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

OIE/FAO
Foot-and-Mouth Disease
Reference Laboratories
Network

WRLFMD

Foot-and-Mouth Disease

October-December 2020
Quarterly report

FAST Reports
Foot-and-mouth And Similar Transboundary animal diseases

European Commission for the
Control of Foot-and-Mouth Disease

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Sudan and South Sudan: *Final boundary between the Republic of Sudan and the Republic of South Sudan has not yet been determined.*

Abyei: *Final status of the Abyei area is not yet determined.*

Falkland Islands (Malvinas): *A dispute exists between the Governments of Argentina and the United Kingdom of Great Britain and Northern Ireland concerning sovereignty over the Falkland Islands (Malvinas).*

Contents

Abbreviations and acronyms

BVI	Botswana Vaccine Institute
EIDRA	Emerging Infectious Disease Research Association
EuFMD	European Commission for the Control of Foot-and-Mouth Disease
FAST reports	Foot-and-mouth and similar transboundary animal diseases reports
FGBI “ARRIAH”	Federal Governmental Budgetary Institution “Federal Centre for Animal Health”
FMD	Foot-and-mouth disease
FMDV	Foot-and-mouth disease Virus
FMDV GD	Foot-and-mouth disease Virus Genome detected
FMDV NGD	Foot-and-mouth disease Virus Genome not detected
GF-TAD	Global Framework for the Progressive Control of Transboundary Animal Diseases
LVRI	The National Reference Laboratory for FMD, The Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences
MEVAC	International Facility for Veterinary Vaccines Production (Egypt)
NT	Not tested
NVD	No virus detected
OIE	World Organisation for Animal Health
PIADC	Plum Island Animal Disease Center
rRT-PCR	Real-time reverse transcription polymerase chain reaction
SAARC	South Asian Association for Regional Cooperation
SADC	Southern Africa in collaboration with the Southern African Development Community
SAT	Southern African Territories
SEACFMD	South-East Asia and China FMD campaign
SSARRL	Sub-Saharan Africa Regional Reference Laboratory
SVD	Swine vesicular disease
VETBIS	Veterinary Information System of Turkey
VI	Virus Isolation
WAHIS	World Animal Health Information System (of the OIE)
WRLFMD	World Reference Laboratory for Foot-and-Mouth Disease

1. Highlights and headlines

Welcome to the first issue of the FMD Quarterly Report for 2021 and I take the opportunity to pass on my best wishes for the New Year. Despite the limitations placed on all of us by the COVID-19 pandemic, I was very pleased to be able to catch-up with many FMD colleagues via a series of meetings in "virtual" format organised at the end of 2020 - including the EU-RL Workshop (organised by ANSES and Sciensano), the Annual meeting of the OIE/FAO FMD Laboratory Network (www.foot-and-mouth.org), the 25th SEACFMD sub-commission meeting and the Open Session of EuFMD (https://www.eufmd.info/os20faster).

This report describes the latest intelligence and results from samples collected from FMD endemic countries. In recent years, particular attention has focused on FMD viruses that circulate in Pool 2 (South Asia) and the frequency by which these viruses can seed new outbreaks elsewhere in Asia. Examples of viruses that have spread from Pool 2 include O/ME-SA/Ind-2001 (d and e sub-lineages) and A/ASIA/G-VII. Earlier in 2020, a new serotype O lineage was described for samples collected in Sri Lanka (see Jan-Mar 2020 report); new data provided from ICAR-DFMD India during the OIE/FAO FMD Laboratory Network meeting provides further evidence that this lineage (tentatively named O/ME-SA/SA-2018) is more widely distributed in South Asian countries. Data in this report also describes new genetic clade within the O/ME-SA/PanAsia^{FAR-11} sub-lineage which has been detected in Iran and presents the phylogenetic tree for the new cases due to the O/ME-SA/PanAsia^{ANT-10} sub-lineage detected in Turkey. Elsewhere, sub-clinical cases (due to SAT 1) have been reported in South Africa.

The WRLFMD has been recently working with EuFMD to develop an open-access interactive FMD dashboard to allow users to interrogate, retrieve and display FMD information (including FMDV genomic data). The scope and functionality of the improved tools implemented during this project will be influenced by **your requirements** and therefore we are seeking feedback to help us to understand how we should prioritise the design of this system. For those you that are interested, please complete the survey in the link: https://forms.office.com/Pages/ResponsePage.aspx?id=Eh70v1zu20izMQzOHucOut-ijsc2qwZOo151ynO2MwhUN01SUFVROTc3TTRYRklEMTU3WU1FTUsyQy4u

Don King, Pirbright January 2021

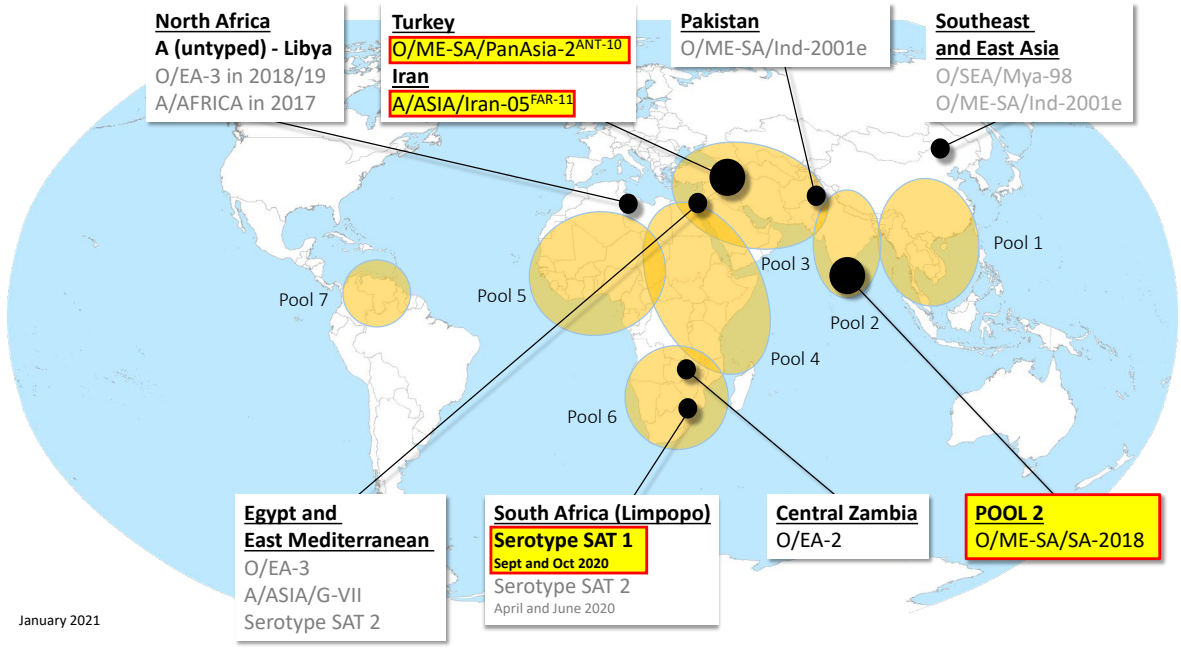


Figure 1: Recent headline events (reported October-December 2020) with endemic pools highlighted in orange. Source: WRLFMD. Map conforms to the United Nations World Map, June 2020.

2. General overview

Endemic 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.

POOL	REGION/COUNTRIES	SEROTYPES PRESENT
1	**SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA** Cambodia, China, China (Hong Kong SAR), Taiwan Province of China, Democratic People's Republic of Korea, Republic of Korea, Lao People's Democratic Republic, Malaysia, Mongolia, Myanmar, Russian Federation, Thailand, Viet Nam	A, Asia 1 and O
2	**SOUTH ASIA** Bangladesh, Bhutan, India, Mauritius, Nepal, Sri Lanka	A, Asia 1 and O
3	**WEST EURASIA & MIDDLE EAST** Afghanistan, Armenia, Azerbaijan, Bahrain, Georgia, Iran (Islamic Republic of), Iraq, Israel, Jordan, Kazakhstan, Kuwait, Kyrgyzstan, Lebanon, Oman, Pakistan, Palestine, Qatar, Saudi Arabia, Syrian Arab Republic, Tajikistan, Turkey, Turkmenistan, United Arab Emirates, Uzbekistan	A, Asia 1 and O (SAT 2)
4	**NORTH AFRICA** Algeria, Egypt, Libya, Morocco, Tunisia	A, O and SAT 2
	EASTERN AFRICA Burundi, Comoros, Djibouti, Eritrea, Ethiopia, Kenya, Rwanda, Somalia, South Sudan, Sudan, Uganda, United Republic of Tanzania, Yemen	O, A, SAT 1, SAT 2 and SAT 3
5	**WEST/CENTRAL AFRICA** Benin, Burkina Faso, Cabo Verde, Cameroon, Central African Republic, Chad, Congo, Côte d'Ivoire, Democratic Republic of the Congo, Equatorial Guinea, Gabon, Gambia, Ghana, Guinea, Guinea-Bissau, Liberia, Mali, Mauritania, Niger, Nigeria, Sao Tome and Principe, Senegal, Sierra Leone, Togo	O, A, SAT 1 and SAT 2
6	**SOUTHERN AFRICA** Angola, Botswana, Malawi, Mozambique, Namibia, South Africa, Zambia, Zimbabwe	SAT 1, SAT 2 and SAT 3 (O, A)[†]
7	**SOUTH AMERICA** Colombia, Venezuela (Bolivarian Republic of)	O and A

[†] *only in Angola and north Zambia as spill-over from pool 4*

3. Summary of FMD outbreaks and intelligence

3.1. 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.

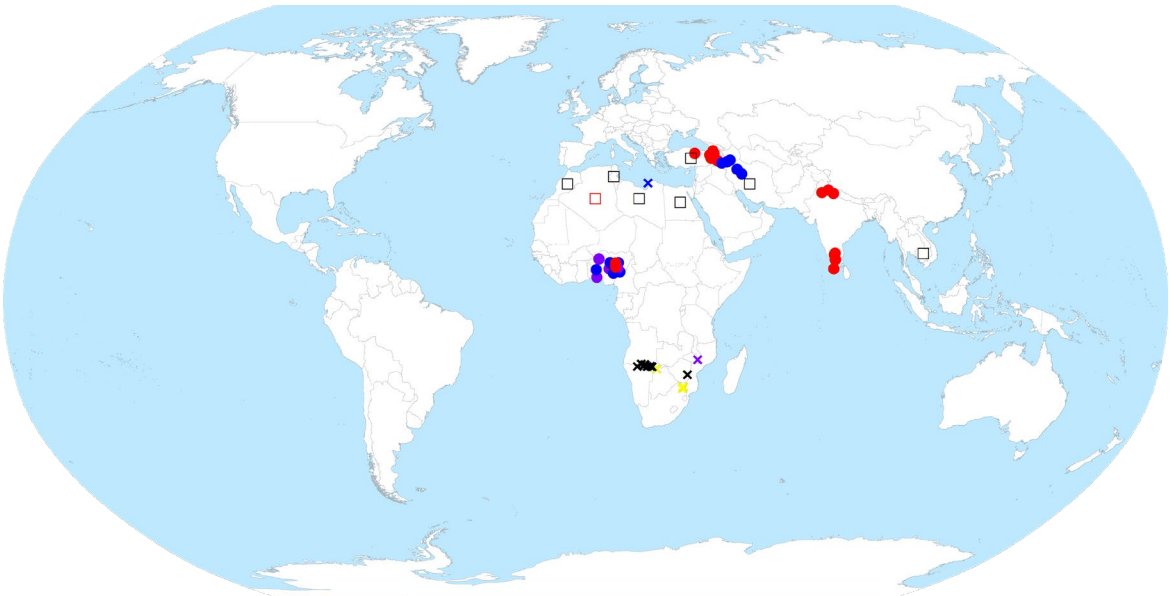


Figure 2: Samples tested by WRLFMD or reported in this quarter. ● indicates samples analysed; × indicates new outbreaks reported to the OIE, but where results to define the genotype have not been reported; □ indicates reports of FMD from other sources. Shape colours define the serotype detected ●O; ●A; ●C; ●Asia1, ●SAT1, ●SAT2, ●SAT3, ○ FMD not detected, ● serotype undetermined/not given in the report.

Source: WRLFMD. Map conforms to the United Nations World map, June 2020.

3.2. Pool 1 (Southeast Asia/Central Asia/East Asia)

The Kingdom of Cambodia

A batch of nine samples was received to WRLFMD on 22 December 2020. Typing and genotyping is underway and will be reported shortly.

FMD is reported to have affected 707 cattle, causing 34 deaths, in Siem Reap province and 1645 cattle in Pailin province. Veterinary officers have been adminstering vaccines to cattle in the affected areas.

ProMED post: 20201117.7949239

The Lao People's Democratic Republic

A batch of five samples was received to WRLFMD on 22 December 2020. Typing and genotyping is underway and will be reported shortly.

The Kingdom of Thailand

A batch of 16 samples was received to WRLFMD on 22 December 2020. Typing and genotyping is underway and will be reported shortly.

3.3. Pool 2 (South Asia)

The Republic of India

The ICAR-Directorate of Foot-and-Mouth Disease, recently published a study of **FMD type O** in which 286 VP1 sequences were reported (Dahiya *et al*., 2020). Genotyping showed that all sequences belonged to the ME-SA topotype; two belonged to the PanAsia lineage, 271 to the Ind-2001 lineage (60 were 'd' sublineage and 211 were 'e' sublineage). Additionally, 13 sequences belonged to a new lineage which we have named O/ME-SA/SA-2018 (SA for South Asia). Exchange of sequence data at the OIE/FAO FMD Laboratory Network meeting (during December) demonstrated that three viruses previously found in Sri Lanka in 2018 and 2019 also belong to this new lineage.

Reference: Dahiya SS, Subramaniam S, Biswal JK, Das B, Prusty BR, Ali SZ, Khulape SA, Mohapatra JK, Singh RK. (2020). Genetic characterization of foot-and-mouth disease virus serotype O isolates collected during 2014-2018 revealed dominance of O/ME-SA/Ind2001e and the emergence of a novel lineage in India. *Transboundary and Emerging Diseases*, 2020 Dec 10. https://doi.org/10.1111/tbed.13954. Epub ahead of print. PMID: 33305514.

3.4. Pool 3 (West Eurasia and Middle East)

The Republic of Turkey

Turkey reported the occurrence of 28 FMD outbreaks in cattle (n=21) and small ruminant (7) populations between October and December 2020 (18 in October, 5 in November and 5 in December), among which 21 were confirmed serotype O. This brings the total number of clinical outbreaks in 2020 to 147, with the number of confirmed outbreaks reported to ADNS being 142 (Source: ADNS). The outbreaks that occurred during the last trimester were distributed in different parts of Anatolia (Ardahan, Bursa, Corum, Denizli, Erzurum, Eskisehir, Isparta, Izmir, Karramanmaras, Kars, Mus, Samsun, Sinop, Tokat, Van, Zondulak

provinces). EuFMD focal points from the Transcaucasus countries were informed about outbreaks in proximity to their borders, as part of the Statement of Intentions between Transcaucasia and neighboring countries (SOI). This triggered targeted control measures, including vaccination, surveillance and awareness raising in the adjoining border regions of the Transcaucasus countries.

FMD is endemic in Anatolia and the circulating sublineages are still believed to be the O PanAsia-2/Qom15 and O PanAsia-2/ANT10 as reported in the previous FAST report. Both are well matched to the vaccines currently in use. Serotypes A and Asia1 were not detected since January 2018 and July 2015, respectively.

On 06 October 2020, six **FMD type O VP1** sequences were received from the FMD (Şap) Institute, Ankara. They originated from samples collected from cattle (and one sheep) between December 2019 and September 2020. Genotyping revealed that all belonged to the ME-SA topotype, PanAsia-2 lineage while four sequences belonged to the QOM-15 sublineage (from the provinces of Ardahan, Erzurum, Kars and Mus) and two to the ANT-10 sublineage (from the provinces of Tokat and Van) (see below).

The Islamic Republic of Iran

During an official meeting with EuFMD on 22 December 2020, the Islamic Republic of Iran reported about 60 FMD outbreaks in large ruminants and 10 outbreaks in small ruminants between October and November 2020. For the first 8 months of 2020, 974 FMD outbreaks were reported in Iran. FMD outbreaks are mostly reported at the end of winter and beginning of spring, due to the combination of more intense livestock movements, increased number of small ruminants (newborns) and more suitable climatic conditions for FMDV environmental survival at these periods. Within the A/ASIA/Iran-05 lineage, the main circulating sublineages identified between January and November 2020 were Sis-12, Sis-13, Far-11 while for O/ME-SA/PanAsia-2, it was Qom-15 and Ant-10. The main Asia 1 lineage was Sindh-08. The O PanAsia-2 Ant-15 sublineage has been predominant between January to November 2020, but the A Iran-05 Far-11 sublineage has been increasingly detected in recent weeks. Implementation of biosecurity measures and vaccination strategies were the main control measures to be applied.

According to the Iran Veterinary Organization (IVO), 6,204,125 large ruminants and 44,599,728 small ruminants were vaccinated against FMD between 1st January and 1st November 2020, using trivalent vaccines (O, A, Asia1) that were either locally produced or imported.

On 25 November 2020, six VP1 sequences of **FMD type A** were received from Central Veterinary Laboratory of the Iran Veterinary Organisation (CVL-IVO). The samples were collected between May and November 2020 from outbreaks in cattle in the provinces of Ardabil, East Azerbaijan, Qom, Qazvin and West Azerbaijan. Genotyping showed the six sequences belonged to the ASIA topotype, Iran-05 lineage, FAR-11 sublineage (see below).

The Republic of Iraq

Five VP1 sequences were retrieved from GenBank on 23 October 2020. The sequences were derived from nasal swabs collected from bovines in June 2019 and had been submitted by Drs. Abdul-Satar S Sadoon and QT Al-Obaidi of the University of Mosul. Two sequences belonged to **FMD type O**, one to **FMD type Asia 1** and two to **FMD type SAT 1**. Genotyping showed that the type O viruses belonged to the ME-SA topotype, PanAsia-2 lineage; the Asia 1 viruses belonged to the Sindh-08 lineage; and the SAT 1 viruses belonged to two different topotypes, I (NWZ) and IX (see below). The presence of these virus in Iraq requires confirmation by one of the OIE or FAO reference laboratories.

3.5. Pool 4 (North and Eastern Africa)

The People's Democratic Republic of Algeria

The last FMD outbreak in Algeria was reported in March 2019 (lineage O EA-3). The vaccination program consists of mass vaccination twice a year for large ruminants (except in 4 southern wilayas) using $6PD_{50}$ vaccine (strains O 3039, O Manisa, A 22 Iraq). Between December 2019 and March 2020, 844,734 large ruminants were reportedly vaccinated (representing 60% vaccination coverage). An additional campaign was initiated in October 2020.

The Arab Republic of Egypt

Four FMD outbreaks were detected in 2020, two confirmed as SAT2 serotype and the others confirmed as serotype A. Source: REMESA JPC meeting. The General Organization for Veterinary Services (GOVS) in Egypt conducted sero-surveillance in November 2020 targeting six governorates along the border (Aswan, Matrouh, New Valley, North Sini, South Sini, and Red Sea). The surveillance was supported by EuFMD through the provision of diagnostic kits. The objective of the surveillance was to estimate the serological prevalence to NSP antibodies among the large and small ruminant populations, focusing on the 6-18 months age category. Sera were collected from 1,680 randomly selected animals and tested using a 3ABC NSP ELISA. The results revealed an overall NSP seroprevalence of 10.8% (182/1,680; 95%CI 9.4-12.4%) for small and large ruminants combined. The highest seroprevalence was in Aswan governorate (23.6%) with the lowest being in Matruh governorate

The State of Libya

Two outbreaks were notified to the OIE on 15th December 2020 (date of start of the outbreaks: 1st November 2020; current status as of 13th January 2021: continuing). Five cases were reported among sheep on two farms located in the Eastern region (Benghazi) with a population of 313 susceptible sheep and 26 goats. Clinical signs included fever, lameness, and abortion in some cases. No genotyping has been reported, but the AFRICA topotype, G-IV lineage has been reported previously.

OIE Immediate notification & Follow-up reports

An investigation team from the National Centre for Animal Health (NCAH), Tripoli visited the areas around the infected premises in Benghazi, Al-Marj, Al-Abyaar, the Gulf of Sirte and Tukra. Sera from 173 cattle, sheep and goats were collected, with 9 sheep and 10 cattle samples from Benghazi and Al-Marj testing positive to NSP antibodies. Structural proteins (SP) ELISA testing to indicate the possible serotype is still pending, noting previous reports identified serotype A as the likely cause. Source: NCAH

Recently, the NCAH adopted a new FMD vaccination strategy, and is planning to receive 400,000 doses to vaccinate the cattle population in Libya (estimated at 100,000 head), providing two doses, two weeks apart. Small ruminants will also be vaccinated using a ring vaccination strategy in response to reported outbreaks. An FMD virtual awareness campaign targeting public and private vets on the topics of FMD diagnosis, sampling, biosecurity, and epidemiology are currently underway, also implemented by the NCAH, in collaboration with EuFMD and the FAO sub-regional office for North Africa

The Kingdom of Morocco

Morocco renews the OIE endorsed, FMD official control program each year. The last outbreak in Morocco was reported in July 2019. The vaccination strategy uses a bivalent vaccine (strains: O/TUR/2009, A22/IRQ/64. Based on in vitro vaccine matching, the r_1 values indicated a good match between the O/TUR/2009 vaccine and strains from the O/EA-3 lineage circulating in the region. Since 2019, the vaccination program consisted of mass vaccination twice a year for large ruminants (approximately 2.8 million animals) and once yearly risk-based vaccination of small ruminants in border regions in the eastern part of the country (approximately 5 million animals). Morocco conducted post vaccination monitoring studies, with satisfactory results from a small-scale immunogenicity study in 2019 and a population immunity study in 2020.

The Republic of Tunisia

No outbreaks were reported in 2020 in Tunisia. The vaccination strategy against FMD consists of annual mass vaccination using $6PD_{50}$ trivalent vaccine (strains: O3039, O Manisa, SAT2 Eritrea, A Iraq22) for large ruminant and bivalent (O3039, O Manisa, SAT2 Eritrea) for small ruminants. The reported vaccination coverage in 2020 was 71.2% in large ruminants and 85.7% in small ruminant populations.

3.6. Pool 5 (West/Central Africa)

The Federal Republic of Nigeria

On 25 November 2020, 18 FMDV sequences were received from National Centre for Foreign Animal Disease (NCFAD), Winnipeg, Canada. These were produced in collaboration with the National Veterinary Research Institute (NVRI), Vom, Nigeria. Two sequences were **FMD type O**, 14 were **FMD type A** and two were **FMD type SAT 2**. Genotyping revealed the type O viruses to belong to the WA topotype; the type A viruses all belonged to the AFRICA topotype, G-IV lineage; and the SAT 2 viruses belonged to

topotype VII. Some of the sequences were incomplete VP1's and are too short to have been included in the trees.

On the 11 December 2020, 25 VP1 sequences were retrieved from GenBank. They had been submitted by the Sciensano Research Institute (Ukkel, Belgium) as part of a joint study with the NVRI. All sequences were derived from samples collected from cattle in the Abuja Federal Capital Territory and the Bauchi, Benue, Kaduna, Oyo and Plateau States between 2013 and 2017. Fourteen were **FMD type O**, six were **FMD type A**, three were **FMD type SAT 1** and two were **FMD type SAT 2**. Genotyping showed that two type O viruses belonged to the WA topotype and 12 to the EA-3 topotype; all six type A viruses belonged to the AFRICA topotype, G-IV lineage; the three SAT 1 viruses belonged to topotype X; and the two SAT 2 viruses belonged to topotype VII, Lib-12 lineage (see below).

3.7. Pool 6 (Southern Africa)

The Republic of Botswana

A single outbreak of FMD type SAT 1 was reported in cattle on 13 September 2020 in Ngamiland (North-West district). VP1 genotyping was performed in the OIE Sub-Saharan Africa Regional Reference laboratory (SSARRL) for FMD at the Botswana Vaccine Institute (BVI) and showed the virus to belong to topotype III (WZ) (see below).

OIE Immediate notification & Follow-up reports

The Republic of Malawi

An outbreak of **FMD type SAT 2** was previously reported in cattle at Kasokeza, Maperera Dip tank, Chikwawa, Southern Region on 7 August 2020. VP1 sequencing was performed at the OIE Sub-Saharan Africa Regional Reference laboratory (SSARRL) for FMD at the Botswana Vaccine Institute (BVI) on two samples and showed that the virus belonged to topotype I (see below).

OIE Immediate notification & Follow-up reports

The Republic of Namibia

Between 25 September 2020 and 25 October 2020, four outbreaks of **FMD type SAT 2** were reported in cattle in the Kavango East and Kavango West regions. No genotyping has been reported.

OIE Immediate notification & Follow-up reports

The Republic of South Africa

Between 03 September 2020 and 23 October 2020, three outbreaks of **FMD type SAT 1** were reported in cattle in Greater Giyani, Limpopo. Diagnosis of these sub-clinical cases was performed using serological methods and no genotyping has been reported.

OIE Immediate notification & Follow-up reports

The Republic of Uganda

A batch of 11 samples was received to WRLFMD on 16 December 2020. Typing and genotyping is underway and results will be reported shortly.

The Republic of Zimbabwe

An outbreak of FMD (untyped) was reported in cattle on 12/10/2020 at Chinyika, Bikita, Masvingo.

OIE Immediate notification & Follow-up reports

3.8. Pool 7 (South America)

No new outbreaks of FMD were reported in South America.

3.9. Extent of global surveillance

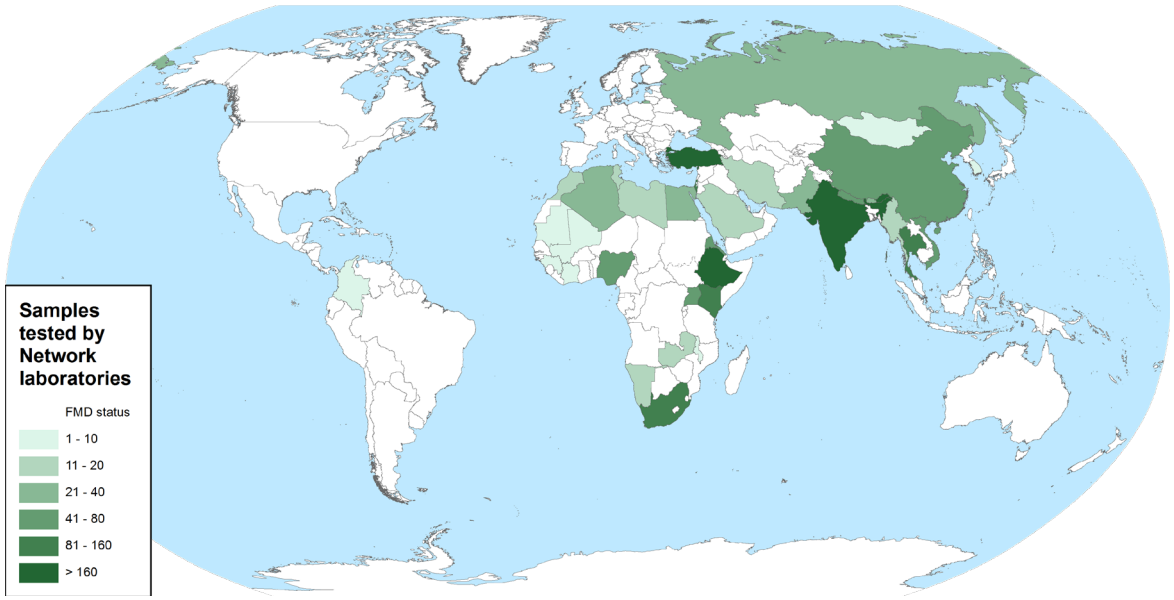


Figure 3: Samples received during 2019 from FMD outbreaks (routine surveillance that is undertaken in countries that are FMD-free without vaccination is not shown). Data from presentations given at the OIE/FAO Reference

laboratory Network annual meeting (https://www.foot-and-mouth.org/Ref-Lab-Network/Network-Annual-Meeting)

Source: WRLFMD. Map conforms to the United Nations World map, June 2020.

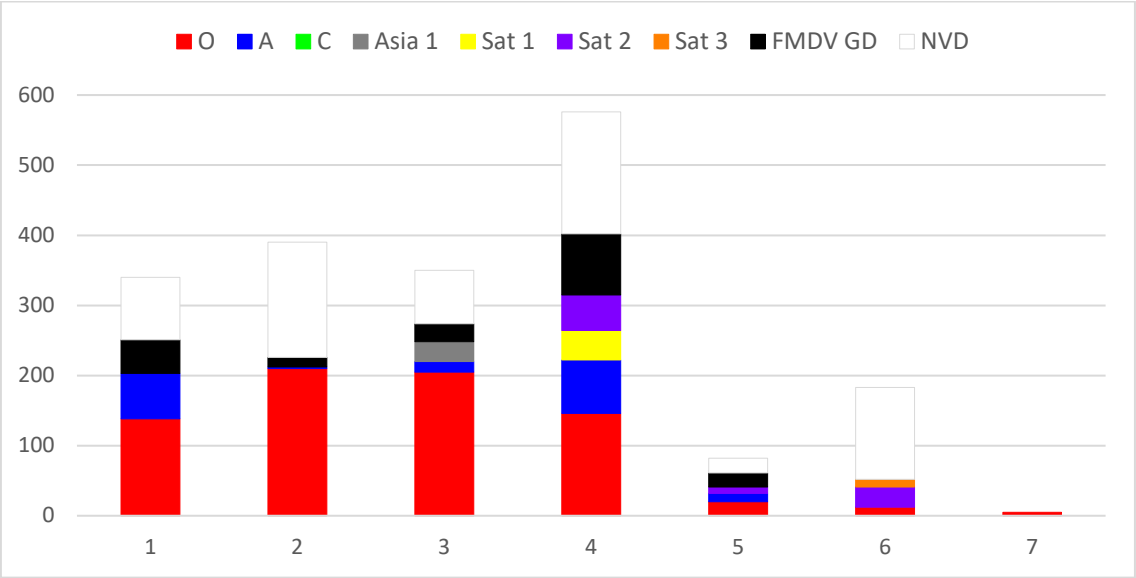


Figure 4: Representation of different FMDV serotypes detected in samples tested from the FMD endemic pools by the OIE/FAO FMD Laboratory Network during 2019 (draft data) (NVD = no virus detected; GD = genome detected)

In regions where FMD is endemic, continuous evolution of the virus generates geographically discrete lineages that are genetically distinct from FMD viruses found elsewhere. This report displays how different FMD lineages circulate in different regions; these analyses accommodate the latest epidemiological intelligence to assess the relative importance of the viral strains circulating within each regions (see Table 1, below).

Table 1: Conjectured relative prevalence of circulating FMD viral lineages in each Pool. For each of the regions, data represent the relative importance of each viral lineage [prevalence score estimated as a percentage (%) of total FMD cases that occur in domesticated hosts]. These scores (reviewed at the OIE/FAO FMD Laboratory Network meeting in December 2020) can be used to inform the PRAGMATIST tool (see Annex 3). Recent changes to increase risks are shown in red, while a reduction in risk is shown in green.

Lineage	Southeast / Central / East Asia [Pool 1]	South Asia [Pool 2]	West Eurasia & Middle East [Pool 3]	North Africa	Eastern Africa [Pool 4]	West / Central Africa [Pool 5]	Southern Africa [Pool 6]	South America [Pool 7]
O ME-SA PanAsia-2			35					
O ME-SA PanAsia	10							
O SEA Mya-98	33							
O ME-SA Ind2001	20	80	7	10				
O EA or O WA			3	55	55	70		
O EURO-SA								80
O CATHAY	10.5							
A ASIA Sea-97	26							
A ASIA Iran-05	0		27					
A ASIA G-VII		16	15					
A AFRICA				25	22	15		
A EURO-SA								20
Asia-1	0.5	4	12.5					
SAT 1				0	8	5	27	
SAT 2			0.5	10	14	10	57	
SAT 3					1		16	
C								

A number of outbreaks have occurred where samples have not been sent to the WRLFMD or other laboratories in the OIE/FAO FMD Laboratory Network. 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-2020.

Results from samples or sequences received at WRLFMD (status of samples being tested) are shown in Table 2 and a complete list of clinical sample diagnostics made by the WRLFMD from October to December 2020 is shown in Annex 1: (Summary of submissions). A record of all samples received by WRLFMD is shown in Annex 1: (Clinical samples).

Table 2: Status of sequencing of samples or sequences received by the WRLFMD from October to December 2020 (* 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/2020/00006	16/12/2020	Uganda	pending	11	-	pending
WRLFMD/2020/00007	22/12/2020	Thailand	pending	16	-	pending
WRLFMD/2020/00008	22/12/2020	Cambodia	pending	9	-	pending
WRLFMD/2020/00009	22/12/2020	Lao P.D.R.	pending	5	-	pending
			Total	**41**	**-**	

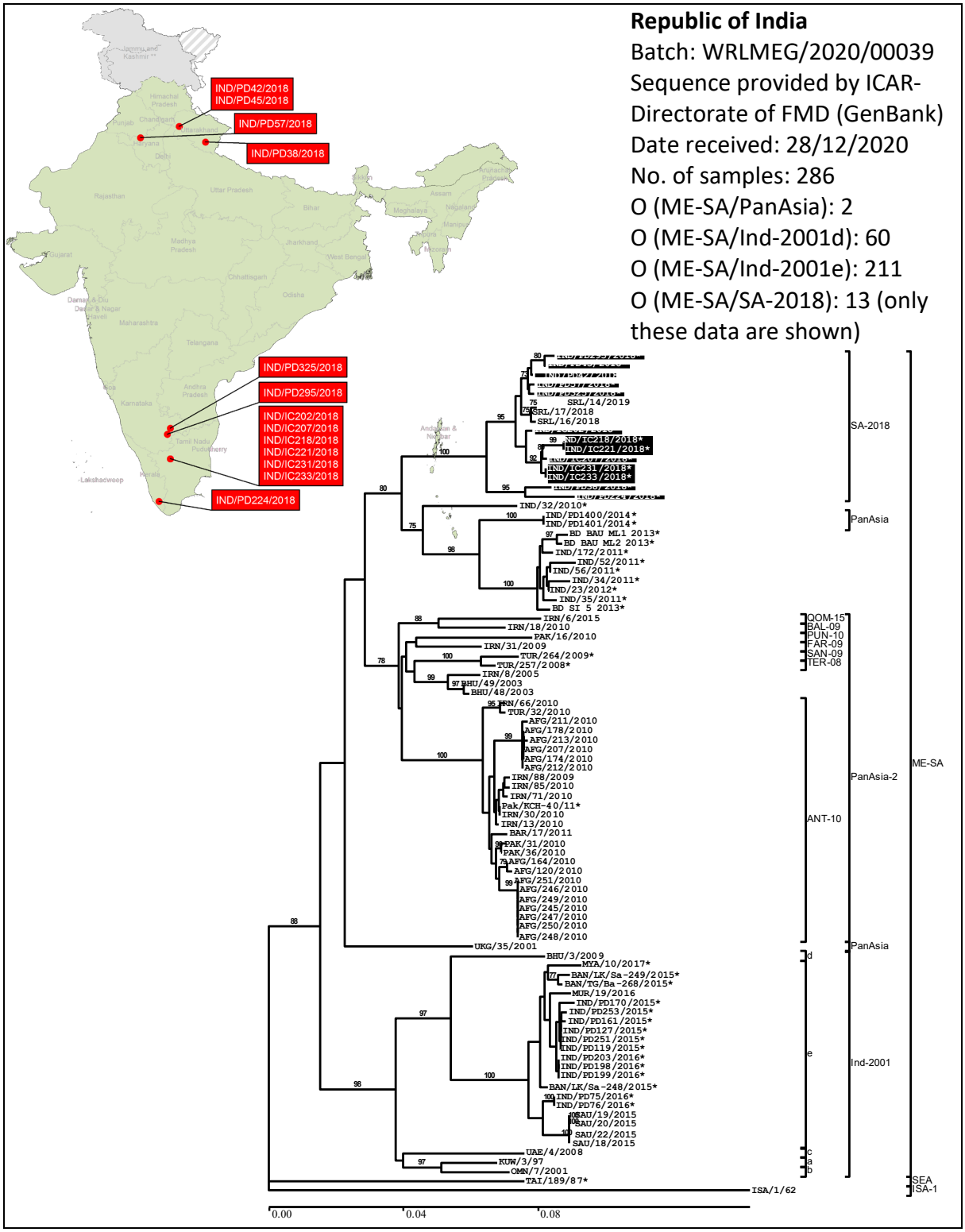
Table 3: VP1 sequences submitted by other FMD Network laboratories to the WRLFMD from October to December 2020 (* indicates sequences retrieved from GenBank).

WRLFMD Batch No.	Date received	Country	Serotype	Date Collected	No. of sequences	Submitting laboratory
WRLMEG/2020/00026	06/10/2020	Turkey	O	2019, 2020	6	FMDI
WRLMEG/2020/00027	19/10/2020	Botswana	SAT 1	2020	2	SSARL
WRLMEG/2020/00028	19/10/2020	Malawi	SAT 2	2020	2	SSARL
WRLMEG/2020/00035	23/10/2020	Iraq	O	2019	2*	Univ. of Mosul
			Asia 1	2019	1*	
			SAT 1	2019	2*[1]	
WRLMEG/2020/00036	25/11/2020	Iran	A	2020	6	CVL
WRLMEG/2020/00037	25/11/2020	Nigeria	O	2020	1	NCFAD (Canada)/ NVRI (Nigeria)
			A	2019, 2020	10	
			SAT 2	2019	2	
WRLMEG/2020/00038	11/12/2020	Nigeria	O	2013, 2014, 2015, 2017	14*	Sciensano (Belgium) / NVRI (Nigeria)
			A	2015, 2017	6*	
			SAT 1	2015	3*	
			SAT 2	2013, 2017	2*	
WRLMEG/2020/00039A	28/12/2020	India	O	2018	13*	ICAR-DFMD
				Total	**72**	

[1] confirmation of these results requires input from OIE of FAO FMD Reference Laboratories

4. Detailed analysis

4.1. Pool 1 (Southeast Asia/Central Asia/East Asia)



4.2. Pool 3 (West Eurasia and Middle East)

Islamic Republic of Iran

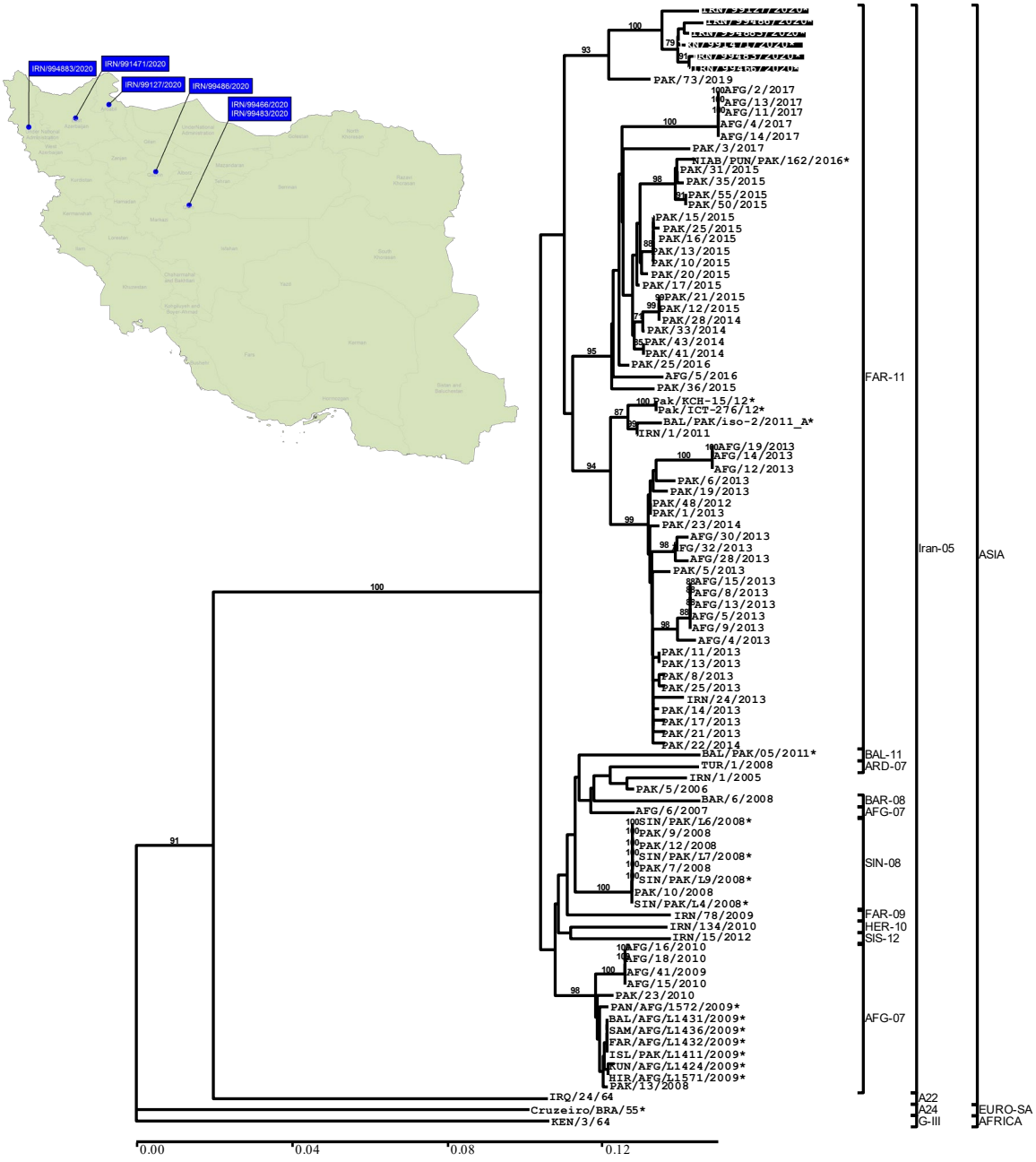
Batch: WRLMEG/2020/00036

Sequence provided by CVL-IVO

Date received: 25/11/2020

No. of samples: 6

A (ASIA/Iran-05^{FAR-11}): 6



Republic of Turkey

Batch: WRLMEG/2020/00026

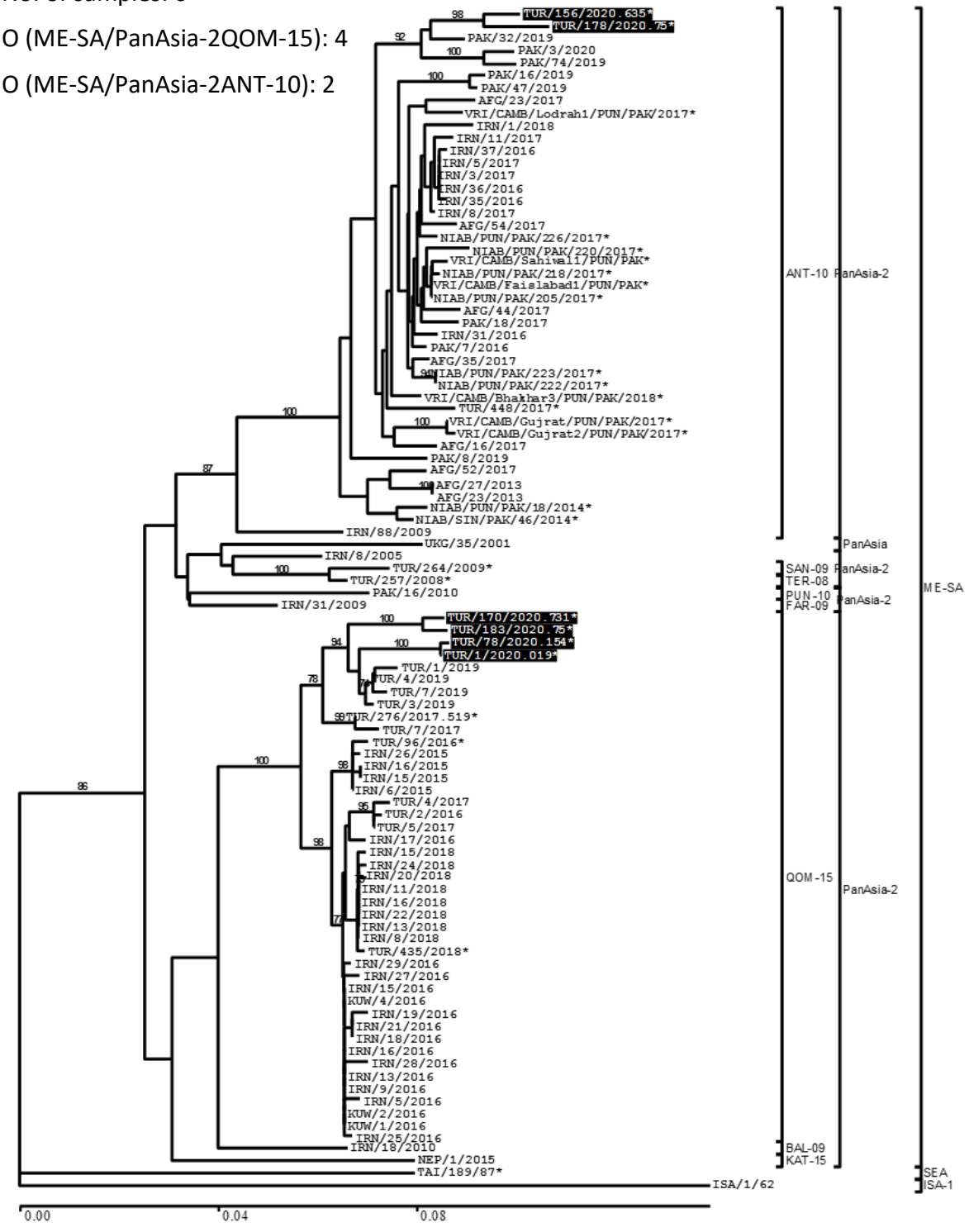
Sequence provided by FMDI-Ankara

Date received: 06/10/2020

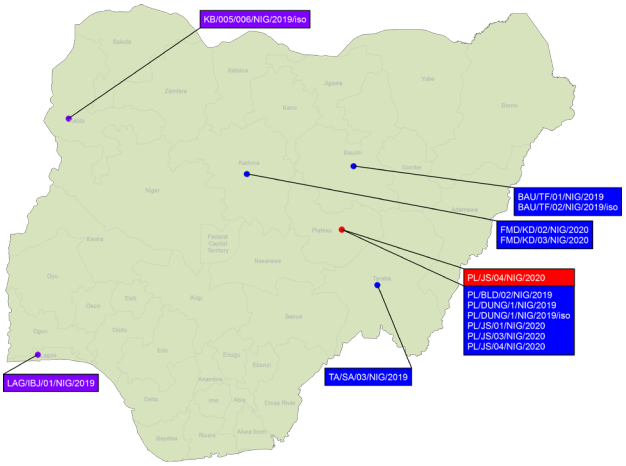
No. of samples: 6

O (ME-SA/PanAsia-2QOM-15): 4

O (ME-SA/PanAsia-2ANT-10): 2



4.3. Pool 5 (West/Central Africa)



Federal Republic of Nigeria

Batch: WRLMEG/2020/00037

Sequence provided by NCFAD/NVRI

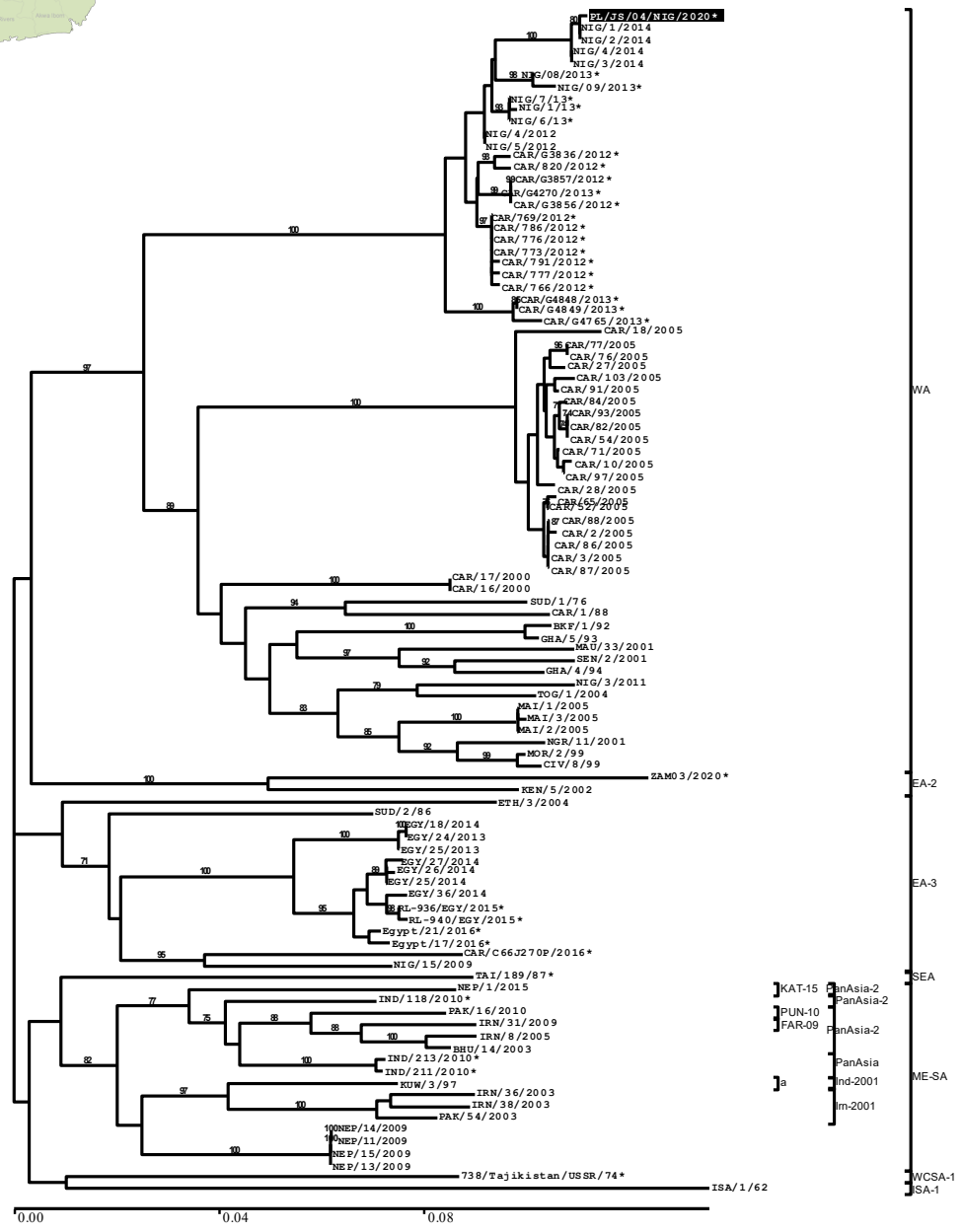
Date received: 25/11/2020

No. of samples: 18

O (WA): 2

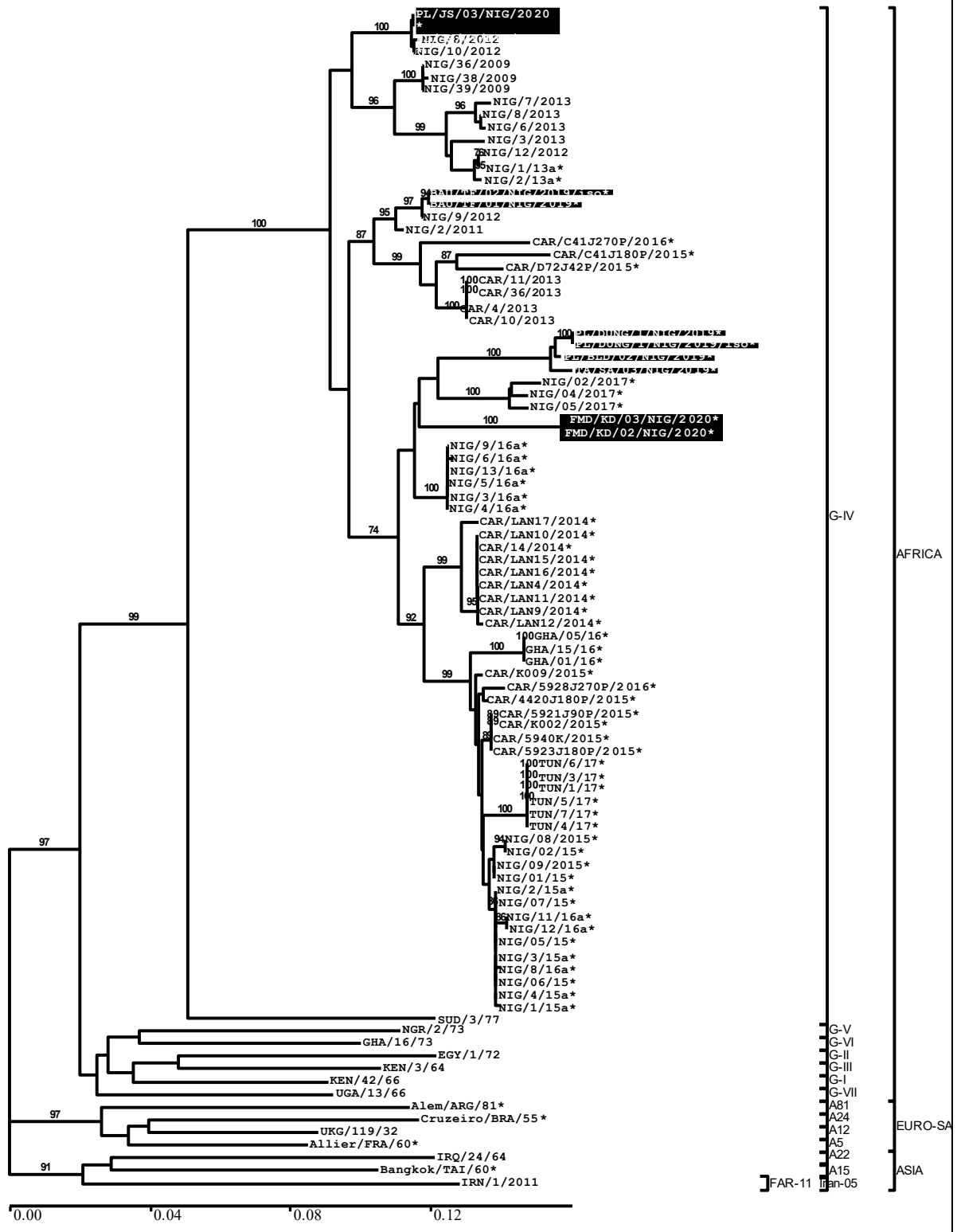
A (AFRICA/G-IV): 14

SAT2 (VII): 2



Nigeria continued on next page

Nigeria Contiunued



Nigeria continued next page

Nigeria continued

Federal Republic of Nigeria

Batch: WRLMEG/2020/00038

Sequence provided by Sciensano (GenBank)

Date received: 11/12/2020

No. of samples: 25

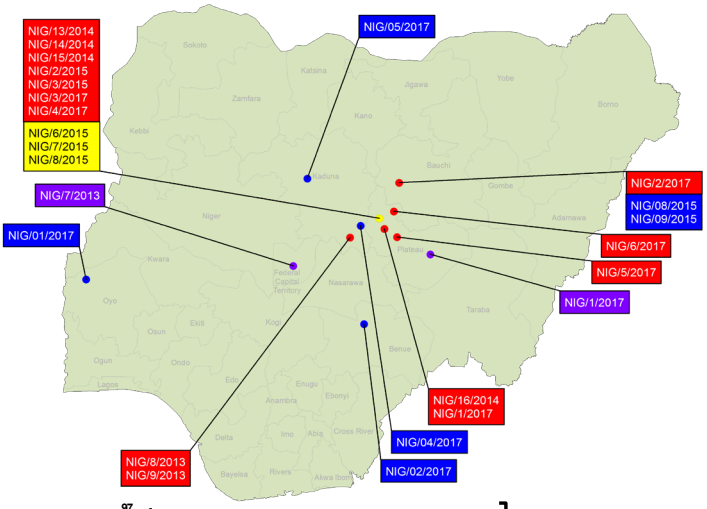
O (EA-3): 12

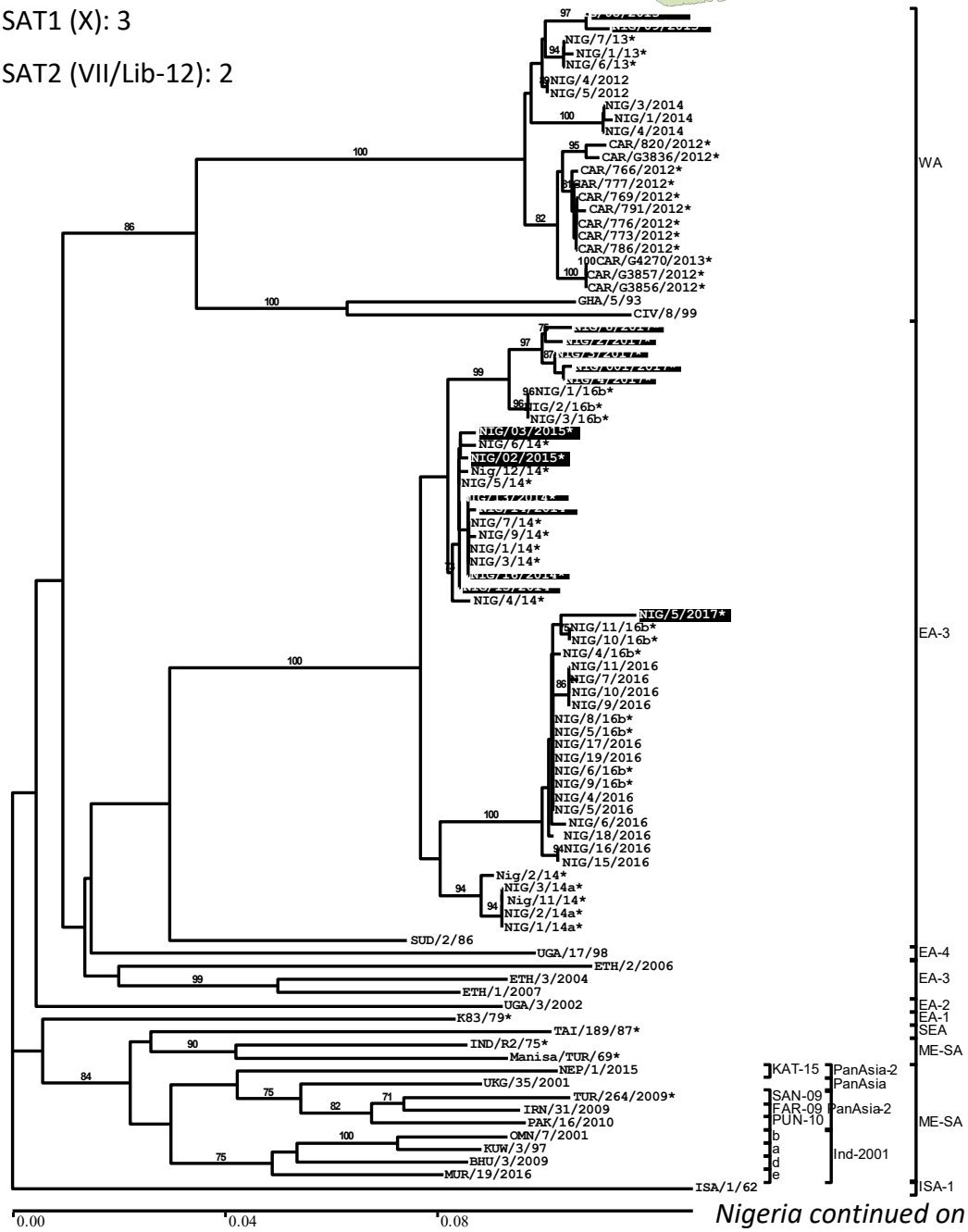
O (WA): 2

A (AFRICA/G-IV): 6

SAT1 (X): 3

SAT2 (VII/Lib-12): 2





Nigeria continued on next page

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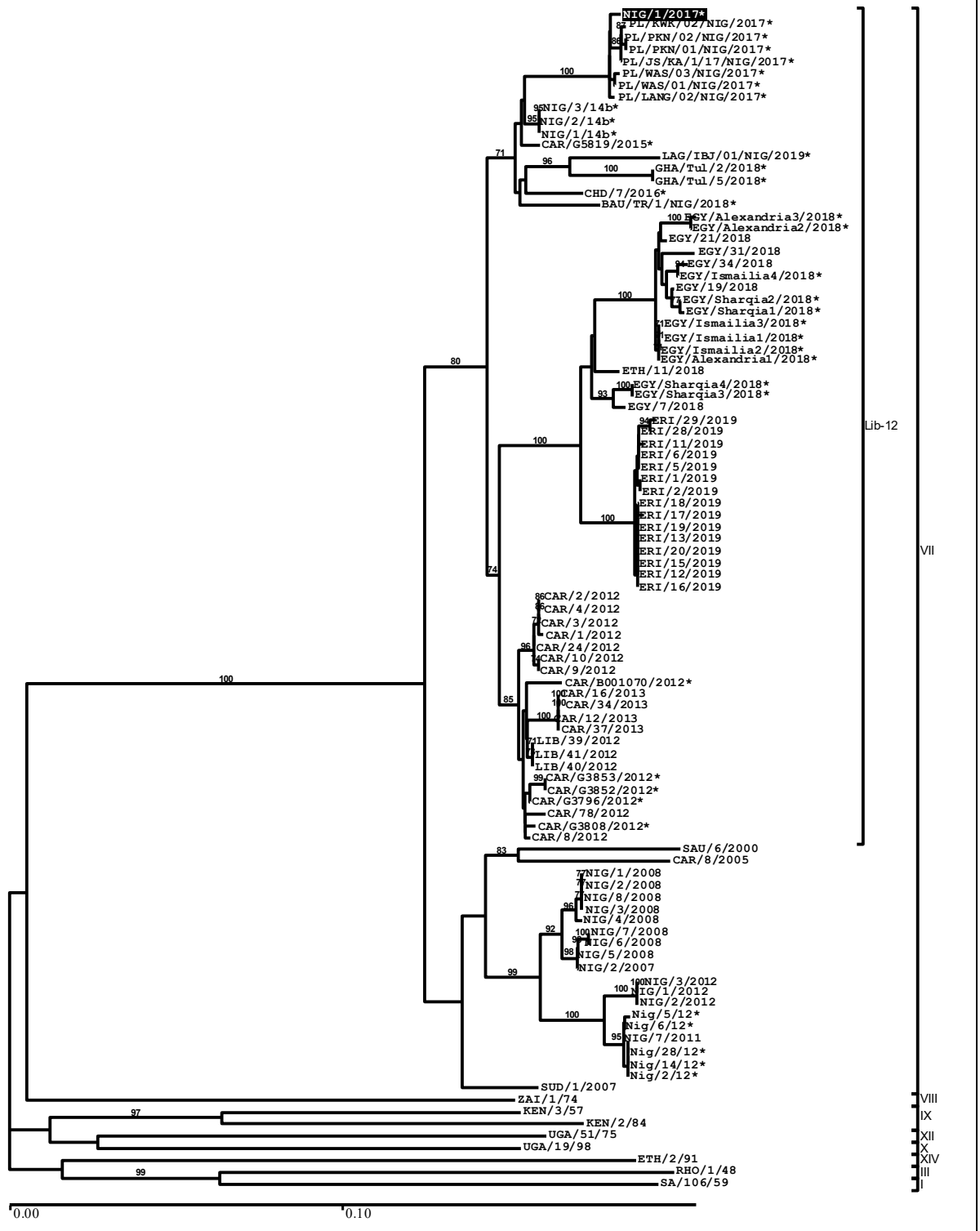
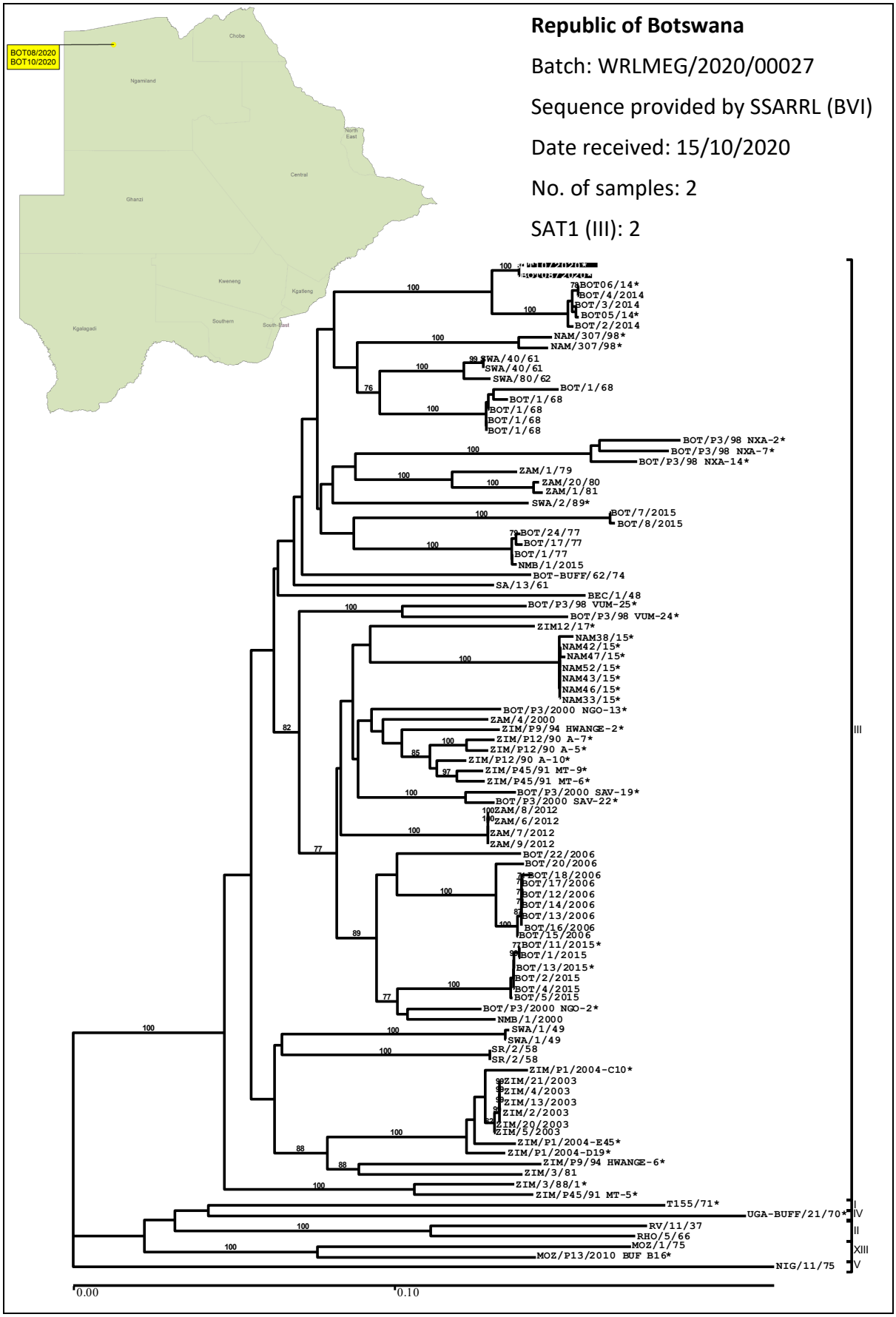
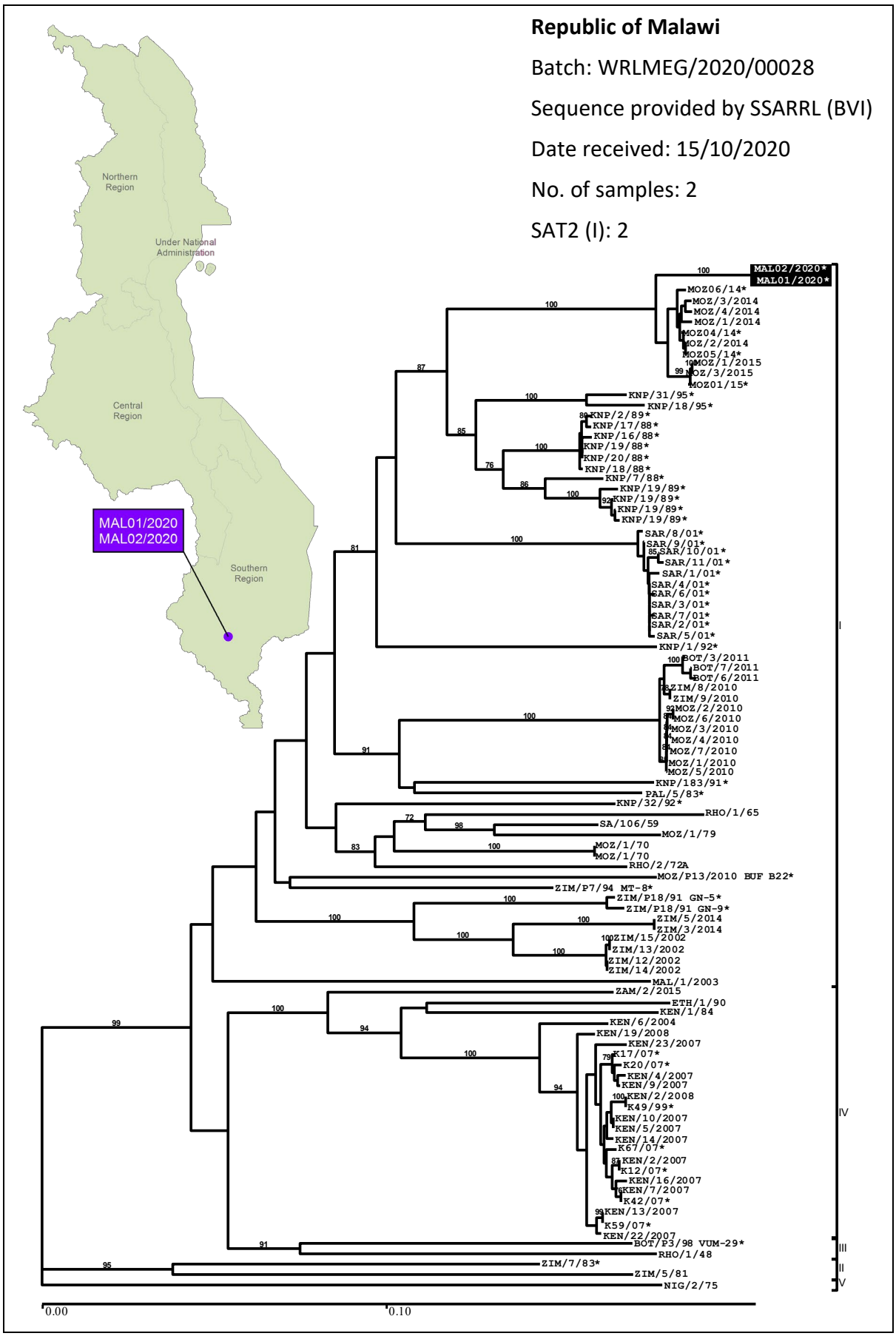
Nigeria continued



4.4. Pool 6 (Southern Africa)




Republic of Malawi
Batch: WRLMEG/2020/00028
Sequence provided by SSARRL (BVI)
Date received: 15/10/2020
No. of samples: 2
SAT2 (I): 2
Northern Region
Under National Administration
Central Region
Southern Region
MAL01/2020
MAL02/2020
MAL02/2020*
MAL01/2020*
MOZ06/14*
MOZ/3/2014
MOZ/4/2014
MOZ/1/2014
MOZ04/14*
MOZ/2/2014
MOZ05/14*
MOZ/1/2015
MOZ/3/2015
MOZ01/15*
KNP/31/95*
KNP/18/95*
KNP/2/89*
KNP/17/88*
KNP/16/88*
KNP/19/88*
KNP/20/88*
KNP/18/88*
KNP/7/88*
KNP/19/89*
KNP/19/89*
KNP/19/89*
KNP/19/89*
SAR/8/01*
SAR/9/01*
SAR/10/01*
SAR/11/01*
SAR/1/01*
SAR/4/01*
SAR/6/01*
SAR/3/01*
SAR/7/01*
SAR/2/01*
SAR/5/01*
KNP/1/92*
BOT/3/2011
BOT/7/2011
BOT/6/2011
ZIM/8/2010
ZIM/9/2010
MOZ/2/2010
MOZ/6/2010
MOZ/3/2010
MOZ/4/2010
MOZ/7/2010
MOZ/1/2010
MOZ/5/2010
KNP/183/91*
PAL/5/83*
KNP/32/92*
RHO/1/65
SA/106/59
MOZ/1/79
MOZ/1/70
MOZ/1/70
RHO/2/72A
MOZ/P13/2010 BUF B22*
ZIM/P7/94 MT-8*
ZIM/P18/91 GN-5*
ZIM/P18/91 GN-9*
ZIM/5/2014
ZIM/3/2014
ZIM/15/2002
ZIM/13/2002
ZIM/12/2002
ZIM/14/2002
MAL/1/2003
ZAM/2/2015
ETH/1/90
KEN/1/84
KEN/6/2004
KEN/19/2008
KEN/23/2007
K17/07*
K20/07*
KEN/4/2007
KEN/9/2007
KEN/2/2008
K49/99*
KEN/10/2007
KEN/5/2007
KEN/14/2007
K67/07*
KEN/2/2007
K12/07*
KEN/16/2007
KEN/7/2007
K42/07*
KEN/13/2007
K59/07*
KEN/22/2007
BOT/P3/98 VUM-29*
RHO/1/48
ZIM/7/83*
ZIM/5/81
NIG/2/75
I
IV
III
II
V
0.00
0.10

4.5. Vaccine matching

Antigenic characterisation of FMD field isolates by matching with vaccine strains by 2dmVNT from October to December 2020.

NOTES:

1. Vaccine efficacy is influenced by vaccine potency, antigenic match and vaccination regime. Therefore, it is possible that a less than perfect antigenic match of a particular antigen may be compensated by using a high potency vaccine and by administering more than one vaccine dose at suitable intervals. Thus, a vaccine with a weak antigenic match to a field isolate, as determined by serology, may nevertheless afford some protection if it is of sufficiently high potency and is administered under a regime to maximise host antibody responses (Brehm, 2008).
2. Vaccine matching data generated in this report only considers antibody responses in cattle after a single vaccination (typically 21 days after vaccination). The long-term performance of FMD vaccines after a second or multiple doses of vaccine should be monitored using post-vaccination serological testing.

Table 4: Summary of samples tested by vaccine matching

Serotype	O	A	C	Asia-1	SAT 1	SAT 2	SAT 3
Pakistan*	2	-	-	-	-	-	-
Vietnam*	4	-	-	-	-	-	-
Total	**6**	**0**	**0**	**0**	**0**	**0**	**0**

*** Supplementary vaccine matching reports**

Abbreviations used in tables

For each field isolate the r1 value is shown followed by the heterologous neutralisation titre (r1-value / titre). The r1 values shown below, represent the one-way serological match between vaccine strain and field isolate, calculated from the comparative reactivity of antisera raised against the vaccine in question. Heterologous neutralisation titres for vaccine sera with the field isolates are included as an indicator of cross-protection.

M	**Vaccine Match** r_1 = ≥ *0.3 - suggests that there is a close antigenic 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* - suggest that the field isolate is antigenically different to the vaccine strain. Where there is no alternative, the use of this vaccine should carefully consider vaccine potency, the possibility to use additional booster doses and monitoring of vaccinated animals for heterologous responses.
NT	**Not tested against this vaccine**

NOTE: A "0" in the neutralisation columns indicates that for that particular field virus no neutralisation was observed at a virus dose of a 100 $TCID_{50}$.

NOTE: This report includes the source of the vaccine virus and bovine vaccinal serum. Vaccines from different manufactures may perform differently and caution should be taken when comparing the data.

Table 5: Supplementary vaccine matching studies for O1 Campos

Isolate	Serotype O		O1 Campos Biogenesis	
	Topotype	*Lineage*	r_1-*value*	*Titre*
PAK/46/2019	ME-SA	Ind-2001	0.26	1.90
VIT/13/2020	ME-SA	Ind-2001	0.78	2.24
VIT/19/2019	ME-SA	PanAsia	0.79	2.24
PAK/3/2020	ME-SA	PanAsia-2	0.56	2.19
VIT/15/2019	SEA	Mya-98	0.15	1.61
VIT/31/2019	SEA	Mya-98	0.24	1.82

Table 6: Supplementary vaccine matching studies for O PanAsia-2

Isolate	Serotype O		O PanAsia-2 Boehringer Ingelheim	
	Topotype	*Lineage*	*r_1-value*	*Titre*
TUN/1/2019	EA-3	-	065	2.12
MOR/1/2019	EA-3	-	0.49	2.00
ALG/1/2019	EA-3	-	0.59	2.08
SRL/14/2019	ME-SA	-	0.28	1.93
SRL/1/2019	ME-SA	Ind-2001d	0.39	2.08
SRL/17/2019	ME-SA	Ind-2001d	0.29	1.95
BHU/1/2019	ME-SA	Ind-2001e	0.58	2.07
PAK/46/2019	ME-SA	Ind-2001e	0.62	2.28
PAK/12/2019	ME-SA	PanASIA-2^{ANT-10}	0.32	2.00
PAT/3/2019	ME-SA	PanASIA-2^{QOM-15}	0.39	1.90
TUR/4/2019	ME-SA	PanASIA-2^{QOM-15}	0.51	2.02
PAK/3/2020	ME-SA	PanASIA-2^{ANT-10}	0.36	2.05

Annex 1: Sample data

Summary of submissions

Table 7: Summary of samples collected and received to WRLFMD (October to December 2020)

Country	Nº of samples	Virus isolation in cell culture/ELISA								RT-PCR for FMD	
		FMD virus serotypes							No Virus Detected		
		O	*A*	*C*	*SAT 1*	*SAT 2*	*SAT 3*	*ASIA-1*		*Positive*	*Negative*
Cambodia	9										
Lao P.D.R.	5										
Thailand	16										
Uganda	11										
TOTAL	**41**	**-**	**-**	**-**	**-**	**-**	**-**	**-**	**-**	**-**	**-**

Clinical samples

Table 8: Clinical sample diagnostics made by the WRLFMD® October to December 2020

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

Annex 2: FMD publications

Recent FMD Publications (October to December 2020) cited by Web of Science.

1. Abd El Rahman, S., B. Hoffmann, R. Karam, M. El-Beskawy, M.F. Hamed, L.F. Forth, D. Hoper, and M. Eschbaumer (2020). Sequence analysis of Egyptian *Foot-and-mouth disease virus* field and vaccine strains: intertypic recombination and evidence for accidental release of virulent virus. *Viruses-Basel*, **12**(9): 15. DOI: 10.3390/v12090990.
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4. Adjid, R.M.A. (2020). Foot-and-mouth disease: an exotic animal disease that must be alert of entry into Indonesia. *Wartazoa-Buletin Ilmu Peternakan Dan Kesehatan Hewan Indonesia*, **30**(2): 61-70. DOI: 10.14334/wartazoa.v30i2.2490.
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9. Arjkumpa, O., T. Yano, R. Prakotcheo, C. Sansamur, and V. Punyapornwithaya (2020). Epidemiology and national surveillance system for foot-and-mouth disease in cattle in Thailand during 2008-2019. *Veterinary Sciences*, **7**(3): 13. DOI: 10.3390/vetsci7030099.
10. Asfor, A.S., N. Howe, S. Grazioli, S. Berryman, K. Parekh, G. Wilsden, A. Ludi, D.P. King, S. Parida, E. Brocchi, and T.J. Tuthill (2020). Detection of bovine antibodies against a conserved capsid epitope as the basis of a novel universal serological test for foot-and-mouth disease. *Journal of Clinical Microbiology*, **58**(6): 9. DOI: 10.1128/jcm.01527-19.
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15. Cacciabue, M., A. Curra, E. Carrillo, G. Konig, and M.I. Gismondi (2020). A beginner's guide for FMDV quasispecies analysis: sub-consensus variant detection and haplotype reconstruction using next-generation sequencing. *Briefings in Bioinformatics*, **21**(5): 1766-1775. DOI: 10.1093/bib/bbz086.
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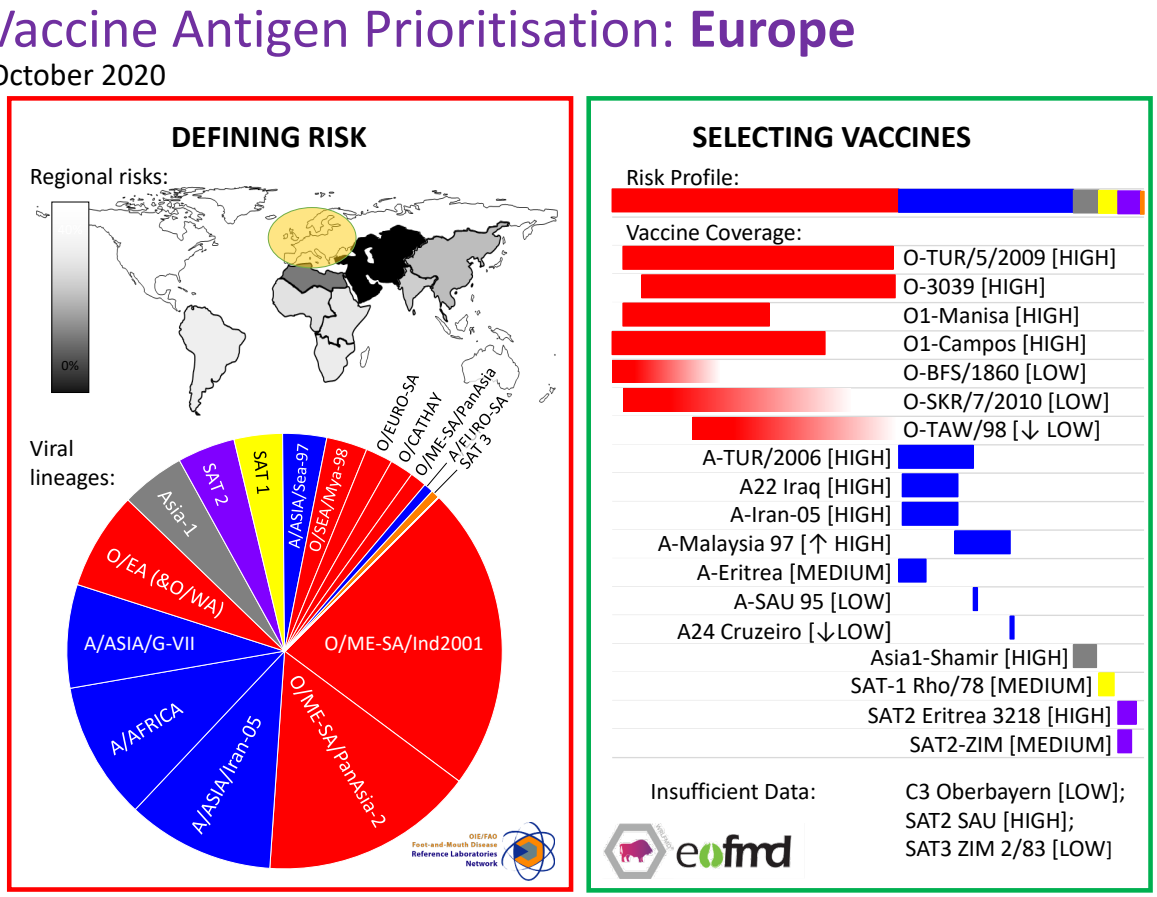
Annex 3: Vaccine recommendations

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 1 in Section 3.9, above), as well as available *in vitro, in vivo* and field data to score the ability of vaccines to protect against these FMDV lineages.



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

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.

Annex 4: Brief round-up of EuFMD and WRLFMD activities

Courses

EuFMD's open access online courses provide convenient self-paced training which you may study anytime, anywhere, free of charge. Link to all courses: https://eufmdlearning.works/mod/page/view.php?id=13130

- There are currently 4 courses in English, 1 in French and 1 in Arabic:
    - Introduction to Foot-and-Mouth Disease (in English, French and Arabic)
    - What is the Progressive Control Pathway?
    - Public Private Partnerships in the Veterinary Domain (in support of OIE Training)
    - Introduction to the Progressive Control Pathway
    - Introduction to the Risk-based Strategic Plan (RBSP) ***coming soon***
- The WRLFMD residential training course on FMD diagnostics (https://www.pirbright.ac.uk/instructor-led-training/diagnosis-foot-and-mouth-disease) scheduled for May 2020 has been postponed.

Podcasts

We have a constantly updated series of short podcasts relating to the FAST world, available here: http://www.fao.org/eufmd/resources/podcasts/en/

Meetings

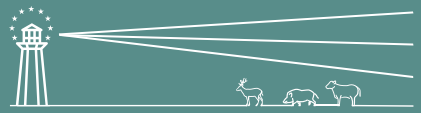
- The EuFMD Open Session will conclude on 16 February (https://www.eufmd.info/os20faster)
- 44th General Session of the EuFMD will be held 21 April 2021 - 23 April 2021
- GFRA conferences for America (15 March) and South East Asia (week of 22 March).

Proficiency test scheme organised by WRLFMD

Sample panels for the Phase XXXII exercise have shipped to international laboratories; however, this is still ongoing as the disruption to air travel continues. Results have been received from laboratories and these are currently being analysed (see table below for a summary of the current status of the exercise).

Status	Number of Labs
Invitations	72
Declined to take part	9
Paperwork in progress	1
Awaiting shipping	2
Panels shipped	35
Destroyed in transit	1
Results returned	26

We will write to inform participating laboratories about any other changes that may be required to accommodate these events, and please feel free to contact WRLFMD if you have any questions.



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Hold-FAST tools

GET PREPARED, E-learning, FMD-PCP, EuFMDiS, Pragmatist, Impact Risk Calculator, Virtual Learning Center, SMS Disease reporting, Global Vaccine Security, Outbreak Investigation app, PCP-Support Officers, PCP Self-Evaluation tool, AESOP, Telegram, Whatssap, Quarterly Global Reports, Real Time Traning.

EuFMD Committees

Executive Committee, Standing Technical Committee, Special Committee for Surveillance and Applied Research (SCSAR), Special Committee on Biorisk Management (SCBRM), Tripartite Groups.

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