

# WRLFMD Quarterly Report October to December 2019

Foot-and-Mouth Disease





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# 1. Summary of samples tested and reported FMD outbreaks

## 1.1. Global Overview of samples received and tested

The location of all samples detailed in this report can be seen on the map below. More detailed maps and sample data, on a country by country basis, can be found in the following sections of this report.



**Figure 1:** Samples tested by WRLFMD in this quarter (coloured spots define serotypes detected (C, A, G, Asia 1, SAT 1, SAT 2, SAT 3, untyped, negative))

## 1.2. Asia

### Myanmar



Between 1<sup>st</sup> October 2019 and 26<sup>th</sup> November 2019, 16 outbreaks of **FMD type O** were reported to have occurred in cattle in various parts of the country (Magway Region, Mandalay Region, Mon State, Sagaing Region and Shan State). Between 15<sup>th</sup> November 2019 and 2<sup>nd</sup> December 2019, five outbreaks of **FMD type A** were reported in cattle in Yangon Region. No genotyping is available for either serotype.

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## 1.3. Africa

### Eritrea



A batch of 47 samples was received on 18<sup>th</sup> December 2019. Serotyping and genotyping results are pending and will be detailed in the next quarterly report.

### Guinea-Bissau



A series of six outbreaks due to **FMD type O** were reported to have occurred in cattle in the Bafatá region during January to April 2019. No genotyping has been reported.

### Nigeria



On the 15<sup>th</sup> December 2019, near-complete FMDV genome sequences were received from the Canadian Food Inspection Agency (CFIA/ACIA) in conjunction with the Nigerian National Veterinary Research Institute (NVRI). Eight of the sequences were **FMDV type O** and eight were **FMDV type SAT 2**. The samples had been collected from cattle in the Plateau (15 samples) and Bauchi (1 sample) States during 2017-2018. Genotyping of the VP1 regions showed that the type O viruses belonged to the EA-3 toposotype and the type SAT 2 belonged to toposotype VII, lineage LIB-12 (see below).

### Namibia



Five further outbreaks of **FMD type SAT 3** were reported in cattle in the Zambezi region between October and December 2019. Previous genotyping by the SSARRL (BVI) showed that the causal virus belonged to toposotype II (see the June-September 2019 Network Report).

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## South Africa



A series of 15 outbreaks of **FMD type SAT 2** were reported to have occurred in cattle in the Limpopo Province (municipalities of Ba-Phalaborwa, Greater Letaba, Makhado, Molemole and Polokwane) between 1<sup>st</sup> November 2019 and 27<sup>th</sup> December 2019. These outbreaks occurred in South Africa's FMD Protection Zone. No genotyping has been reported.

## Zimbabwe



Between 21<sup>st</sup> August 2019 and 22<sup>nd</sup> October 2019, 22 outbreaks of **FMD type SAT 1** were reported in cattle in Masvingo province. On 22<sup>nd</sup> September 2019, a single outbreak of **FMD type SAT 2** was reported in cattle in Mashonaland Central. No genotyping is available for either serotype.

## 1.4. South America

No new outbreaks of FMD were reported in the continent.

## 1.5. Uncharacterised FMD viruses

A number of outbreaks have occurred where samples have not been sent to the WRLFMD. It is probable that the countries involved have performed their own genetic characterisation; however, through the OIE/FAO Laboratory Network we would also like to encourage the submission of samples (or complete VP1 sequences) to the WRLFMD.

An up-to-date list and reports of FMD viruses characterised by sequencing can be found at the following website: <http://www.wrlfmd.org/country-reports/country-reports-2019>.

Results from samples or sequences received at WRLFMD (status of samples being tested) are shown in Table 1 and a complete list of clinical sample diagnostics made by the WRLFMD from October to December 2019 is shown in Annex 1 (Summary of Submissions). A record of all samples received by WRLFMD is shown in Annex 1 (Clinical Samples).

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**Table 1:** Status of sequencing of samples or sequences received by the WRLFMD from October to December 2019 (\* indicates a batch carried over from the previous quarter).

WRLFMD Batch No.	Date received	Country	Serotype	No. of samples	No. of sequences	Sequencing status
WRLFMD/2019/00031	18/12/2019	Eritrea	pending	47	-	-
<b>Total</b>				<b>47</b>	<b>0</b>	

**Table 2:** VP1 sequences submitted by other FMD Network laboratories to the WRLFMD from October to December 2019.

WRLFMD Batch No.	Date received	Country	Serotype	Date Collected	No. of sequences	Submitting laboratory
WRLMEG/2019/00045	01/12/2019	Vietnam	O	2019	13	RAHO6
WRLMEG/2019/00046	15/12/2019	Nigeria	O	2017-2018	8	CFIANVRI
			SAT 2	2017-2018	8	CFIANVRI
Total					29	

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## 2. Detailed Analysis

Key for maps and trees:

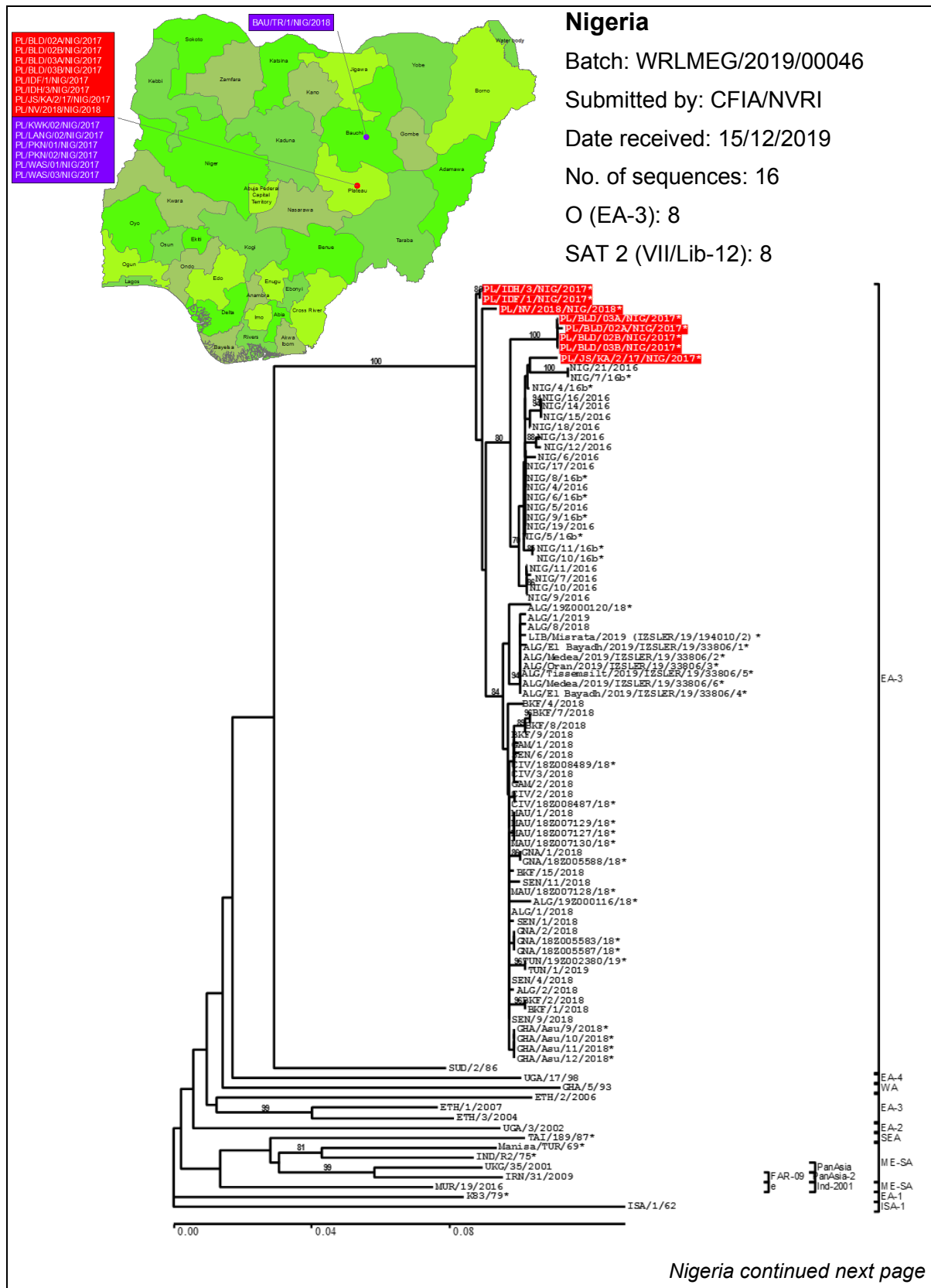
<b>Serotype O</b>	<b>Serotype Asia-1</b>	<b>Serotype SAT 3</b>
<b>Serotype A</b>	<b>Serotype SAT 1</b>	<b>FMDV Genome Detected</b>
<b>Serotype C</b>	<b>Serotype SAT 2</b>	<b>No Virus Detected</b>

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## 2.1. Africa



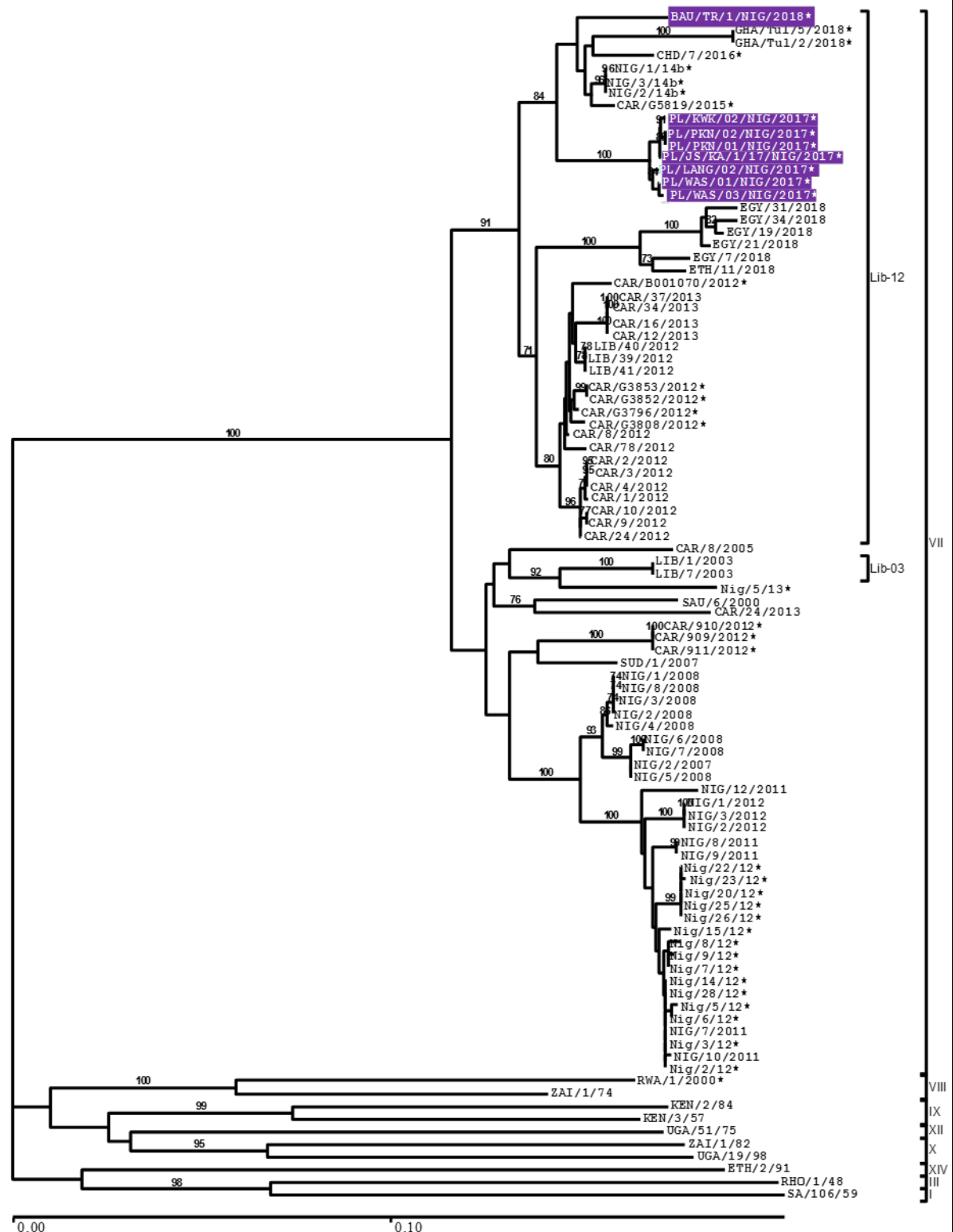
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## Nigeria Continued



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## 2.2. Vaccine matching

During this reporting period vaccine matching has been undertaken for 6 FMD virus field isolates.

**Table 3: Summary of samples tested by vaccine matching.**

Serotype	O	A	C	Asia-1	SAT 1	SAT 2	SAT 3
Hong Kong, SAR of PRC	2						
Thailand	2	2					
<b>Total</b>	<b>4</b>	<b>2</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>

For individual data see Annex 1, section 2.7 (Antigenic Characterisation).

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## Annex 1: Sample data

### 2.3. Summary of Submissions

Table 4: Summary of samples collected and received to WRLFMD (October to December 2019)

Country	Nº of samples	Virus isolation in cell culture/ELISA								No Virus Detected	RT-PCR for FMD	
		FMD virus serotypes							Positive		Negative	
		O	A	C	SAT 1	SAT 2	SAT 3	ASIA -1				
-	-	-	-	-	-	-	-	-	-	-	-	
TOTAL	0	0	0	0	0	0	0	0	0	0	0	

#### Abbreviations used in table

VI / ELISA	FMD (or SVD) virus serotype identified following virus isolation in cell culture and antigen detection ELISA
FMD	Foot-and-mouth disease
SVD	Swine vesicular disease
NVD	No FMD, SVD or vesicular stomatitis virus detected
NT	Not tested
rRT-PCR	Real-time reverse transcription polymerase chain reaction for FMD (or SVD) viral genome

### 2.4. Clinical Samples

Table 5: Clinical sample diagnostics made by the WRLFMD® October to December 2019

Country	Date		WRL for FMD Sample Identification	Animal	Date of Collection	Results		
	Received	Reported				VI/ELISA	RT-PCR	Final report
-	-	-	-	-	-	-	-	-
<b>TOTAL</b>				<b>0</b>				

#### Abbreviations used in table

FMD(V)	Foot-and-mouth disease (virus)
FMDV GD	Genome detected

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FMDV NGD	Genome not detected (samples submitted in Trizol, only rRT-PCR carried out)
VI/ELISA	FMDV serotype identified following virus isolation in cell culture and antigen ELISA
rRT-PCR	Real-time reverse transcription polymerase chain reaction on epithelial suspension for FMD (or SVD) viral genome
NVD	No foot-and-mouth disease, swine vesicular disease or vesicular stomatitis virus detected
NT	Not tested

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## 2.5. Antigenic Characterisation

Antigenic characterisation of FMD field isolates by matching with vaccine strains by 2dmVNT from October to December 2019.

### Abbreviations used in tables

M	Vaccine Match $r_1 = \geq 0.3$ . Suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.
N	No Vaccine Match $r_1 = < 0.3$ . Suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect
B	Borderline Any $r_1$ values between 0.28 to 0.32
NT	Not tested against this vaccine

**Table 6: Vaccine matching studies for A FMDV by VNT**

Strain	Serotype	Topotype	Lineage	A/IRN/05	A/MAY/97	A/TUR/20/06	A22 IRAQ
TAI/7/2019	A	ASIA	Sea-97	0.35	0.21	0	0.43
TAI/8/2019	A	ASIA	Sea-97	0.32	0.2	0	0.51

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**Table 7: Vaccine matching studies for O FMDV by VNT**

Strain	Serotype	Topotype	Lineage	O 3039	O1 Manisa	O/TUR/5/2009
HKN/1/2019	O	CATHAY	-	0.19	0.12	0.16
HKN/4/2019	O	CATHAY	-	0.19	0.08	0.09
TAI/14/2018	O	SEA	Mya-98	0.42	0.27	0.29
TAI/15/2018	O	ME-SA	Ind-2001	1	0.72	1

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## Annex 2: FMD publications

Recent FMD Publications (October to December 2019) cited by Web of Science (Pirbright Institute papers and authors are highlighted in **BOLD AND GREY**)

1. Ababneh, M.M., W. Hananeh, Z.B. Ismail, M. Hawawsheh, M. Ai-Zghoul, N.J. Knowles, and K. van Maanen. First detection of *Foot-and-mouth disease virus* O/ME-SA/Ind2001e sublineage in Jordan. *Transboundary and Emerging Diseases*.
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4. Ali, M.R., A. Ul Alam, M. Al Amin, M.A. Siddique, M. Sultana, and M.A. Hossain. Emergence of novel lineage of *Foot-and-mouth disease virus* serotype Asia1 BD-18 (G-IX) in Bangladesh. *Transboundary and Emerging Diseases*.
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10. Dhakal, S. and G.J. Renukaradhya (2019). Nanoparticle-based vaccine development and evaluation against viral infections in pigs. *Veterinary Research*, **50**(1): 14.

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11. Dill, V. and M. Eschbaumer. Cell culture propagation of *Foot-and-mouth disease virus*: adaptive amino acid substitutions in structural proteins and their functional implications. *Virus Genes*: 15.
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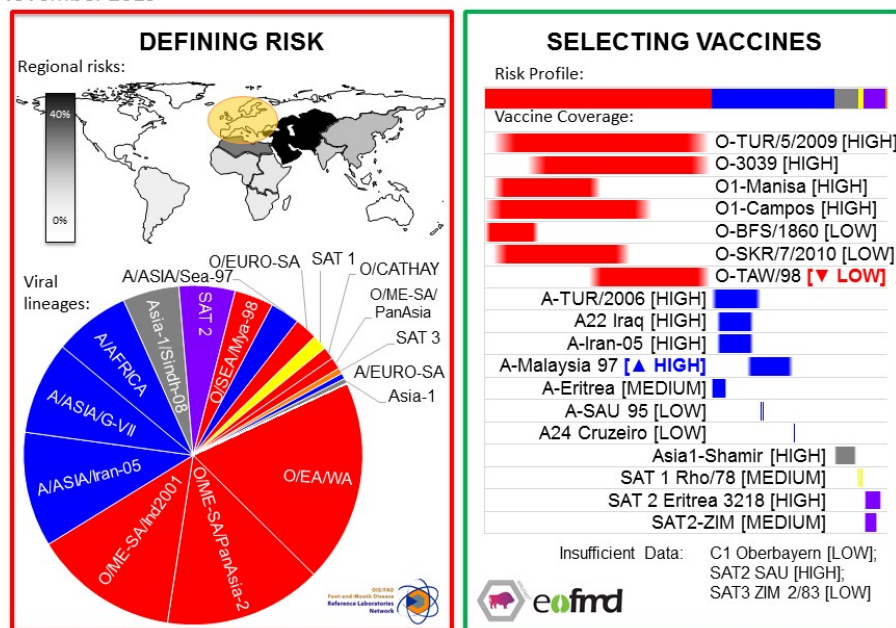
## Annex 3: Vaccine Recommendations

This report provides recommendations of FMDV vaccines to be included in antigen banks. These outputs are generated with a new tool (called PRAGMATIST) that has been developed in partnership between WRLFMD® and EuFMD. These analyses accommodate the latest epidemiological data collected by the OIE FAO FMD Laboratory Network regarding FMDV lineages that are present in different *source regions* (see Table below), as well as available *in vitro*, *in vivo* and field data to score the ability of vaccines to protect against these FMDV lineages.

Lineage	West Eurasia	East Asia	North Africa	India and Southern Asia	East Africa	West and Central Africa	Southern Africa	South America
O ME-SA PanAsia-2	35							
O ME-SA PanAsia		10						
O SEA Mya-98		33						
O ME-SA Ind2001	6	20	10	80				
O EA or O WA	3		55		55	70		
O EURO-SA								80
O CATHAY		10.5						
A ASIA Sea-97		25						
A ASIA Iran-05	25.5	0						
A ASIA G-VII	17.5			16				
A AFRICA			25		22	15		
A EURO-SA								20
Asia-1	12.5	1.5		4				
SAT 1			0		8	5	27	
SAT 2	0.5		10		14	10	57	
SAT 3					1		16	
C								

### Vaccine Antigen Prioritisation: Europe

November 2019



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

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The table defines the relative distribution of FMDV lineages in each of the eight *source regions*, while the figure highlights the importance of these *source regions* for **Europe** (using data collected at the EU-RL Workshop); please contact WRLFMD or 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.

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## Annex 4: Brief round-up of WRLFMD activities

### Proficiency test scheme organised by WRLFMD:

Phase XXXII (available in early 2020: invitation letters will be circulated shortly): Sample panels will be prepared and dispatched to participating laboratories: Panel 1 (available as either “live” FMDV or inactivated FMDV) will test virological methods, while Panel 2 will evaluate serological assays. We are proposing that this proficiency test focusses on laboratory confirmation of FMDV virus infection using different laboratory methods, and that laboratories will be scored according to expectations defined by the PCP status of their country, or their international reference laboratory status (see Table below). Please contact WRLFMD if you have any comments on this proposal, or if you would like more information about participating in this phase of the proficiency test scheme.

**Table** Minimum diagnostic testing capabilities for laboratories location in countries at different stages of the PCP (scored using common panels of identical samples sent to all participating laboratories – irrespective of their status).

Level	VIROLOGY (Panel 1)		SEROLOGY (Panel 2)	
	Minimum test requirements	Expected lab capability	Minimum test requirements	Expected lab capability
PCP 0	-	n/a	NSP ELISA	Define infection history (FMDV+/-)
PCP 1	either AgELISA or RT-PCR	<ul style="list-style-type: none"> <li>FMD virus present</li> <li>FMDV serotype</li> </ul>	NSP ELISA	Define infection history (FMDV+/-)
PCP 2	either AgELISA or RT-PCR	<ul style="list-style-type: none"> <li>FMD virus present</li> <li>FMDV serotype</li> </ul>	NSP ELISA SP ELISA	<ul style="list-style-type: none"> <li>Define infectious status</li> <li>vaccination status</li> <li>serotype</li> <li>+/- PVM</li> </ul>
PCP 3 PCP 4+	AgELISA rRT-PCR +/- sequencing +/- VI*	<ul style="list-style-type: none"> <li>FMD virus present</li> <li>FMDV serotype</li> <li>topotype, lineage</li> </ul>	NSP ELISA SP ELISA +/- VNT*	<ul style="list-style-type: none"> <li>Define infectious status</li> <li>vaccination status</li> <li>serotype</li> <li>+/- PVM</li> </ul>
OIE/FAO Reference Laboratories	Enhanced genome sequencing*	<ul style="list-style-type: none"> <li>FMD virus present</li> <li>FMDV serotype</li> <li>topotype, lineage, and relationship between FMDV positive samples in panel</li> </ul>	NSP ELISA SP ELISA +/- VNT*	<ul style="list-style-type: none"> <li>Define infectious status</li> <li>vaccination status</li> <li>serotype</li> <li>PVM</li> <li>identify cross-reactivity</li> </ul>

\* If able to receive the infectious panel

### Residential Training Course:

Information about the residential course that will run in May 2020 is posted on the website below; <https://www.pirbright.ac.uk/training-courses/diagnosis-foot-and-mouth-disease>

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## December 2019: 14<sup>th</sup> Annual Meeting of the OIE/FAO FMD Laboratory Network (Busan, South Korea)



### Headline events:

- As in past years, serotype O is the predominant serotype followed by serotype A.
- Further expansion of the O/ME-SA/Ind-2001e lineage during 2019 into Pakistan. These new outbreaks raise concern as it is the first time that this lineage has been detected in a West Eurasian country that has the potential for onward spread into countries such as Iran and Turkey.
- Continued outbreaks of O/EA-3 (2018/19) in North Africa (Libya and Morocco) following on from cases due to A/AFRICA/G-IV during 2017. There are now two distinct viral lineages responsible for the cases detected in North West Africa (Maghreb) and North East Africa (Egypt).
- Retrospective data confirms the presence of the SAT 1 lineage X in Cameroon in 2016.
- There has also been a new incursion of SAT 2/VII lineage into Egypt – most closely related to sequences from Ethiopia.
- New outbreaks of O/EA-2 in central Zambia and Comoros have been caused by two different lineages (15% nt difference). The Comoros lineage is most closely related to samples collected in Tanzania.
- An outbreak of SAT 2 in South Africa has resulted in a suspension of FMD-free status

### Summary of additional meetings attended by WRLFMD Scientists

- Don King attended EuFMD Excom in Paris (October 2019)
- Anna Ludi attended and presented at the 12<sup>th</sup> SEACFMD Laboratory Network Meeting in Pakchong Thailand (October 2019).
- Anna Ludi attended and presented at the 2<sup>nd</sup> Regional Expert Group Meeting on foot-and-mouth disease in Bangkok Thailand (October 2019)
- Valerie Mioulet attended the 1<sup>st</sup> Middle East FMD Epidemiology and Laboratory Networks meeting in Cairo, Egypt (November 2019)

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