new outbreak, still due to FMDV O, were notified on multispecies farms at La Guajira and at Cesar, respectively on September 13<sup>th</sup> and October 6<sup>th</sup> 2018.

#### **COUNTER**

**\*\*\* 172 MONTHS SINCE THE LAST SEROTYPE C OUTBREAK WAS REPORTED**

### III. DETAILED POOL ANALYSIS

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

##### China <sup>1</sup>

FMDV serotype O is again responsible for the outbreaks reported in this country, the latest still in cattle reported on October 25<sup>th</sup> 2018 at Midong District, Urumqi, Xinjiang, the second in the month to the one that occurred on October 10<sup>th</sup> 2018 at Bayantuohai Township, Evenk Autonomous Banner, Hulunbeir, Inner Mongolia.

Laboratory confirmation was carried out on October 30<sup>th</sup> 2018 by the Lanzhou National Reference Laboratory for Foot and Mouth Disease (OIE Reference Laboratory) using reverse transcription - polymerase chain reaction (RT-PCR) followed by sequencing.

The source of this outbreak was attributed to the legal introduction of new live animals and the containment measures adopted for this event were movement control inside the country, screening, traceability, quarantine, official destruction of animal products, official disposal of carcasses, by-products and waste, stamping out, zoning disinfection and vaccination in response to the outbreak and no treatment to the affected animals.

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

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

**Table 2:** summary of the cattle involved in the FMD outbreak that occurred in a cattle unit on October 25<sup>th</sup> at Midong District, Urumqi, Xinjiang. (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	271	20	0	271	0	7.38%	0.00%	0.00%	100.00%

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

**Map 2:** location of the FMD outbreak that occurred in a cattle unit on October 25<sup>th</sup> at Midong District, Urumqi, Xinjiang. (Source – WAHIS)



##### SEACFMD <sup>11</sup>

No new outbreaks were notified during November 2018 among the countries of the South East Asia FMD Campaign, listed in Table 3.

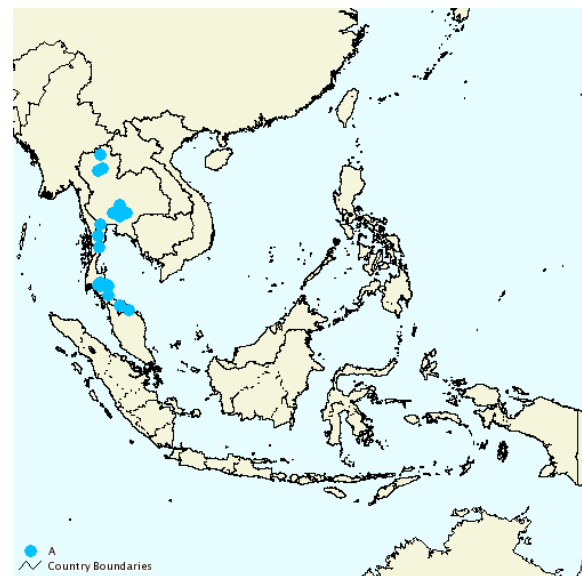
November 2018

The number of on-going events in the different reporting countries of this region is as listed in Table 3. Location of the circulating serotypes A and O in the single countries is represented in Maps 3 and 4.

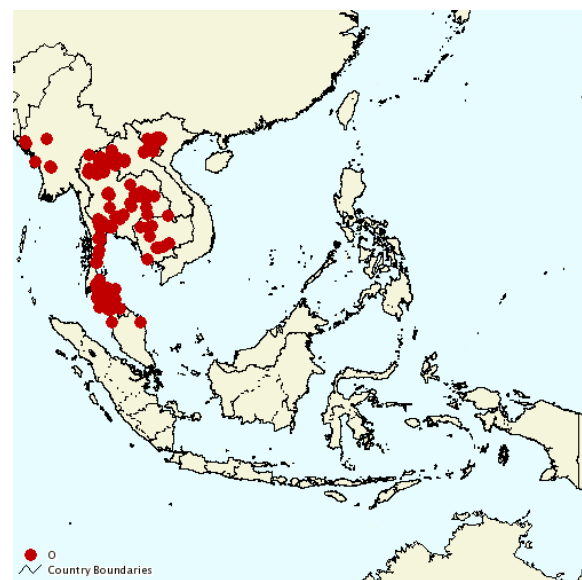
**Table 3:** FMD outbreaks on-going and notified up to November 2018 in the countries of the Southeast Asia Region (Source – SEAFMD Campaign)

	N° of ongoing outbreaks prior to 2018	Jan '18	Feb '18	Mar '18	Apr '18	May '18	Jun '18	Jul '18	Aug '18	Sep '18	Oct '18	Nov '18	Totals
Cambodia	114	8	3	6	3	14	5	0	0	0	0	0	153
Laos	8	0	0	12	14	22	0	0	0	0	0	0	56
Myanmar	3	0	0	0	0	3	0	0	0	0	0	0	6
Malaysia	54	0	1	1	2	2	0	0	0	0	0	0	60
Thailand	236	13	7	5	3	3	6	2	1	7	29	0	312
Viet Nam	15	9	0	0	0	0	0	0	0	0	0	0	24
Totals	430	30	11	24	22	44	11	2	1	7	29	0	611

**Map 3:** location of the on-going FMD outbreaks reported during November 2018 due to serotype A in the countries reported in Table 3. (Source – SEAFMD Campaign)



**Map 4:** location of the on-going FMD outbreaks reported during November 2018 due to serotype O in the countries reported in Table 3. (Source – SEAFMD Campaign)



**Table 4:** Summary of the history of FMD Pool 1 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2013 -2017 see Map 5 below. (Source – Wahis, EuFMD Global Monthly Report)

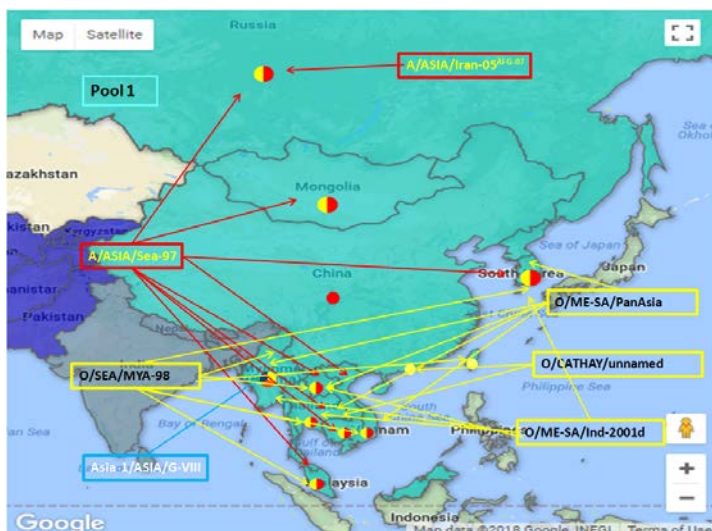
<b>COUNTRY</b>	<b>FMD HISTORY FMDV serotypes, reported to OIE between 2012 – 2017 **(1<sup>st</sup> semester 2017)</b>	<b>LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1</b>	<b>Comment</b>
<b>Cambodia</b>	PENDING/2013-2017 O, A/2016, NOT SAMPLED/2017	Dec 2016/ A & O	<b>See text</b>
<b>China</b>	Data up to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

**Map 5:** 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 Tables, WRLFMD).

Conjectured circulating FMD viral lineages in Pool 1<sup>6,15</sup>:

- 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<sup>SIS10</sup> 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<sup>2</sup>**

As from 2015, FMDV O continues to be the only serotype detected in the country as reported by the ICAR PD-FMD), Indian Council of Agricultural Research, Mukteswar, India.

The laboratory detected FMDV serotype O among the 15 cattle samples examined using antigen and/or RNA detection diagnostic methods while three field isolates of the same serotype were submitted for vaccine matching tests.

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

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

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

**Nepal<sup>3</sup>**

The National Foot and Mouth Disease and TADS Laboratory reports for November 2018 the circulation of FMDV serotype O.

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

The last reported topotypes by the WRLFMD circulating in the country are Asia 1/ASIA/unnamed, first detection in the country and O/ME-SA/2001 d; both lineages were detected in samples collected during 2017.

**Table 5:** Summary of the history of FMD Pool 2 between 2012– 2018. For geographic distribution of circulating FMDVs between 2013 -2017, see Map 6 below. (Source – WAHIS, EuFMD Global Monthly Report)

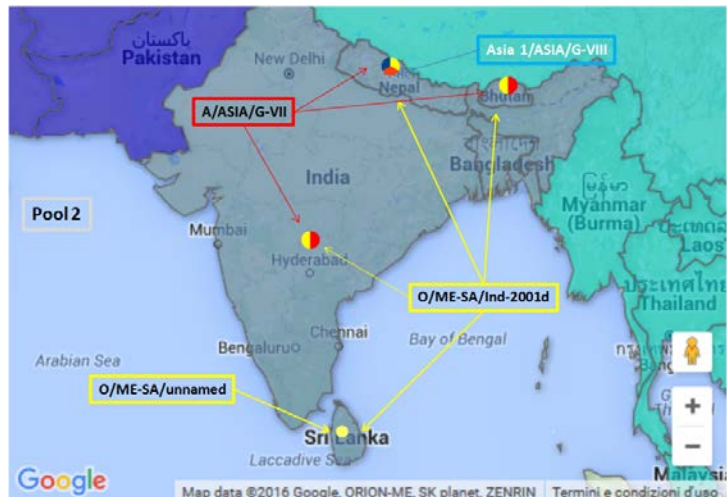
COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE between 2012 – 2017 **(1 <sup>st</sup> semester)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
Bangladesh	A, AISA 1 & O/2016 -2017,	Dec 2016/A, ASIA 1 and O	Follow-up needed

	DISEASE PRESENT BUT WITHOUT QUANTITATIVE DATA		
<b>Bhutan</b>	2017/ A, 2013-2017/O, NOT TYPED or NOT REPORTED 2013 & 2014/NOT SAMPLED	Apr 2018/O, Sep 2017/A	Follow-up needed
<b>India</b>	O, NOT SAMPLED 2012-2015/A 2012-2014/Asia 1	Nov 2018/O, Apr 2015/A Asia 1	<b>See text</b>
<b>Mauritius</b>	2016/O	Sep 2016/O	Follow-up needed
<b>Nepal</b>	O, 2017/A 2012-2013, 2017/Asia 1	Nov 2018/O, Mar 2018/Asia 1, April 2017/A	<b>See text</b>
<b>Sri Lanka</b>	Data up to 2016 2012 – 2016/O	May 2018/O	Follow-up needed

**Map 6:** 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 Tables, WRLFMD)

Conjectured circulating FMDV lineages in Pool 2<sup>6, 15</sup>:

- O/ME-SA/Ind-2001 predominates outbreaks of this serotype detected also in Mauritius during 2016 (**not reported in Map**). The O/ME-SA/Ind-2011 lineage that emerged during 2011 has not been detected during 2012-17.
- A/ASIA/G-VII (genotype 18)
- Asia-1 (lineage C subdivided into Eastern and Western clusters) – not reported in map – reappearance in 2017 in Nepal.



### C. POOL 3 – West Eurasia & Middle East

#### **Afghanistan**<sup>4</sup>

The CVDRL, Afghanistan reported for November 2018, the detection of FMDV serotype O among the 17 samples examined.

A/ASIA/Iran-05 and O/ME-SA/PanAsia-2 are the most recent lineages detected by the WRLFMD in samples collected in the country during 2018.

#### **Israel**<sup>1</sup>

Two outbreaks due to serotype O were reported on November 14<sup>th</sup> and 17<sup>th</sup> 2018 in free ranging cattle farms respectively at Golan and Tsefat, Hazafon, following that reported in September 2018, caused by the same serotype. The outbreak which occurred at Golan is already resolved.

The laboratory confirmation was conducted by the Kimron Veterinary Institute. FMD Laboratory (National laboratory) November 14<sup>th</sup> 2018 using RT-PCR and cell culture isolation. The virus lineage responsible of the outbreaks is O/ME/PanAsia-2.

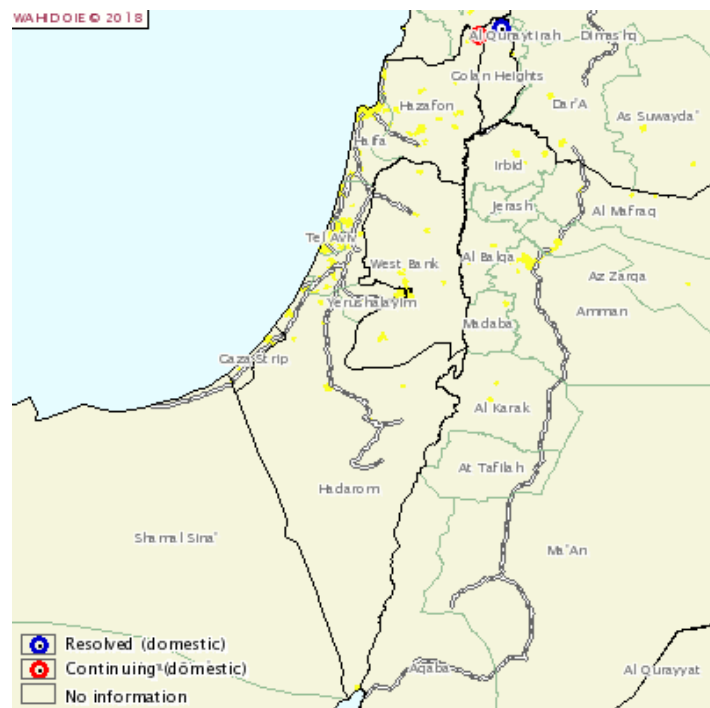
The containment measures adopted are as following: movement control inside the country, surveillance within and outside the containment and/or protection zone, quarantine, zoning, and vaccination in response to the outbreak. One of the epidemiological was vaccinated in June 2018, but details of the strains used are not reported. A summary of the animals involved and location of outbreak are reported in Table 6 and Map 7. The most recent circulating topotypes belonging to FMDV serotype O reported by the WRLFMD are represented by O/EA-3 and O/ME-SA/PanAsia-2 detected in samples respectively collected during 2017 and 2018.

**Table 6:** summary of the animals involved in the FMD outbreaks reported on November 14<sup>th</sup> and 17<sup>th</sup> 2018 in free ranging cattle farms respectively at Golan and at Tsefat, Hazafon. (Source – WAHIS)

Species	Susceptible	Cases	Deaths	Killed and disposed of	Slaughtered	Apparent morbidity rate	Apparent mortality rate	Apparent case fatality rate	Proportion susceptible animals lost*
Cattle	180	30	0	0	0	16.67%	0.00%	0.00%	0.00%

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

**Map 7:** location of the FMD outbreaks reported on November 14<sup>th</sup> and 17<sup>th</sup> 2018 in free ranging cattle farms respectively at Golan and Tsefat, Hazafon. (Source – WAHIS)



**Table 7:** Summary of the history of FMD Pool 3 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2012 -2016, see Map 8 below. (Source – Wahis, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 – 2017 **(1 <sup>st</sup> semester)	LAST OUTBREAK REPORTED/SEROTYPE # see pg. 1	Comment
Afghanistan	2013-2017/O, A, Asia 1, NOT TYPED 2012/SEROTYPE NOT REPORTED	Nov 2018/O, Sep 2018/ A, July 2018/ Asia 1	See text
Algeria	Data available up to 1 <sup>st</sup> semester 2015 20177A, 2014 -2016/O	Sep 2018/O, Apr 2017/A	Follow –up needed
Armenia	2015 -2016/A, 2012-2014, 2017/DISEASE ABSENT	Dec 2015/A	Follow –up needed
Azerbaijan	DISEASE ABSENT	2007/O	Follow –up needed

## Global Foot-and-Mouth Disease Situation

November 2018

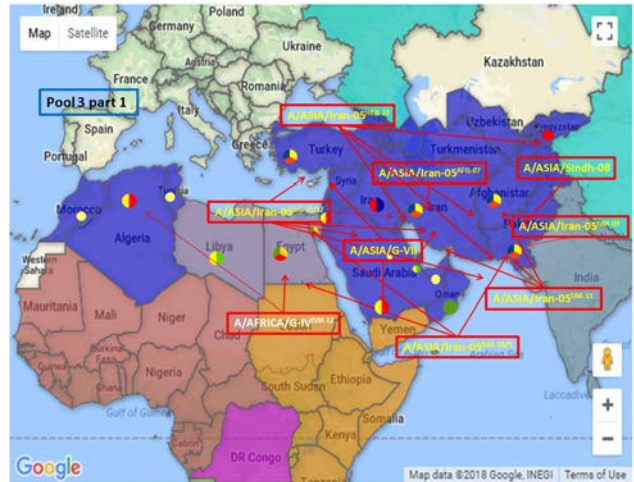
<b>Bahrain</b>	DISEASE ABSENT/2016, 2017, 2012, 2014 & 2015 /O	Mar 2015/O	Follow –up needed
<b>Egypt</b>	2012, 2014, 2016, 2017/SAT 2 2012 – 2017/O, A	April 2017/O, Nov 2016/A May-Jun 2016/Sat 2, Aug 2016/typing pending	Follow –up needed
<b>Georgia</b>	DISEASE ABSENT	2001/ASIA 1	Follow –up needed
<b>Iran (Islamic Republic of)</b>	2012-2017/A, Asia 1 & O	Feb 2018/A, Asia 1 & O,	Follow –up needed
<b>Iraq</b>	2015-2017/O, 2012-2016/A 2015/ SEROTYPE NOT REPORTED	Dec 2013/A, ASIA 1	Follow –up needed
<b>Israel</b>	2012-2015, 2017**/O 2017**/A	Nov 2018/O, June 2017/A	<b>See text</b>
<b>Jordan</b>	2017/O 2012-2016/DISEASE ABSENT	Mar 2017/O	Follow –up needed
<b>Kazakhstan</b>	2014-2017/ DISEASE ABSENT, 2012/O, 2012 –2013/A	Jun 2013/ A & Aug 2012/O	Follow –up needed
<b>Kuwait</b>	2013 – 2014, 2017/ DISEASE ABSENT 2012, 2016/O	April 2016/O	Follow –up needed
<b>Kyrgyzstan</b>	2015 -2017/ DISEASE ABSENT, 2012-2014/O, A	Aug 2014/not typed & Apr 2013 /O, A,	Follow –up needed
<b>Lebanon</b>	2012- 2017**/DISEASE ABSENT	2010/not typed	Follow –up needed
<b>Libya</b>	2015-2017/NO DATA REPORTED 2012-2014/O	Oct 2013/O	Follow –up needed
<b>Morocco</b>	2012-2014, 2017**/DISEASE ABSENT, O/2015	Oct 2015/O	Follow –up needed
<b>Oman</b>	2012-2017/O	May 2015/SAT 2	Follow –up needed
<b>Pakistan</b>	2013-2017/O 2013-2014/A & ASIA 1 2012/ NO DATA REPORTED	Oct 2018/ A & O, May 2018/ Asia 1	Follow –up needed
<b>Palestine</b>	O, 2012-2013/SAT 2	July 2018/Untyped, Dec 2017/O, Mar 2013/Sat 2	Follow –up needed
<b>Qatar</b>	2012-2017/O 2016-2017/A	Dec 2013/O	Follow –up needed
<b>Saudi Arabia</b>	2012-2014, 2016-2017**/O 2015-2016/A	Oct 2016/A & April 2016/O	Follow –up needed
<b>Syrian Arab Republic</b>	DISEASE ABSENT	2002/ A & O	Follow –up needed
<b>Tajikistan</b>	2014-2017**/DISEASE ABSENT 2012- 2013/NOT TYPED	Nov 2012/ not typed & Nov 2011/Asia 1,	Follow –up needed
<b>Tunisia</b>	2017/A, 2015-16/ DISEASE ABSENT, 2014/O	April 2017/A, Oct 2014/O	Follow –up needed
<b>Turkey</b>	A & O, NOT TYPED 2012-2015/Asia 1	Oct 2015/ A May, 2014-2015/ Asia 1 and O	Follow –up needed
<b>Turkmenistan</b>	2013-2017**/DISEASE ABSENT, 2012/NO DATA REPORTED	Not available	Follow –up needed
<b>United Arab Emirates</b>	2013-2014, 2016-2017/O 2012, 2015/DISEASE ABSENT	Sep 2016/O	Follow –up needed
<b>Uzbekistan</b>	2014, 2016-2017/DISEASE ABSENT 2012, 2013 & 2015/NO DATA REPORTED	Not available	Follow –up needed

**Map 8:** FMD distribution between 2013 – 2017 by serotype and toptype 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 Tables, WRLFMD).

(Note: Kazakhstan is not included in map as declared by OIE as FMD free, divided in zones with and without vaccination)

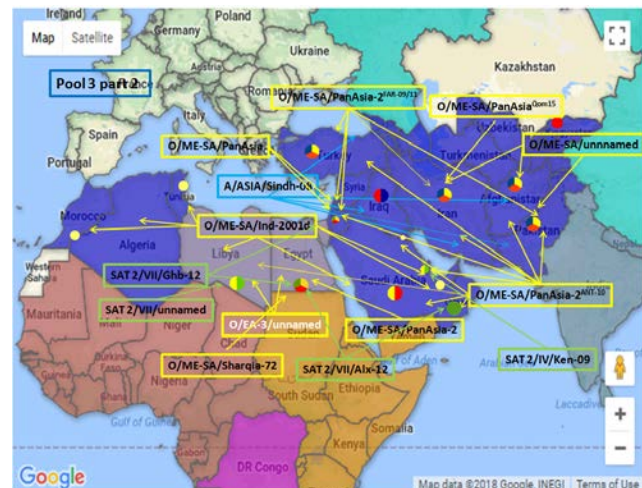
Conjectured circulating FMDV serotype A and Asia 1 lineages in Pool 3<sup>6, 15</sup>:

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



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

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



#### D. POOL 4 – Eastern Africa

##### Ethiopia<sup>5</sup>

The NAHDIC reported FMD outbreaks in the regions of North Shoa of Amhara and Oromia (Map 9) for which samples collected from these episodes were positive for FMDV serotype A and O using antigen detection ELISA.

The laboratory tested 966 sheep and goat sera of which 38 (3.93%) were positive. The samples were examined for screening purposes using the FMD ELISA for antibodies against the viral non-structural proteins (NSP).

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

November 2018

**Map 9:** areas (Amhara and Oromia) of where the FMD outbreaks were reported by NAHDIC during November 2018. (Source – Google Fusion Tables and NAHDIC)



### Kenya<sup>6,7</sup>

The National FMD Reference Laboratory, Embakasi, Kenya reported the detection of FMDV serotype O in the samples examined for the reporting month.

Following is a summary of the VMSD tests for field viruses detected in samples collected between January 2017 and June 2018:

For field isolates A/KEN/14/2017 and A/KEN/17/2017 belonging to the O/EA-2 lineage, vaccine strains O 3039, O Manisa and O TUR 5/09 all obtained good matching results;

For field isolate SAT 1/KEN/8/2017, belonging to SAT 1/I lineage, vaccine strain SAT 1/RHO did not provide good matching results;

For field isolate SAT 2/KEN/19/2017, belonging to the SAT 2/IV lineage, SAT 2 ERI and SAT 2 ZIM vaccines provided good matching results.

**Table 8:** Summary of the history of FMD Pool 4 between 2012 – 2018. For geographic distribution of circulating FMDVs between 2013 -2017, see Map 10 below. (Source – WAHIS, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 – 2016 ** (1 <sup>st</sup> semester)	LAST OUTBREAK REPORTED/SEROTYPE #see pg. 1	Comment
Burundi	DISEASE PRESENT	Aug 2013 / not available	Typing required
Comoros	NO DATA AVAILABLE	2010	Follow –up needed
Democratic Republic of Congo	2012 – 2017**/A, O & SAT 1	June 2017/not typed	Follow –up needed
Djibouti	DISEASE ABSENT	Not available	Follow –up needed
Egypt	2012, 2014, 2016, 2017/SAT 2 2012 – 2017/O & A	May-Jun 2016/ O & Sat 2, March 2016/A, Aug 2016/typing pending	Follow –up needed
Eritrea	2014, 2016-2017/ DISEASE PRESENT 2015/ NO DATA REPORTED 2013/ DISEASE ABSENT, 2012/O	Nov 2016/not reported, Jan 2012/O	Follow –up needed
Ethiopia	O, 2015-2017/SAT 1 2012 & 2017/SAT 2, 2012, 2017/A	Nov 2018/A& O, April 2018/ SAT 2, Feb 2018/SAT 1	See text

November 2018

<b>Kenya</b>	A, O, SAT1 & SAT2	Nov 2018/O, Oct 2018/ A, May 2018/ SAT 1, Nov 2017/SAT 2	<b>See text</b>
<b>Libya</b>	2015-2017/NO DATA REPORTED 2012-2014/O	Oct 2013/ O, Sat 2/Apr 2012	Follow-up needed
<b>Rwanda</b>	2012-2013, 2017/A, O, SAT1 & SAT 2 2015-2016/NO DATA AVAILABLE	Nov 2012/not typed	Typing required
<b>Somalia</b>	2012-13, 2015-2017/DISEASE PRESENT, 2014/PENDING	June 2016/not reported	Follow –up needed
<b>Sudan</b>	2012-2014, 2017/O, 2015-2016/A, SAT 1 2013/SAT 2	Mar 2018/A Dec 2016/ not sampled, June 2017/O & SAT 2	Follow –up needed
<b>South Sudan</b>	2015 - 2017/DISEASE PRESENT 2014/A, O, SAT 1, SAT 2 & SAT 3 2012-2013 & 2016 NO DATA REPORTED	2011	Follow –up needed
<b>United Republic of Tanzania</b>	2012-2017/A, O, SAT 1 & SAT 2	Oct 2016/SAT 1, Aug 2016/O & SAT 2, Jun 2016/ A	Follow –up needed
<b>Uganda</b>	2016/DISEASE PRESENT, 2012, 2015, 2017/ SAT 1, 2012, 2014, 2015, 2017/O	May 2017/O Nov 2014/SAT1, Jan 2015/A and SAT 3, July 2015/ SAT 2 and untyped	Follow –up needed
<b>Yemen</b>	2013 – 2017/ DISEASE PRESENT BUT WITHOUT QUANTITATIVE DATA, 2012/O	2009/O	Follow –up needed

**Map 10:** 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 Tables, WRLFMD).

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

Conjectured circulating FMDV lineages in Pool 4 [6](#), [15](#).

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



### E. POOL 5 – West / Central Africa

#### Cameroon <sup>8</sup>

The Laboratoire National Vétérinaire (LANAVET), Garoua Cameroon detected FMDV in 66 (23.9%) of the 276 bovine samples examined.

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

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

#### Gambia <sup>6</sup>

FMDVs detected in the two samples collected in cattle during July 2018 were genotyped as O/EA-3, similar to the lineages isolated in neighbouring countries of West Africa, i.e. Mauritania, Senegal and in Algeria during 2018 with a sequence identity (seq id) to these viruses of 99.7%.

This the first report by the WRLFMD of the identification of a FMDV toptype circulating in this the country.

#### Mauritania <sup>6,9</sup>

FMDV VP1 sequences of FMDVs detected in seven samples collected during July 2018 at Hodh Ech Chargui (Map 11) and submitted by the FAO/OIE Reference Laboratory, ANSES, France were genotyped as O/EA-3 which as for Gambia were similar to those isolated in the region as well as in Algeria. The species from which the samples were collected is not reported.

Most closely related field viruses are those that were detected also for Gambia, including also Guinea, with the highest seq id of 99.4 for the same toptype detected in Algeria.

**Map 11:** area of Mauritania where O/EA-3 positive samples were collected during July 2018. (Source – Google Maps and WRLFMD)



#### Senegal <sup>6,10</sup>

The LNRV, Senegal confirmed for the reporting month the detection of FMDV serotype O.

In addition, as reported for Gambia and Mauritania, O/EA-3 was the lineage genotyped in six of the 11 cattle and pig samples collected between May and July 2018.

A summary of these results is reported in Table 9 and location in Map 12.

The seq id of the viruses isolated in this country confirms the common of origin of these to the ones isolated in Gambia, Mauritania and Algeria with the most closely related field virus represented by the ones isolated in Algeria having a seq id ranging from 99.2 to 100%.

**Table 9:** genotyping results of the FMDV positive bovine and pig samples collected in Senegal between May and July 2018. (source – WRLFMD)

Sample Identification	Location origin of sample	Species in which sample was collected	Date of collection	Genotype	Most Closely Related Viruses not belonging to the country - Seq id %	Host species
SEN/1/2018	Sebikotane	cattle	09/05/2018	O/EA-3	ALG/1/2018 (99.8)	cattle
SEN/2/2018	Koumpentoum	porcine	28/06/2018		ALG/1/2018 (99.2)	
SEN/4/2018	Bandafassi	cattle	11/07/2018		ALG/1/2018 (100)	
SEN/6/2018	Kaolack	cattle	12/07/2018		ALG/1/2018 (99.7)	
SEN/9/2018	Bandia	cattle	20/07/2018		ALG/1/2018 (100)	
SEN/11/2018	Tilene	cattle	31/07/2018		ALG/1/2018 (99.7)	

**Map 12:** location of where O/EA-3 positive bovine and pig samples was carried out in Senegal between May and July 2018. (Source – Google Fusion Maps and WRLFMD)**Sierra Leone**<sup>6</sup>

The FMDV genome was detected in three of the 34 bovine samples collected during August 2018. As the generation of the sequences of these samples was not possible, further testing of these by a novel lineage specific Real Time reverse transcriptase PCR designed to detect FMD viruses from the O/EA-3 topotype was conducted on these samples and provided positive results which should be interpreted with precaution in the absence of confirmation by sequencing, even if there is evidence of the recent circulation of this topotype in the neighbouring countries of the same Pool.

**Table 10:** Summary of the history of FMD Pool 5 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 – 2017 ** (1 <sup>st</sup> semester)	Last outbreak reported/serotype #see pg. 1	Comment (Genotyping would be useful for this region)
Benin	2017/NO DATA REPORTED 2012-2016/A, O, SAT 1, SAT 2	Jun 2014/O, A, SAT 1, SAT 2	Follow –up needed
Burkina Faso	DISEASE PRESENT	Dec 2016/ not available	Follow –up needed
Cameroon	**DISEASE PRESENT	Nov 2018/untyped, Nov 2014/O, SAT 2, May 2014/SAT 1, Apr 2014/ A	See text

November 2018

<b>Cabo Verde</b>	DISEASE ABSENT	Not available	Follow –up needed
<b>Central African Republic</b>	DISEASE PRESENT BUT WITHOUT QUANTITATIVE DATA	Not available	Follow –up needed
<b>Chad</b>	2016 - 2017/DISEASE PRESENT 2014-15/ DISEASE ABSENT 2012 – 2013/ DISEASE PRESENT	Aug 2016/Not reported	Follow –up needed
<b>Democratic Republic of the Congo</b>	2012 – 2017**/A, O & SAT 1	Mar 2018/untyped Dec 2016/A, O & Sat 1	Follow –up needed
<b>Congo</b>	NO DATA AVAILABLE	Jun 2013/not typed	Typing required
<b>Côte d'Ivoire</b>	2013-2017/DISEASE PRESENT, 2012/A,	Jul 2016/not reported	Follow –up needed
<b>Equatorial Guinea</b>	2014 – 2017/ NO DATA AVAILABLE 2012 – 2013/DISEASE SUSPECTED	Not available	Follow –up needed
<b>Gabon</b>	2017/NO DATA AVAILABLE 2012, 2014-16/DISEASE ABSENT 2013/NO DATA AVAILABLE	Not available	Follow –up needed
<b>Gambia</b>	NO DATA AVAILABLE	July 2018/O	<b>See text</b>
<b>Ghana</b>	2012 – 2017/DISEASE PRESENT	July 2018/untyped June 2017/O, Dec 2016/ SAT 2 2014/not available	Follow –up needed
<b>Guinea-Bissau</b>	2014-2017**/DISEASE PRESENT 2012-2013/DISEASE ABSENT	Aug 2018/O Dec 2016/SAT1 & SAT 2	Follow –up needed
<b>Guinea</b>	2012-2013, 2015-2017 DISEASE ABSENT 2014/ DISEASE PRESENT	Sep 2018/O	<b>See text</b>
<b>Liberia</b>	NO DATA AVAILABLE	Not available	Follow –up needed
<b>Mali</b>	2017/ NO DATA AVAILABLE 2016/DISEASE ABSENT 2015/A, SAT 1 2014-2015/SAT 2 2012/ NO DATA AVAILABLE	Oct 2016/not reported	Follow –up needed
<b>Mauritania</b>	2017/ NO DATA AVAILABLE 2016/DISEASE SUSPECTED, 2014-2015**/SAT 2, 2012-2013/NO REPORTED OUTBREAKS	July 2018/O, Dec 2014/SAT 2	<b>See text</b>
<b>Niger</b>	2017/ DISEASE SUSPECTED 2016/DISEASE PRESENT BUT WITH NO QUALITATIVE DATA, 2015/O 2012 – 2014/NOT SAMPLED	2014/not sampled, May 2015/O	Follow –up needed
<b>Nigeria</b>	2015-2017/DISEASE PRESENT	Sep 2018/O & Sat 2	Follow –up needed

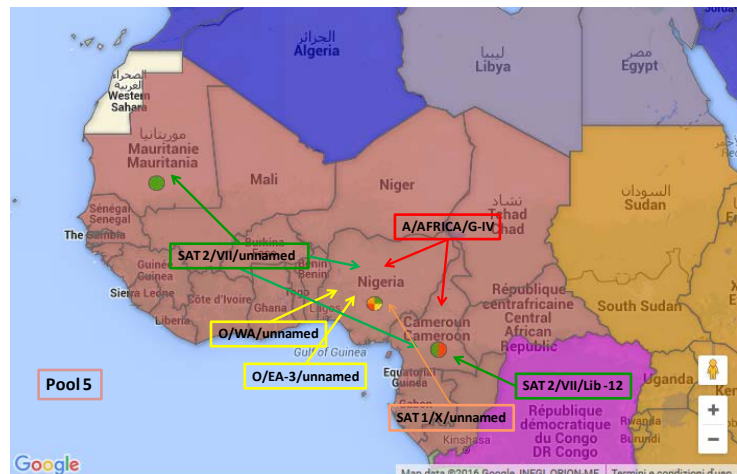
November 2018

	2012-2014/O	Sept 2016/ SAT 1, Nov 2015/A	
<b>Sao Tome Principe</b>	2013-2017/NO DATA AVAILABLE 2012/DISEASE ABSENT	Not available	Follow –up needed
<b>Senegal</b>	2017/ DISEASE SUSPECTED 2015-2016/DISEASE PRESENT 2012, 2014/NOT SAMPLED 2013/NO DATA AVAILABLE	Sep 2018/O, Feb 2015/ A, 2014/ SAT 2	<b>See text</b>
<b>Sierra Leone</b>	2017/NO DATA AVAILABLE 2012 – 2016/DISEASE ABSENT	July 2018/O	<b>See text</b>
<b>Togo</b>	O & SAT 1	2012/O	Follow –up needed

**Map 13:** 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 2 serotypes and white script in map refers to new introduction of viral lineage in pool or country of the pool during 2017. (Source – Google Fusion Tables, WRLFMD).

Conjectured circulating FMDV lineages in Pool 5<sup>15</sup>:

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



#### F. POOL 6 – Southern Africa

##### Malawi<sup>1</sup>

The FMD outbreak reported on October 10<sup>th</sup> 2018 in a cattle population of Northern was diagnosed on clinical basis. The source of the outbreak is due to the introduction of new live animals by the middlemen who supply to processors. The animals were sourced from neighbouring districts. Only blood samples were collected for FMD NSP ELISA, which gave positive results. Other sources of infection were illegal movement of animals and presence of infected animals at pastures and watering points. In fact, the affected population usually have a common watering point, the Songwe River, which borders Malawi and Tanzania. The district also borders with Tanzania and Zambia. The containment measures adopted are movement control inside the country, surveillance outside containment and/or protection zone, quarantine, disinfection, vaccination permitted, if a vaccine exists, and no treatment of affected animals.

A summary of the animals involved in the outbreak and location of this are reported in Table 11 and Map 14. The most recent topotype reported to circulate in the country is SAT1/1 detected in 2017.

November 2018

**Table 11:** summary of the FMD outbreak that occurred on October 10<sup>th</sup> 2018 in a cattle population of Northern. (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	1,300	38	0	0	0	2.92%	0.00%	0.00%	0.00%

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

**Map 14:** location of the FMD outbreak that occurred on October 10<sup>th</sup> 2018 in a cattle population of Northern. (Source – WAHIS)**South Africa** <sup>13</sup>

The ARC-Onderstepoort Veterinary Institute reported the testing by LPBE and NSP ELISA respectively on 5,235 and 371 sera.

There are no reports by the WRLFMD on the most recent circulating topotypes in the country.

**Table 12:** Summary of the history of FMD Pool 6, 2013 – 2018, for geographic distribution see Map 15 below. (Source – WAHIS, EuFMD Global Monthly Report)

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

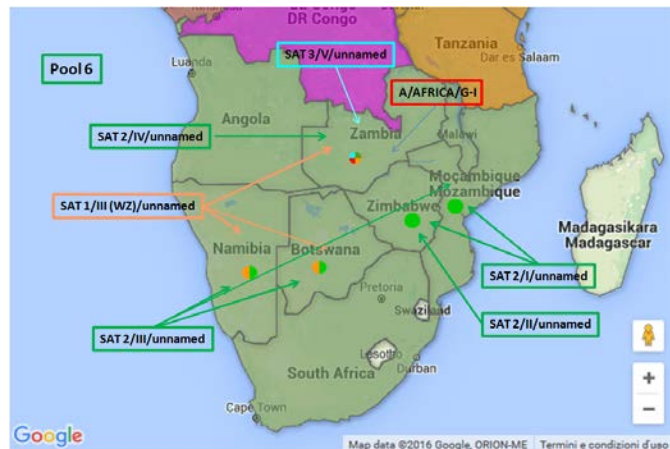
<b>Malawi</b>	2016 – 2017/SAT 2 2013-2015/ NO DATA AVAILABLE 2012/NO OUTBREAKS REPORTED	Oct 2018/untyped, Aug 2018/SAT 2 June 2016/SAT 1	<b>See text</b>
<b>Mozambique</b>	2016 – 2017/SAT 2 2012 -2015/DISEASE ABSENT	June 2018/ Typing pending, Oct 2017/SAT 2, May 2015/ SAT 1	Follow –up needed
<b>Namibia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

**Map 15:** 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 Tables, 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<sup>6, 15</sup>:

- 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

##### Colombia<sup>1</sup>

In addition to the outbreaks notified in the country between September and October 2018 in Boyacá, Cesar and La Guajira, two new outbreaks, still due to FMDV O, were notified on multispecies farms at La Guajira and at Cesar, respectively on September 13<sup>th</sup> and October 6<sup>th</sup> 2018.

Diagnosis of these outbreaks was conducted by the National Veterinary Diagnosis Laboratory, on November 11<sup>th</sup>, using ABC ELISA (for FMDV NSPs) for the outbreak at La Guajira and on October 30<sup>th</sup> 2018, using PCR for the outbreak at Cesar.

The outbreak in La Guajira, was detected by seroepidemiological investigation in accordance with the control and eradication plan established for this disease and chronologically, this is the primary outbreak. Slaughter of the infected animals and their contacts, cleaning and disinfection activities, fallowing and introduction of sentinels were carried out. Quarantine measures are maintained and the origin of the virus introduction is under investigation. The same actions were also carried out for the outbreak at Cesar.

Source of infection for both outbreaks is unknown and control measures put in force are movement control inside the country, surveillance within and outside containment and/or protection zone, traceability, quarantine, disinfection, vaccination in response to outbreaks in the surveillance zone with no of treatment of affected animals. Further measures that will be applied are official destruction of animal products, official disposal of carcasses, by-products and waste and stamping out.

**Table 13:** summary of the animal species and relative consistencies involved in the FMD outbreaks that occurred for the reporting month in Colombia. (Source – WAHIS)

Location of outbreak	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*
Recreo CM, Carraipia, Maicao, La Guajira	13/09/2018	Cattle	17	2	0	17	0	11.76%	0.00%	0.00%	100.00%
		Swine	3	0	0	3	0	0.00%	0.00%	-	100.00%
Los Vila - Villa Castilla, Mayales - La Cuarta, Valledupar, Cesar	06/10/2018	Cattle	2	0	0	2	0	0.00%	0.00%	-	100.00%
		Sheep	15	0	0	15	0	0.00%	0.00%	-	100.00%
		Swine	112	11	0	112	0	9.82%	0.00%	0.00%	100.00%

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

**Map 16:** location of the FMD outbreaks that occurred between for the reporting month. (Source –WAHIS-OIE and Google Fusion Tables)



### Rest of Latin America <sup>1, 11, 12</sup>

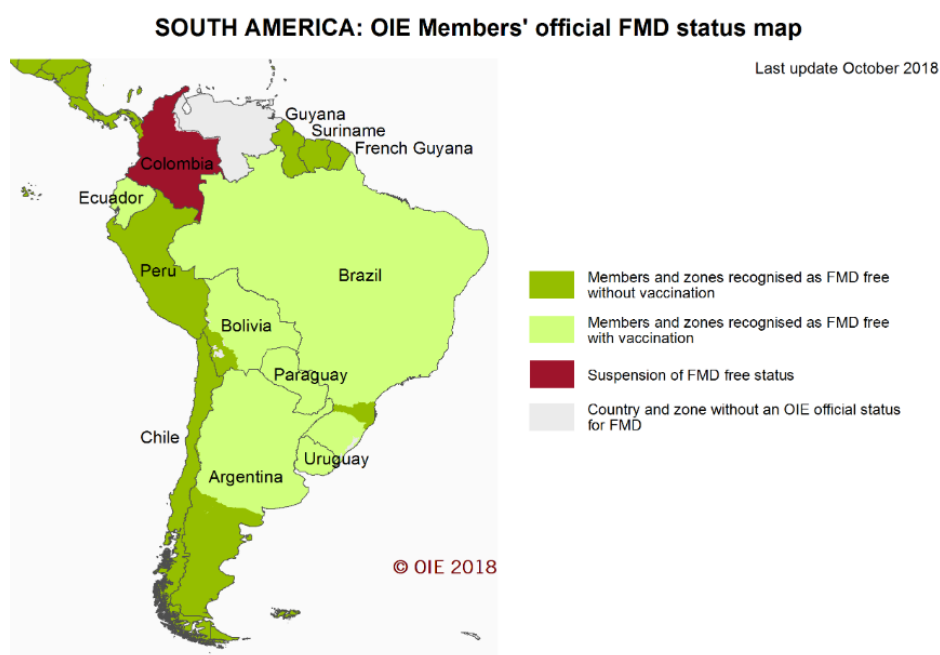
The OIE FMD status of the countries in South America as reported in October 2018 is presented in Map 17. Most South American countries are FMD free with vaccination (Uruguay) or without vaccination (Chile, Guyana) or with free zones with vaccination (Argentina, Bolivia, Brazil, Peru and continental Ecuador) 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 17). 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 14.

**Table 14:** Summary of the history of FMD Pool 16 between 2012 – 2018, for geographic distribution see Map 17. (Source – WAHIS, EuFMD Global Monthly Report)

COUNTRY	FMD HISTORY FMDV serotypes, reported to OIE in 2012 2016** (1 <sup>st</sup> semester)	LAST OUTBREAK REPORTED/SEROTYPE <small>#see pg. 1</small>	Comment
Colombia	DISEASE ABSENT	October 2018/O	See text
Venezuela (Bolivarian Republic of)	DISEASE ABSENT**	2011/O, 2013/A	National situation needs verification

**Map 17:** FMD status for South America <sup>1</sup>(Source – OIE)



**IV. OTHER NEWS:**

<sup>6</sup>The 3<sup>rd</sup> WRLFMD Quarterly Report for the period July – October 2018 contains a new format for recommendations of FMDV vaccines to be included in antigen banks for Europe. The discussion of Table 15 is available within the report.

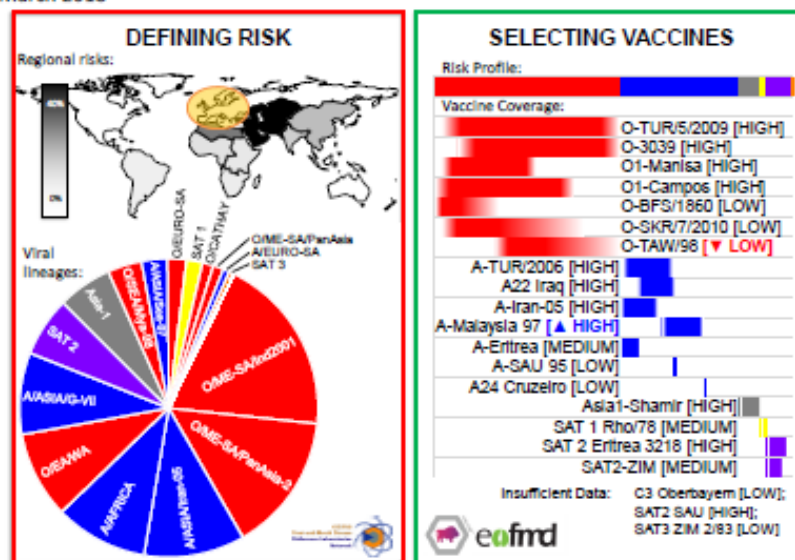
**Table 15:** Recommendations from WRLFMD<sup>®</sup> on FMD virus strains to be included in FMDV antigen banks (for Europe).

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

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

## V. REFERENCES - Superscripts

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