

WRLFMD Quarterly Report October to December 2017

Foot-and-Mouth Disease





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1. Summary of samples tested and reported FMD outbreaks

1.1. Asia

China, People's Republic of

Between 24/09/2017 and 29/11/2017, three outbreaks of **FMD type O** were reported in various species in Guizhou province. On 26/10/2017 a single outbreak, again due to **FMD type O** was reported in pigs in Guangdong province. No genotyping has been reported.

Hong Kong Special Administrative Region

Four samples collected from pigs were received on 11/10/2017. **FMDV type O** was isolated from three samples and one was NVD. All three viruses belonged to the CATHAY topotype (see below).

Mongolia

A complete genome sequence of a **FMDV type O** virus isolated from cattle in March 2015 in Bayan-Ölgii Province (western Mongolia) was retrieved from GenBank (accession number LC320038). The sequence was deposited by researchers at the NIAH-Japan. Genotype comparisons revealed the virus to belong to the ME-SA topotype, Ind-2001d lineage (see section 2.1 below). These results provide the first indication that the O/ME-SA/Ind-2001d lineage has been present in East Asia for more than 2 years.

Myanmar

A VP1 sequence of a **FMDV type Asia 1** virus was received from TRRL via OIE-Bangkok. The original sample had been collected in Kayah State on 03/08/2005. Phylogenetic analyses showed that the sequence was not closely related to any other Asia 1 viruses.

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Pakistan

Forty five samples, collected from cattle and water buffalo between January 2016 and September 2017, were received on 15/09/2017. **FMDV type O** was isolated from 14 samples, **type A** from five samples and **Asia 1** from 16 samples. An additional six samples were typed as A and Asia 1. Only FMDV genome was detected in a further three samples and one was NVD. Genotyping revealed that all the type O viruses belonged to the ME-SA/PanAsia-2^{ANT-10} lineage; four of the type A viruses were ASIA/Iran-05^{SIS-13} and one was ASIA/Iran-05^{FAR-11}; all the Asia 1 viruses were ASIA/Sindh-08. From the six apparent mixed A/Asia 1 viruses, type A was identified in four samples (three ASIA/Iran-05^{SIS-13} and one ASIA/Iran-05^{FAR-11}) and type Asia 1 was identified in five samples (all ASIA/Sindh-08). All six samples were probably mixed infections, but poor sequence data in some cases failed to unequivocally identify the viruses involved.

Palestinian Autonomous Territories

Between 13/11/2017 and 20/12/2017, five outbreaks of **FMD type O** were reported in sheep, goats and cattle in Hebron, West Bank. VP1 sequencing was performed at the Kimron Veterinary Institute (Israel) and submitted to the WRLFMD. The causal virus belonged to the EA-3 topotype and was closely related to previous outbreaks in Palestine, Israel, Egypt and Ethiopia.

Russian Federation

Between 20/09/2017 and 09/10/2017, five outbreaks of **FMD type O** were reported in the Republic of Bashkortostan. VP1 sequencing was performed at the FGBI-ARRIAH and submitted to the WRLFMD. The causal virus was shown to be a novel lineage within the ME-SA topotype (see section 2.1 below), which had previously been observed in Pakistan (2012-2014) and Iran (2013-2014).

Sri Lanka

Twenty samples, collected from cattle between December 2014 and September 2017, were received on 20/11/2017. **FMDV type O** was isolated from 11 samples, FMDV genome was detected in a further two and seven were NVD. All the type O viruses belonged to the ME-SA topotype, Ind-2001d lineage (see section 2.1 below).

Turkey

A single **FMDV type O** VP1 sequence was received from the Şap Institute, Ankara. The original samples had been collected from sheep during 2017 in Gaziantep.

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Phylogenetic analysis showed the genotype to be ME-SA/PanAsia-2^{ANT-10} (see section 2.1 below).

1.2. Africa

Botswana

One sample, collected from cattle at Dingonapel (Sehitwa, Ngamiland) on 23/09/2017, was received from OIE Sub-Saharan Africa Regional Reference laboratory (SSARRL) at the Botswana Vaccine Institute. **FMDV SAT 2** was isolated and genotyping revealed it to belong to toptype III (see section 2.2 below).

Ghana

Two samples, collected from cattle in 2016, were received from SSARRL. **FMDV type O** was isolated from one sample, while the other was NVD. Genotyping showed the virus to belong to the WA toptype being most closely related to viruses from Niger in 2015 (see section 2.2 below).

Kenya

Seven samples were received on 15/12/2017. Serotyping and genotyping results are pending.

Malawi

One sample, collected from cattle at Nsanje in 2016, was received from the SSARRL. **FMDV SAT 1** was isolated and genotyping showed the virus to belong to toptype I (see section 2.2 below).

Mozambique

On 13/10/2017 an outbreak of **FMD SAT 2** was reported in cattle at Moamba, Maputo. On 23/11/2017 an untyped FMD outbreak was reported in cattle at Doa, Tete, close to the border with Malawi. No genotyping has been reported for either outbreak.

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Namibia

Two samples, collected from cattle at Kasika, Makoma Island in July 2017, were received from the SSARRL; both were NVD. Three **FMDV SAT 2** VP1 sequences (one only partially complete) were also received from the SSARRL and were all shown to be toptype III (see section 2.2 below).

Uganda

Two samples, collected from cattle during June 2017, were received from the SSARRL. **FMDV type O** was isolated from one while the other only FMDV genome was detected. VP1 sequencing showed the virus isolate to belong to toptype EA-2 (see section 2.2 below).

Zambia

One samples, collected from cattle at Lukulo (Western province) in May 2017, was received from the SSARRL. **FMDV SAT 3** was isolated and shown to belong to toptype II, being closely related to previous viruses present in the province since 2015 (see section 2.2 below).

Zimbabwe

One sample, collected from cattle at Hebron, Good Hope (near Harare) in 2017. **FMDV SAT 2** was isolated and shown to belong to toptype II (see section 2.2 below).

1.3. South America

No new reports of FMD during this period.

1.4. 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/fmd_genotyping/2017.htm.

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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 2017 is shown in Annex 1 (Summary of Submissions). A record of all samples received by WRLFMD (October to December 2017) is shown in Annex 1 (Clinical Samples).

Table 1: Status of sequencing of samples or sequences received by the WRLFMD from October to December 2017 (* indicates samples carried over from the last quarter and † indicates not included in the totals.)

WRLFMD Batch No.	Date received	Country	Serotype	No. of samples	No. of sequences	Sequencing status
WRLFMD/2017/00021*	15/09/2017	Pakistan	O	14	14	completed
WRLFMD/2017/00021*	15/09/2017	Pakistan	A	5	5	completed
WRLFMD/2017/00021*	15/09/2017	Pakistan	A & Asia 1	6	7	completed
WRLFMD/2017/00021	15/09/2017	Pakistan	Asia 1	16	16	completed
WRLFMD/2017/00022	11/10/2017	Hong Kong SAR	O	3	3	completed
WRLFMD/2017/00023	19/10/2017	Botswana	SAT 2	1	1	completed
WRLFMD/2017/00024	19/10/2017	Ghana	O	1	1	completed
WRLFMD/2017/00025	19/10/2017	Malawi	SAT 1	1	1	completed
WRLFMD/2017/00027	19/10/2017	Uganda	O	1	1	completed
WRLFMD/2017/00028	19/10/2017	Zambia	SAT 3	1	1	completed
WRLFMD/2017/00029	19/10/2017	Zimbabwe	SAT 2	1	1	completed
WRLFMD/2017/00030	20/11/2017	Sri Lanka	O	11	11	completed
WRLFMD/2017/00031	15/12/2017	Kenya	Pending	(n=7 [†])		pending
Total				61	62	

*, carried over from previous quarter.

†, not included in the totals.

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2. Detailed Analysis

Key for maps and trees:

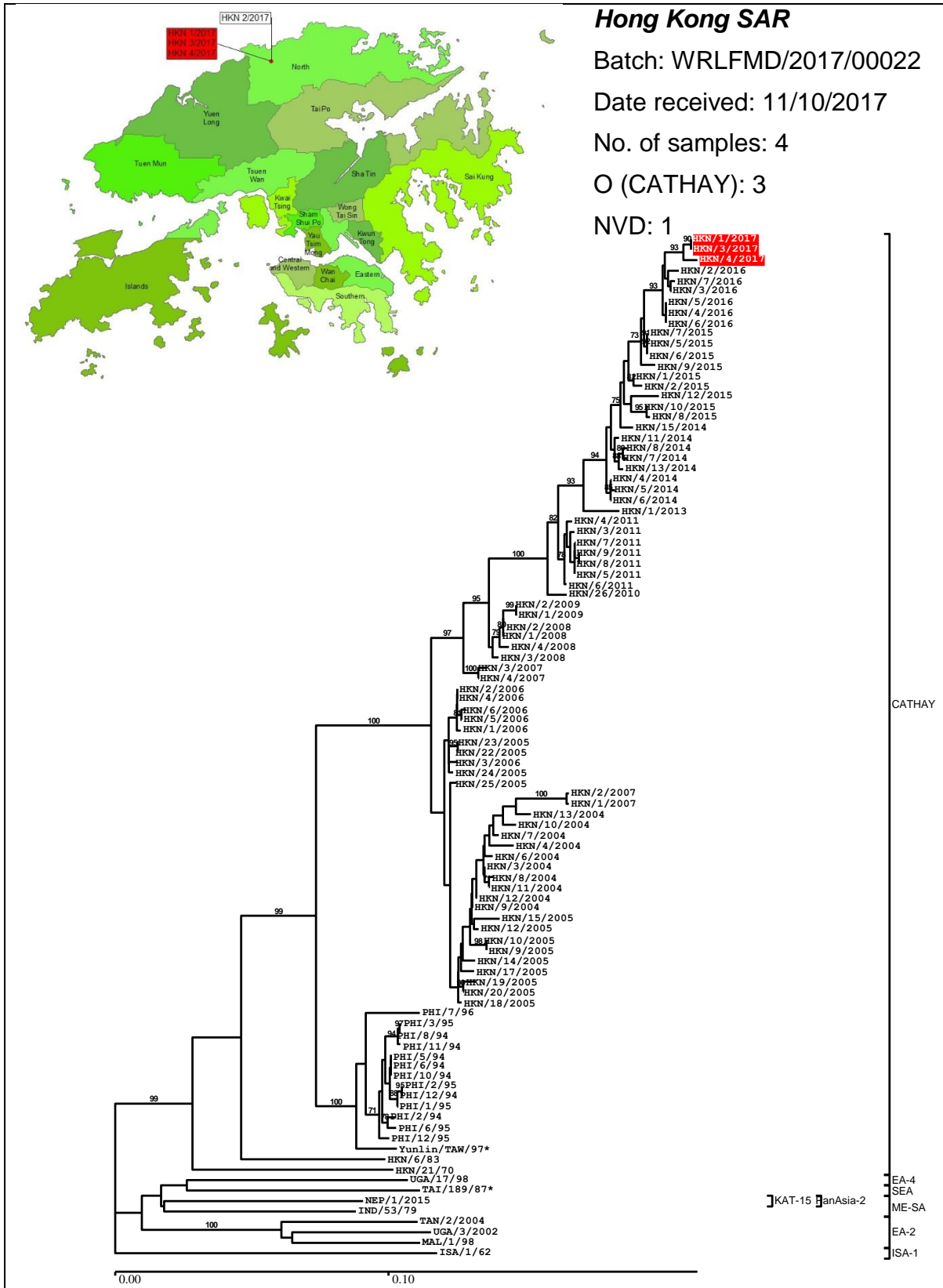
Serotype O
Serotype A
Serotype C
Serotype Asia-1
Serotype SAT 1
Serotype SAT 2
Serotype SAT 3
FMDV Genome Detected
No Virus Detected

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2.1. ASIA



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Mongolia

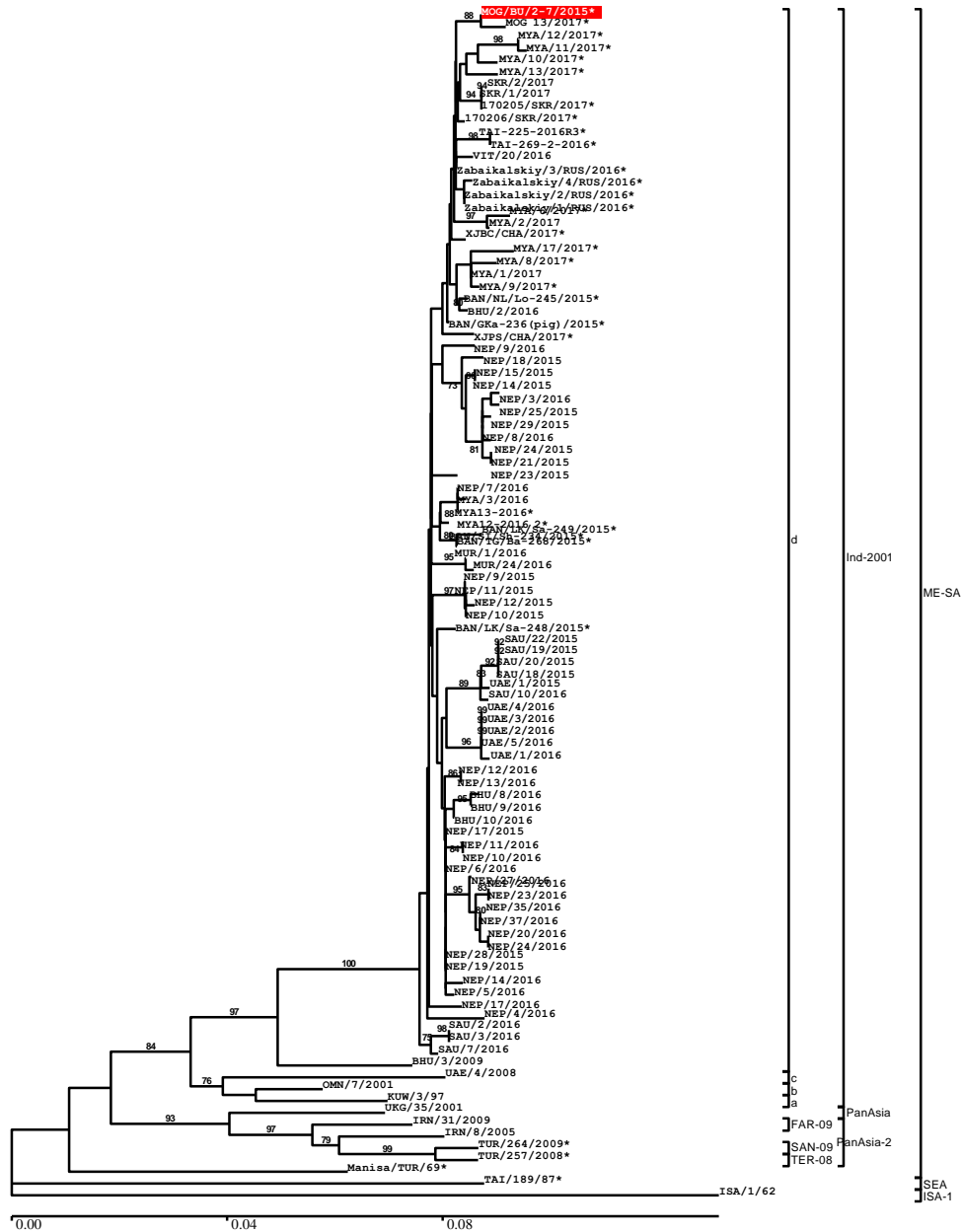
Batch: WRLMEG/2017/00052

Retrieved from GenBank
(LC320038)

Date received: 15/10/2017

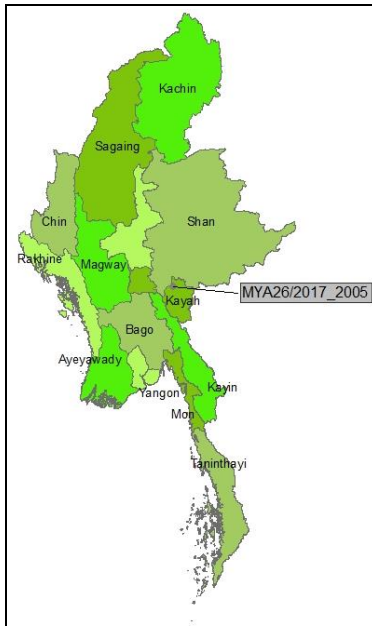
No. of sequences: 1

O (ME-SA/Ind-2001d): 1



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Myanmar

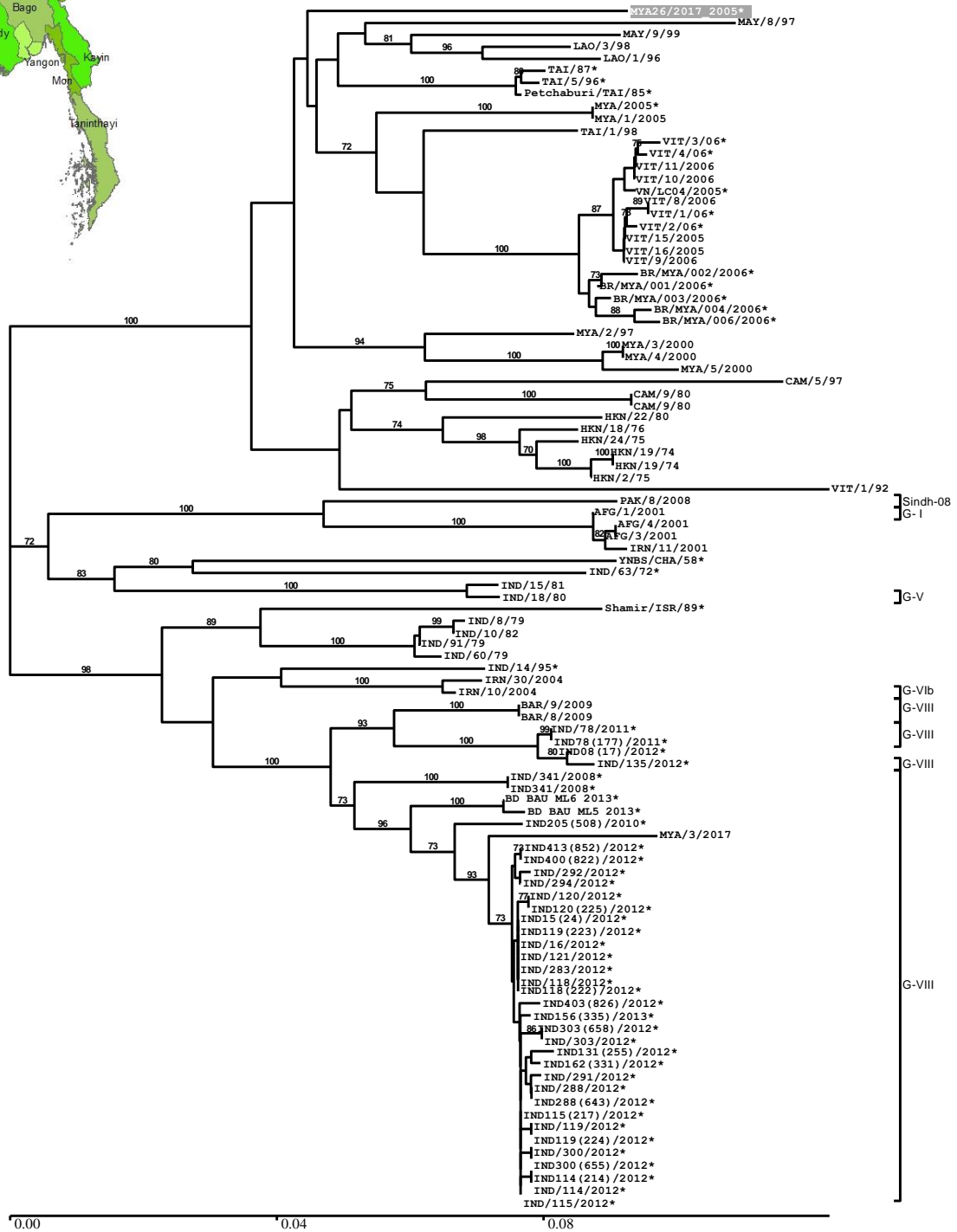
Batch: WRLMEG/2017/00056

Submitted by: Yu Qiu, OIE, Bangkok, Thailand

Date received: 08/11/2017

No. of sequences: 1

Asia 1 (ASIA/unnamed): 1



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Pakistan

Batch: WRLFMD/2017/00021

Date received: 15/09/2017

No. of samples: 44

O (ME-SA/PanAsia-2/ANT-10): 14

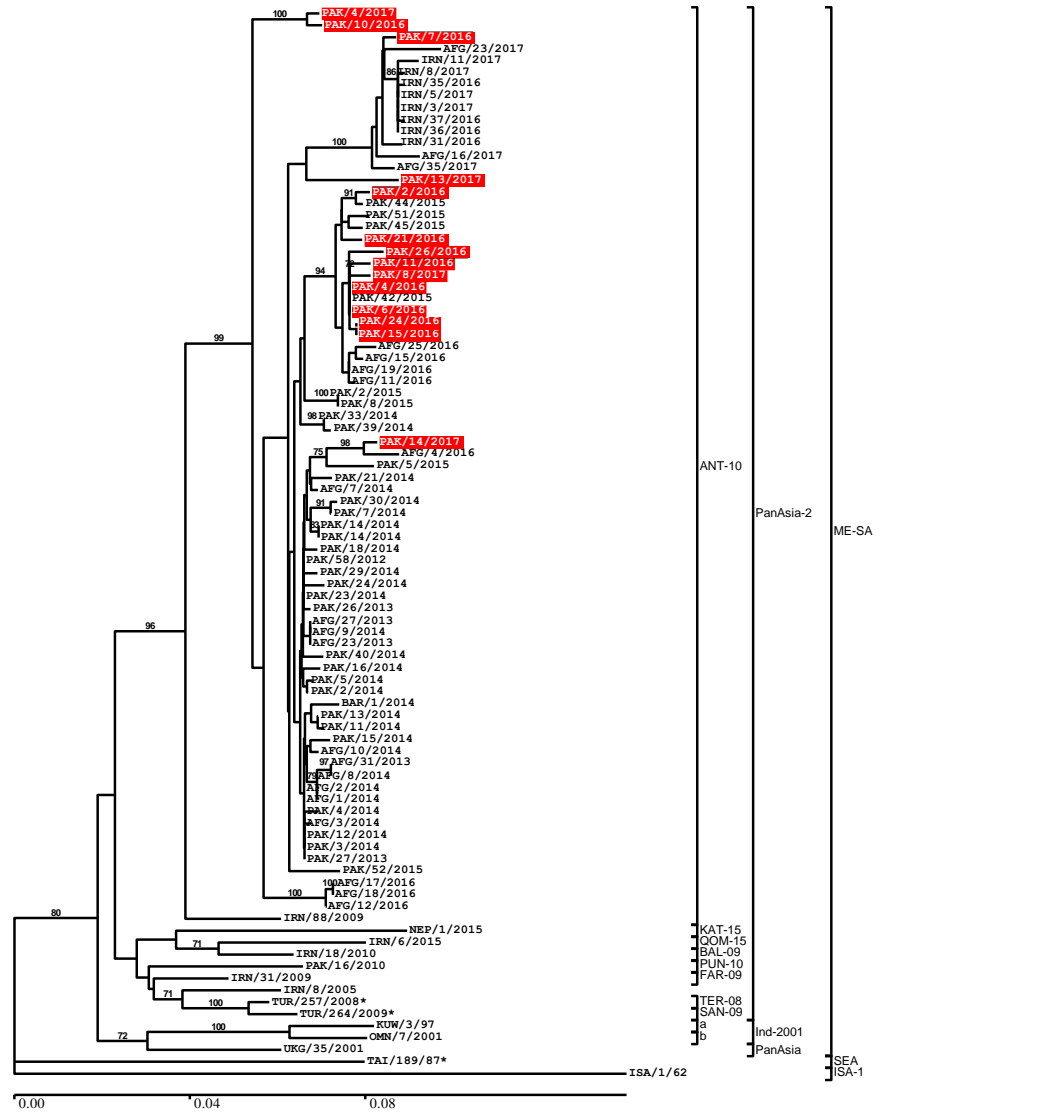
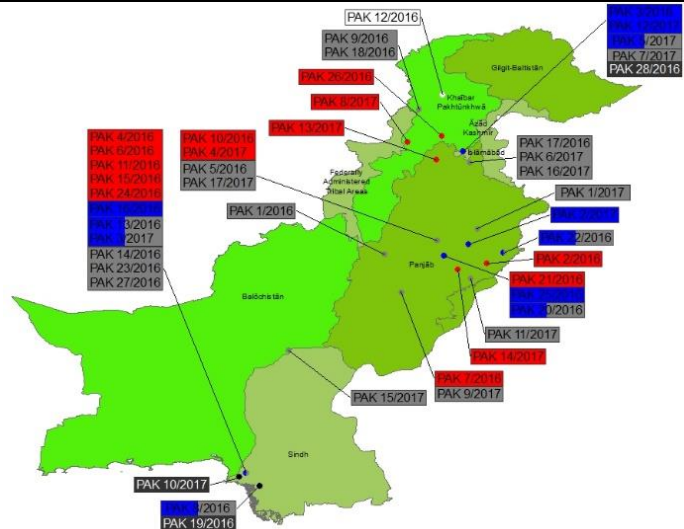
A (ASIA/Iran-05/FAR-11): 2

A (ASIA/Iran-05/SIS-13): 7

Asia 1 (ASIA/Sindh-08): 21

FMDV-GD: 3

NVD: 1



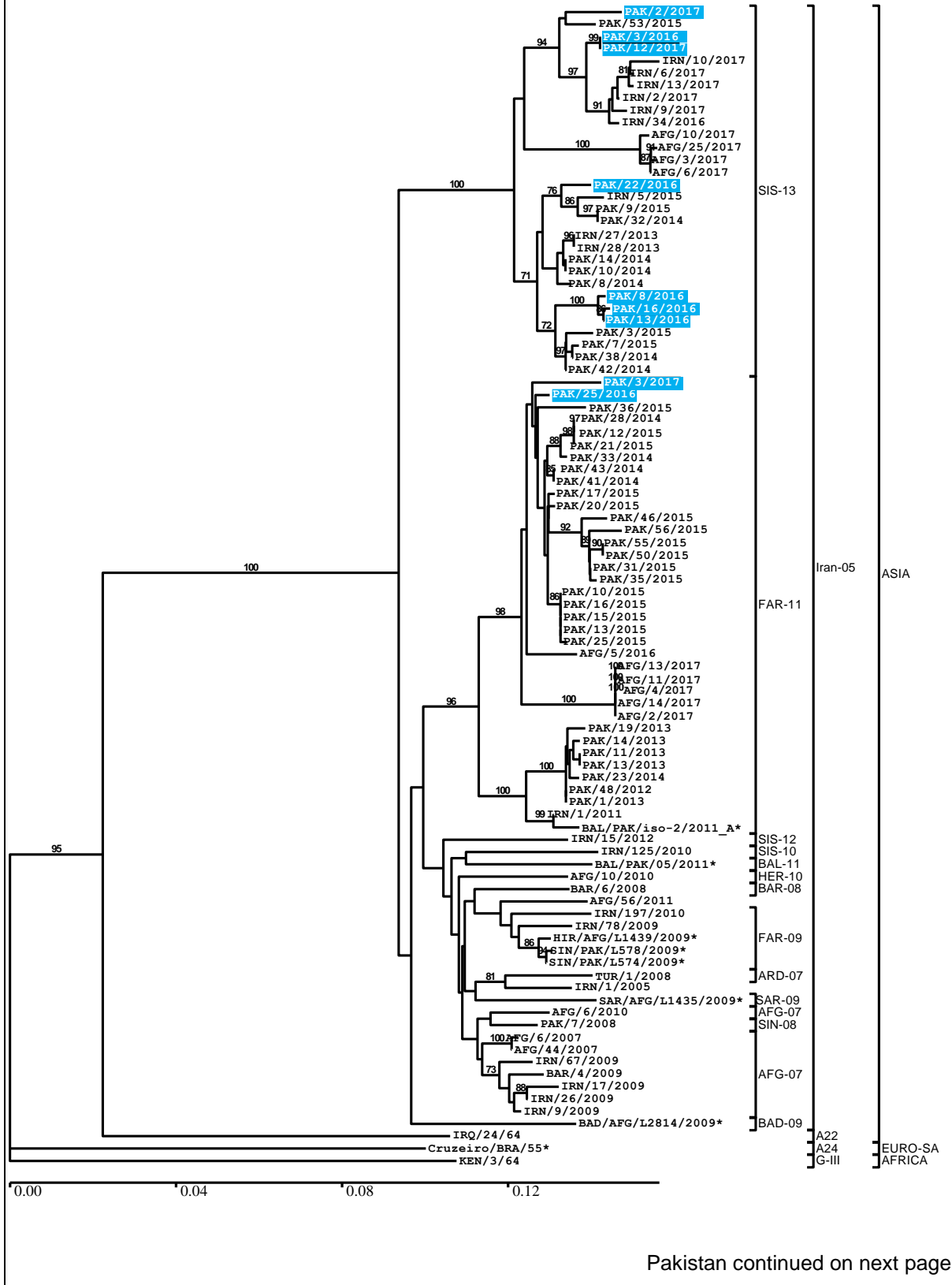
Pakistan continued on next page

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Pakistan continued

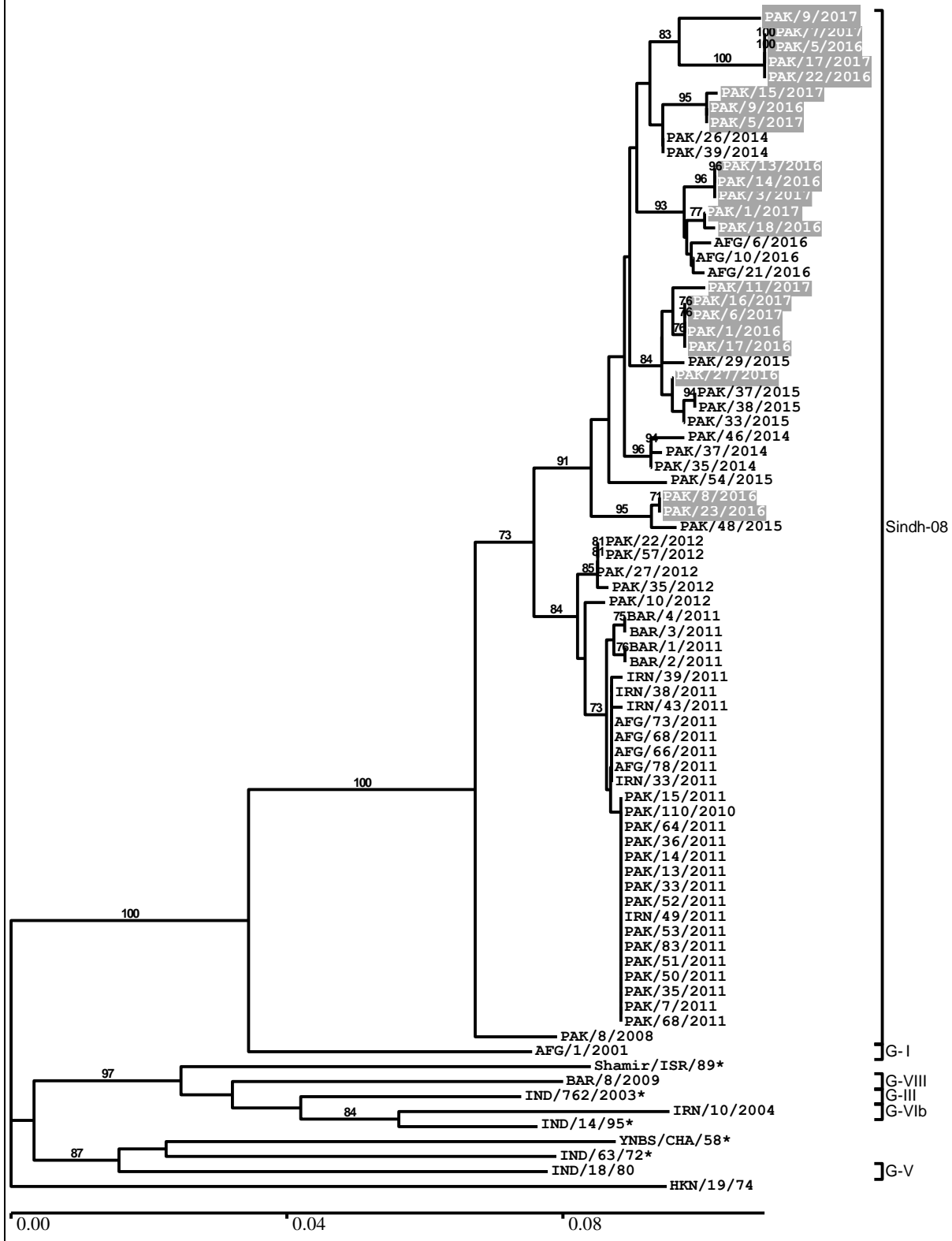


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Pakistan continued



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Palestinian Autonomous Territories

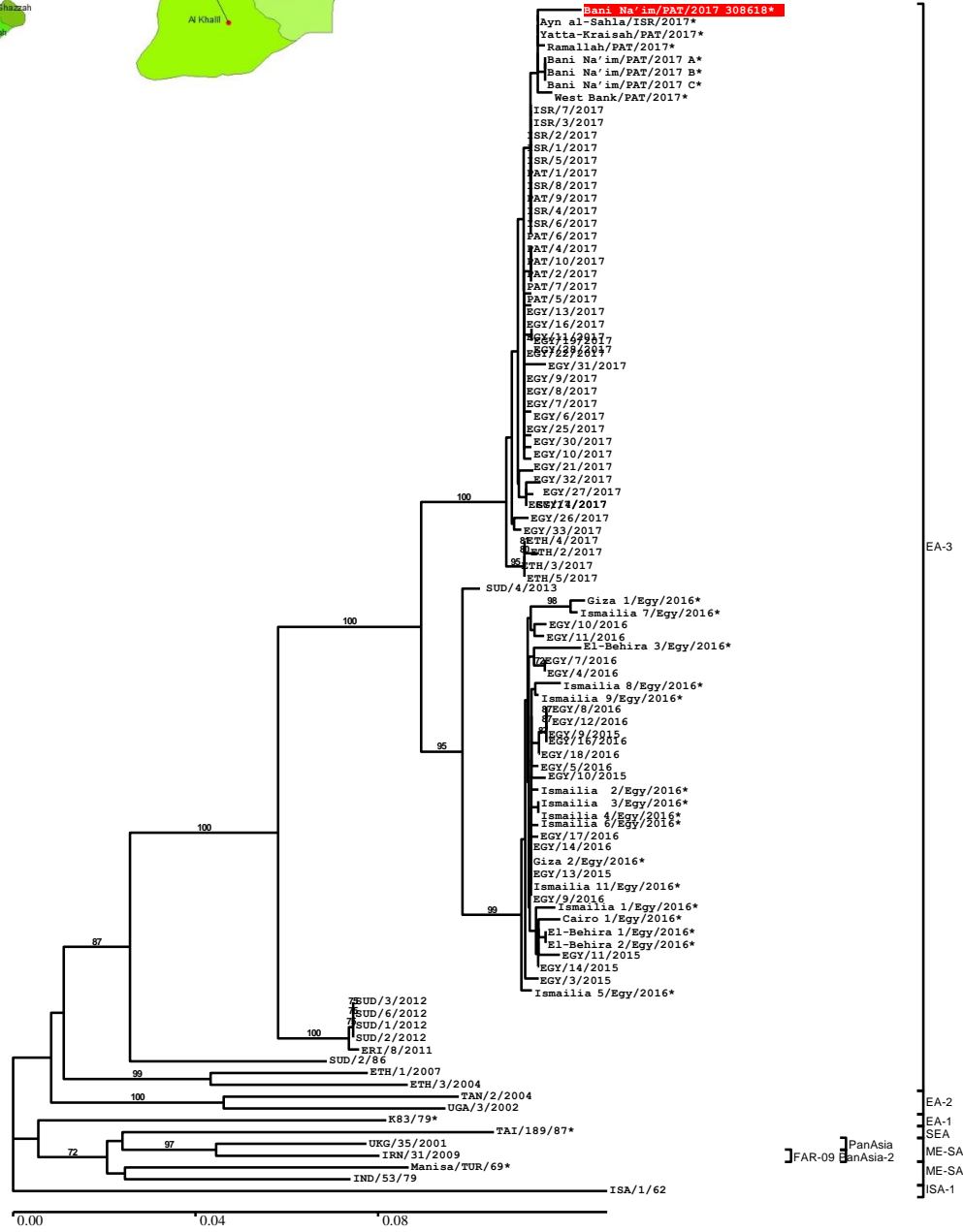
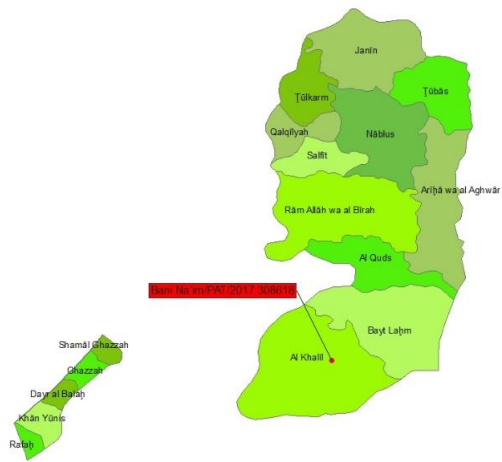
Batch: WRLMEG/2017/00062

Submitted by: Sharon Karniely, Kimron
Veterinary Institute, Israel

Date received: 18/12/2017

No. of sequences: 1

O (EA-3): 1



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Russia

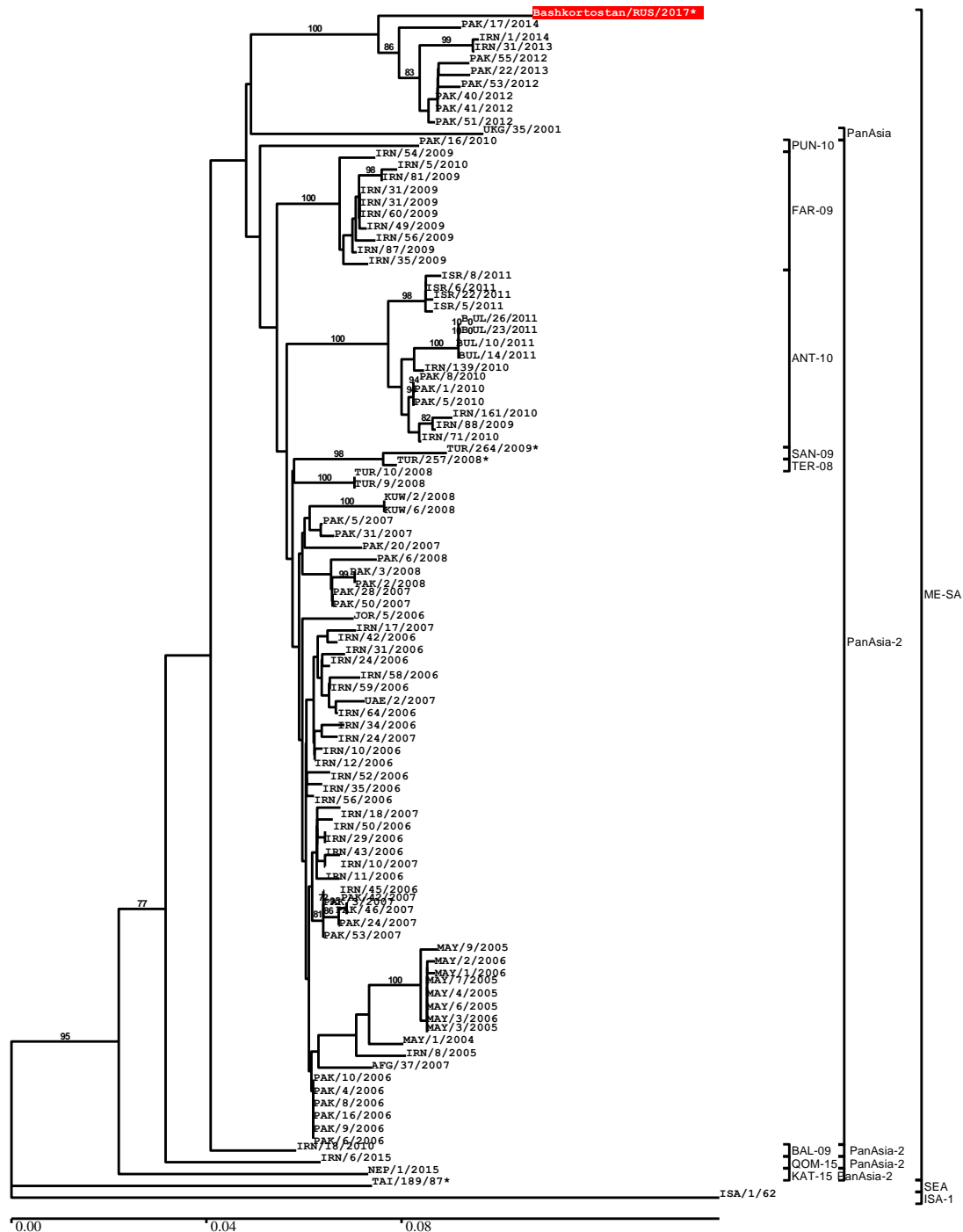
Batch: WRLMEG/2017/00051

Submitted by: Alexey Scherbakov,
FGBI-ARRIAH, Russia

Date received: 13/10/2017

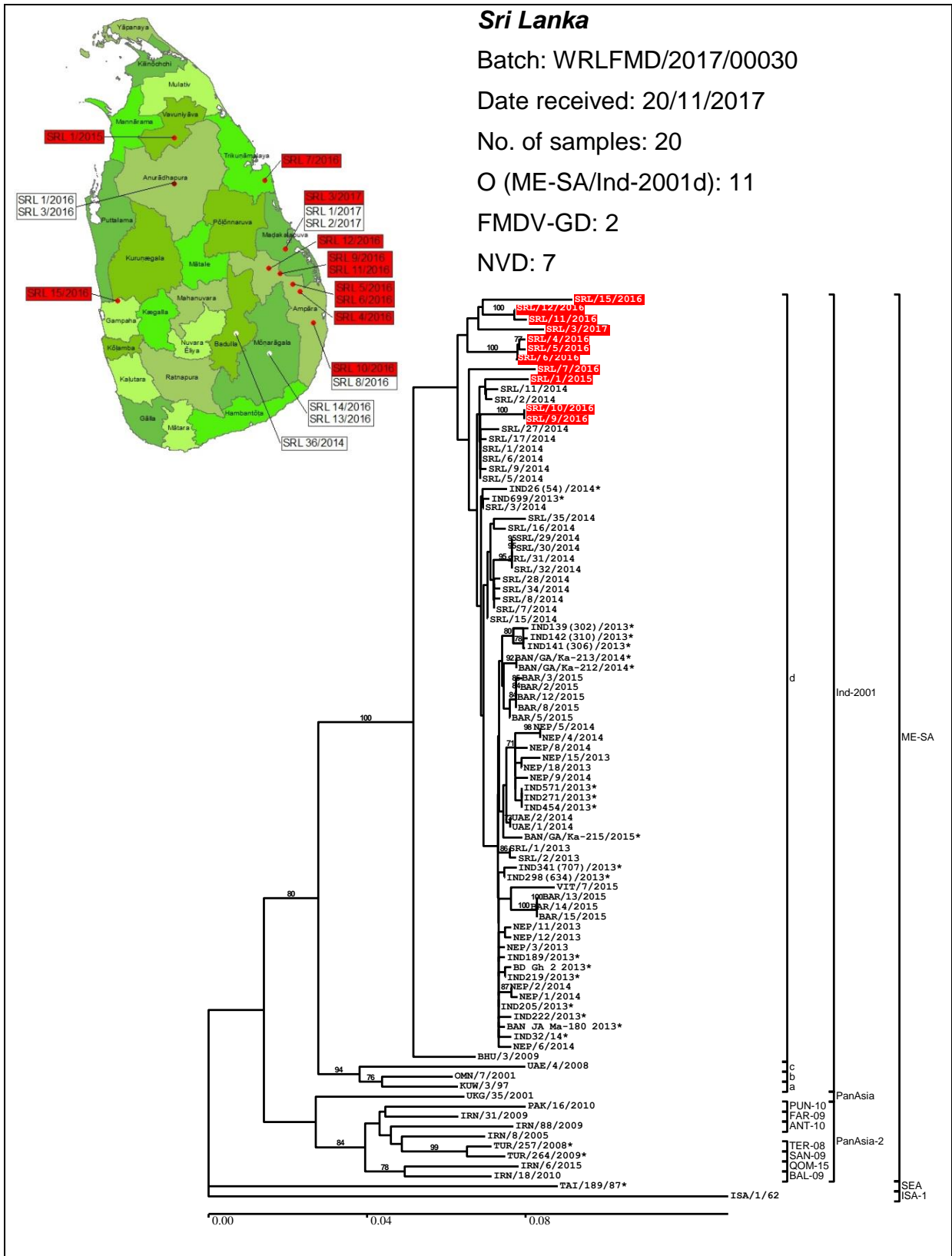
No. of sequences: 1

O (ME-SA/unnamed): 1



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Turkey

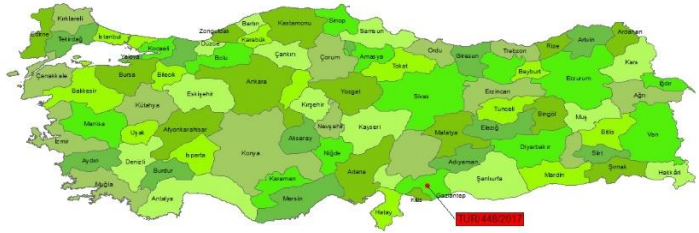
Batch: WRLMEG/2017/00063

Submitted by: Ünal Parlak, FMD
Institute, Ankara, Turkey

Date received: 29/12/2017

No. of sequences: 1

O (ME-SA/PanAsia-2/ANT-10): 1

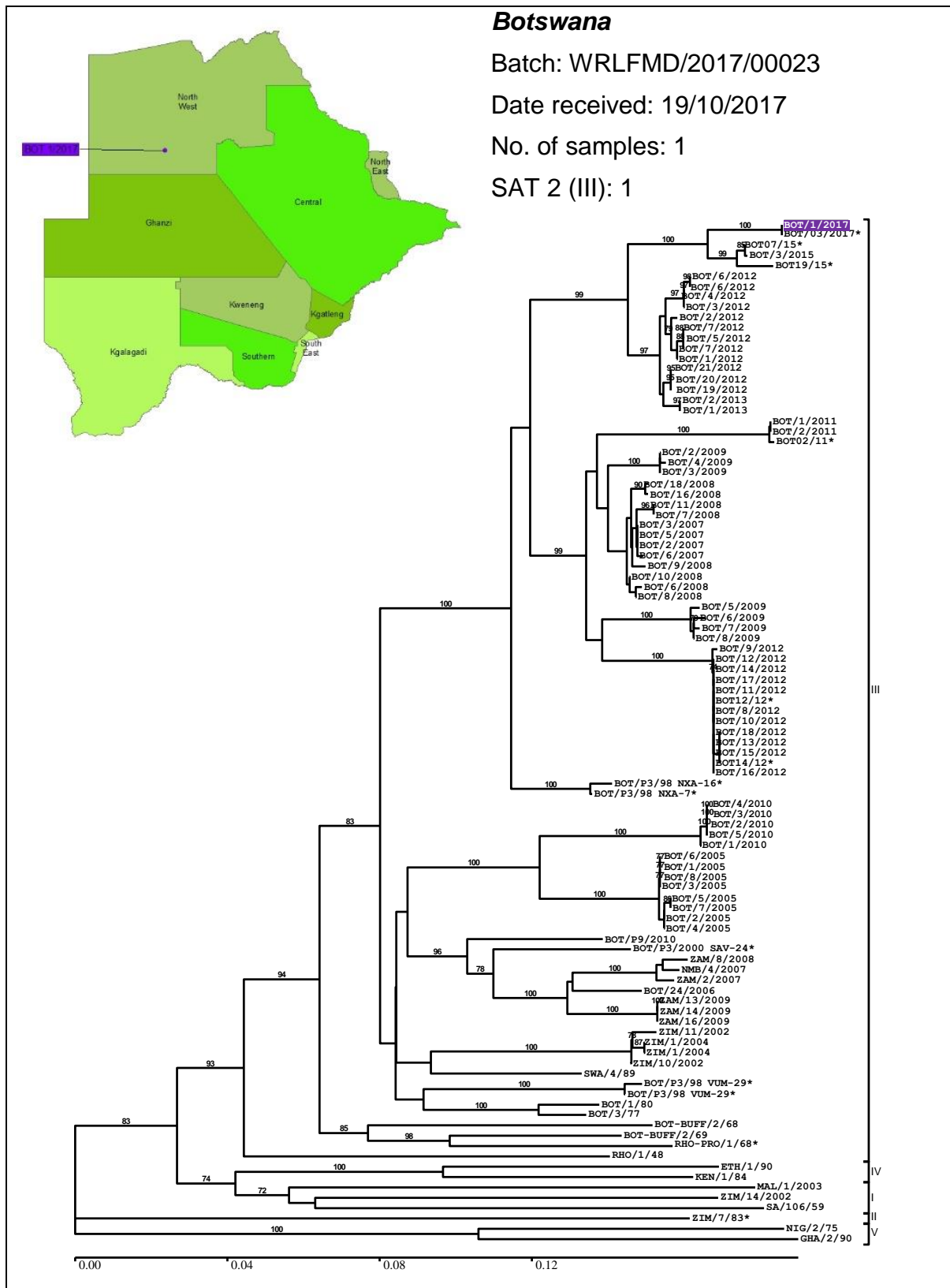


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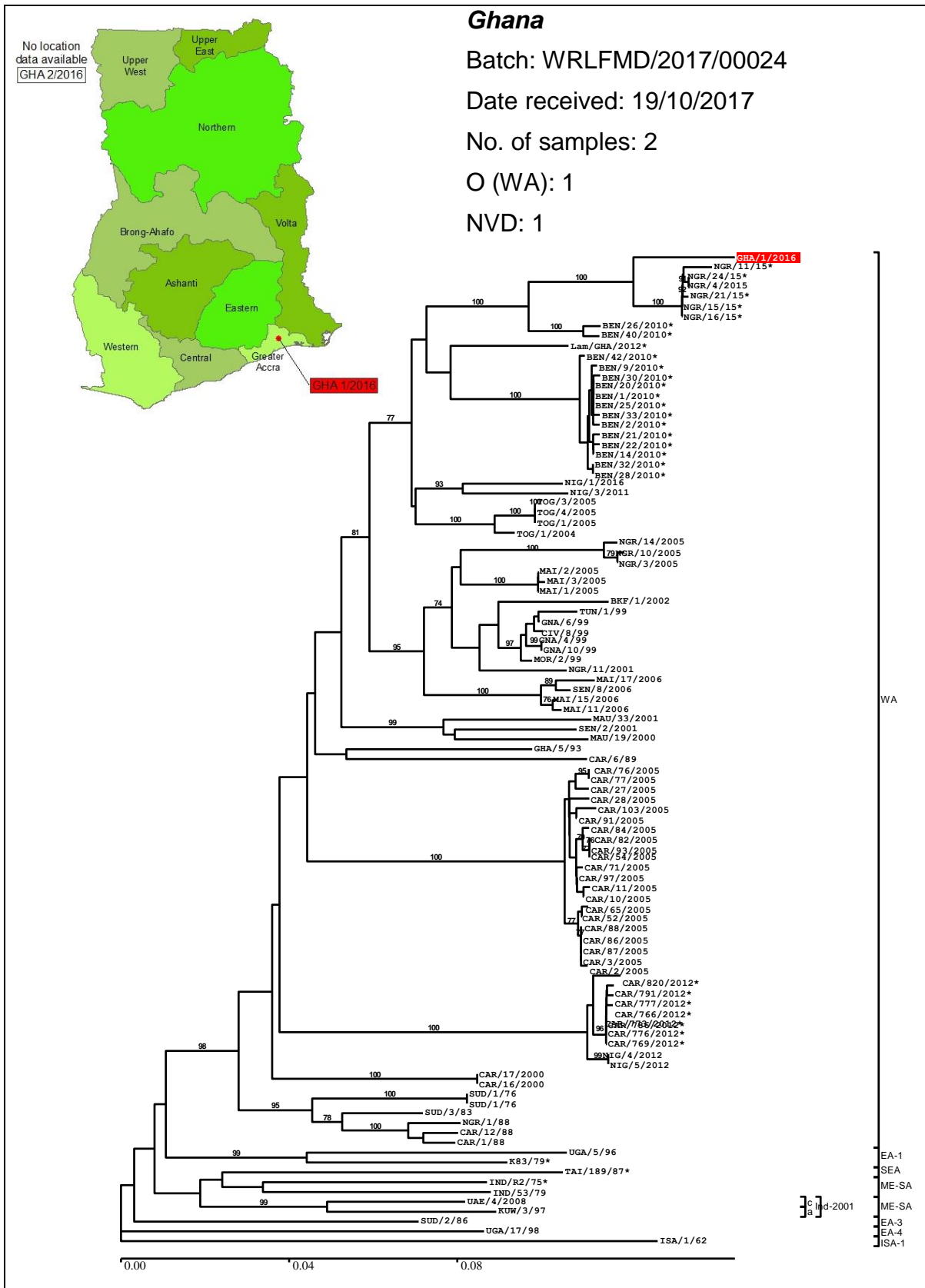


2.2. AFRICA



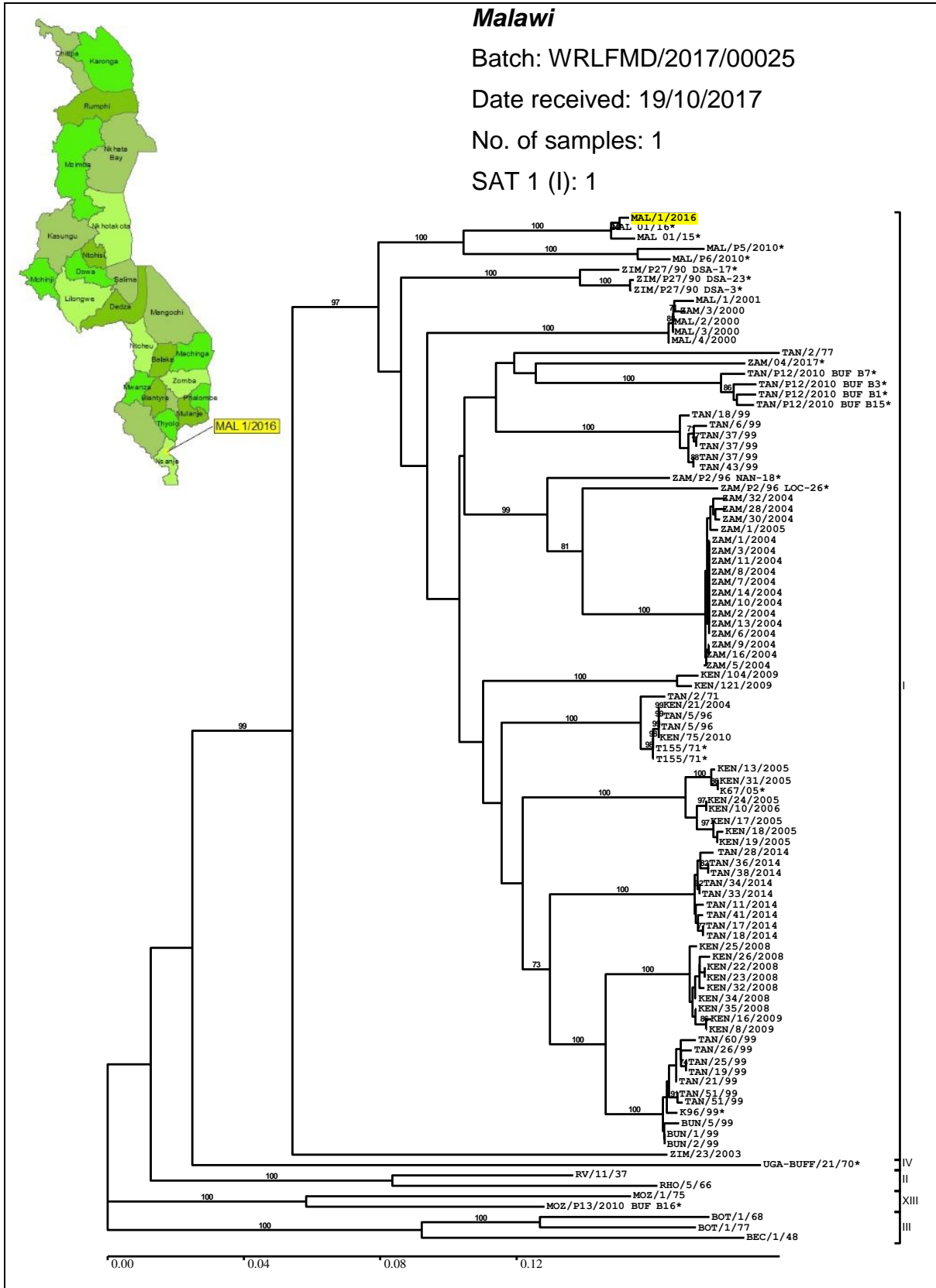
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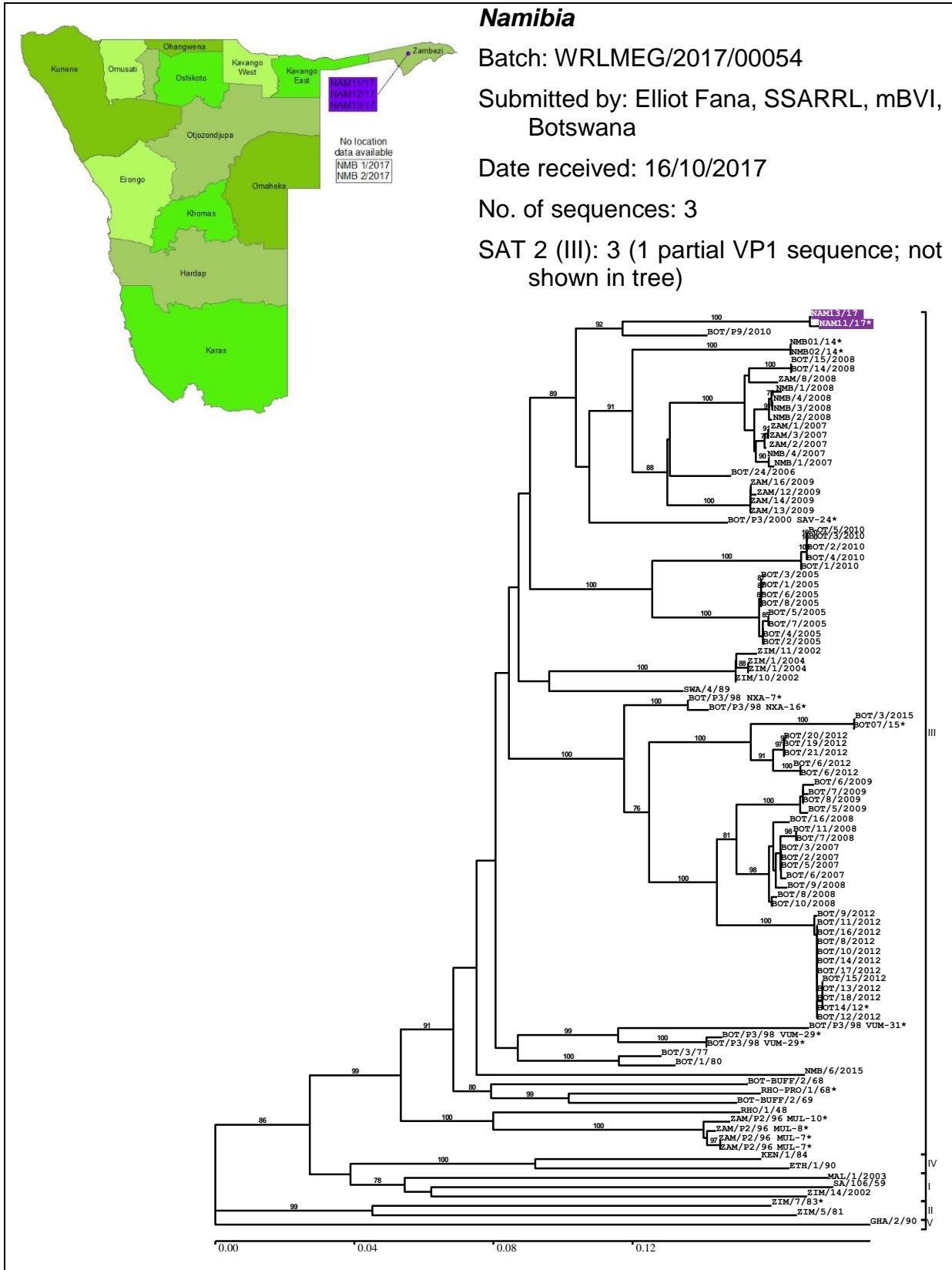
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Namibia

Batch: WRLMEG/2017/00054

Submitted by: Elliot Fana, SSARRL, mBVI, Botswana

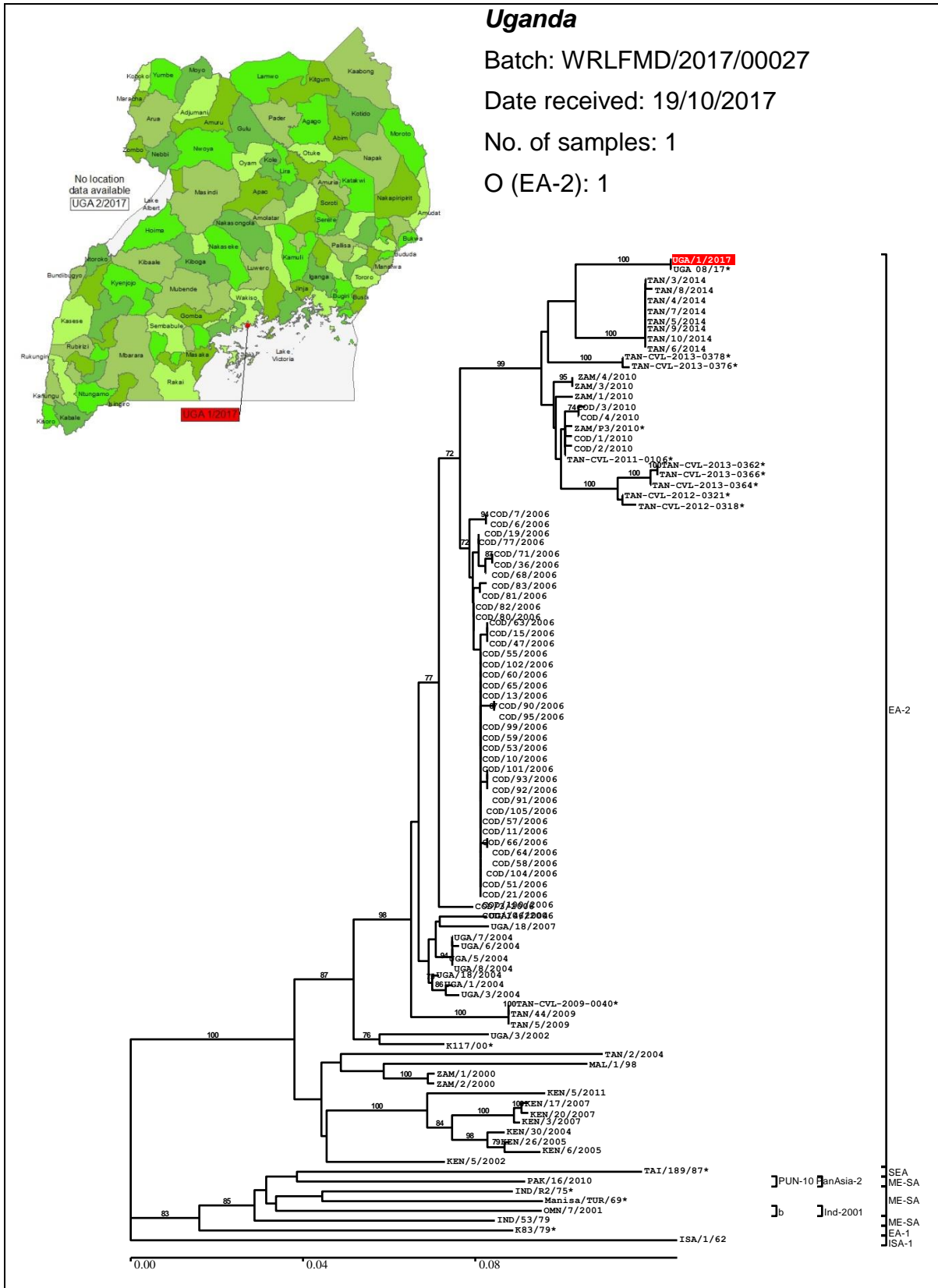
Date received: 16/10/2017

No. of sequences: 3

SAT 2 (III): 3 (1 partial VP1 sequence; not shown in tree)

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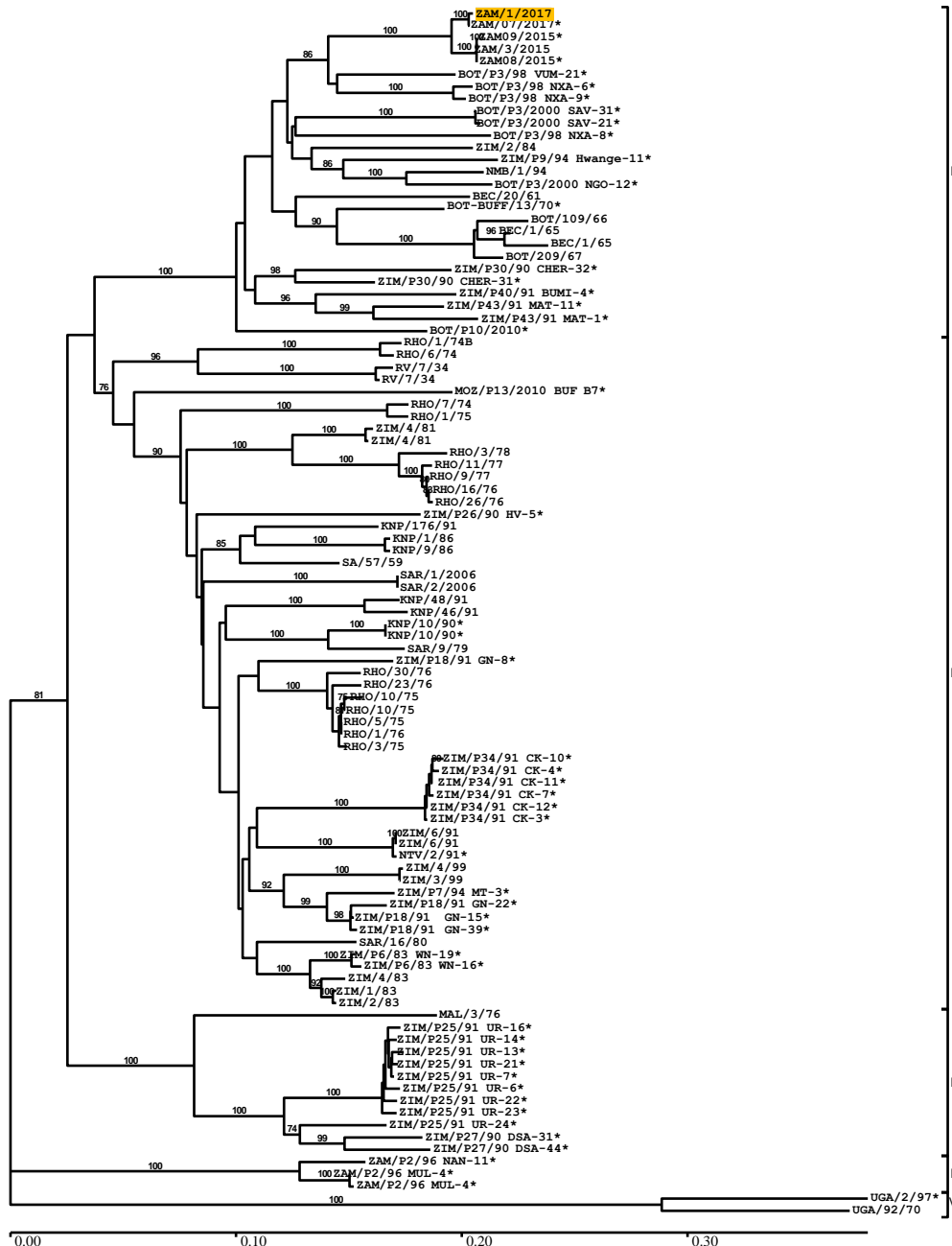
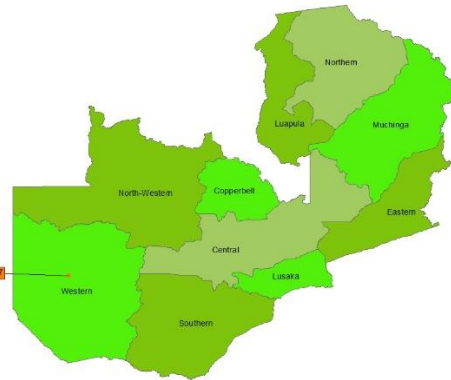
Zambia

Batch: WRLFMD/2017/00028

Date received: 19/10/2017

No. of samples: 1

SAT 3 (II): 1



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Zimbabwe

Batch: WRLMEG/2017/00053

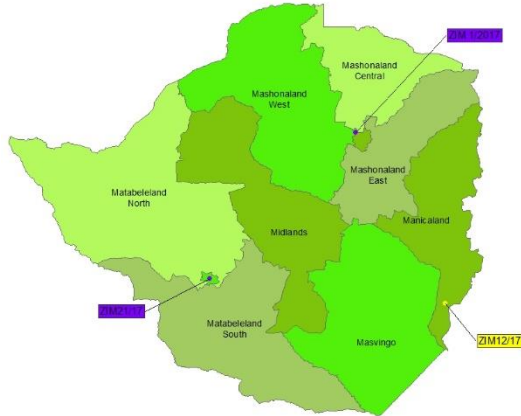
Submitted by: Elliot Fana, SSARRL,
BVI, Botswana

Date received: 16/10/2017

No. of sequences: 2

SAT 1 (III): 1

SAT 2 (II): 1 (partial VP1 sequence;
not shown in tree)

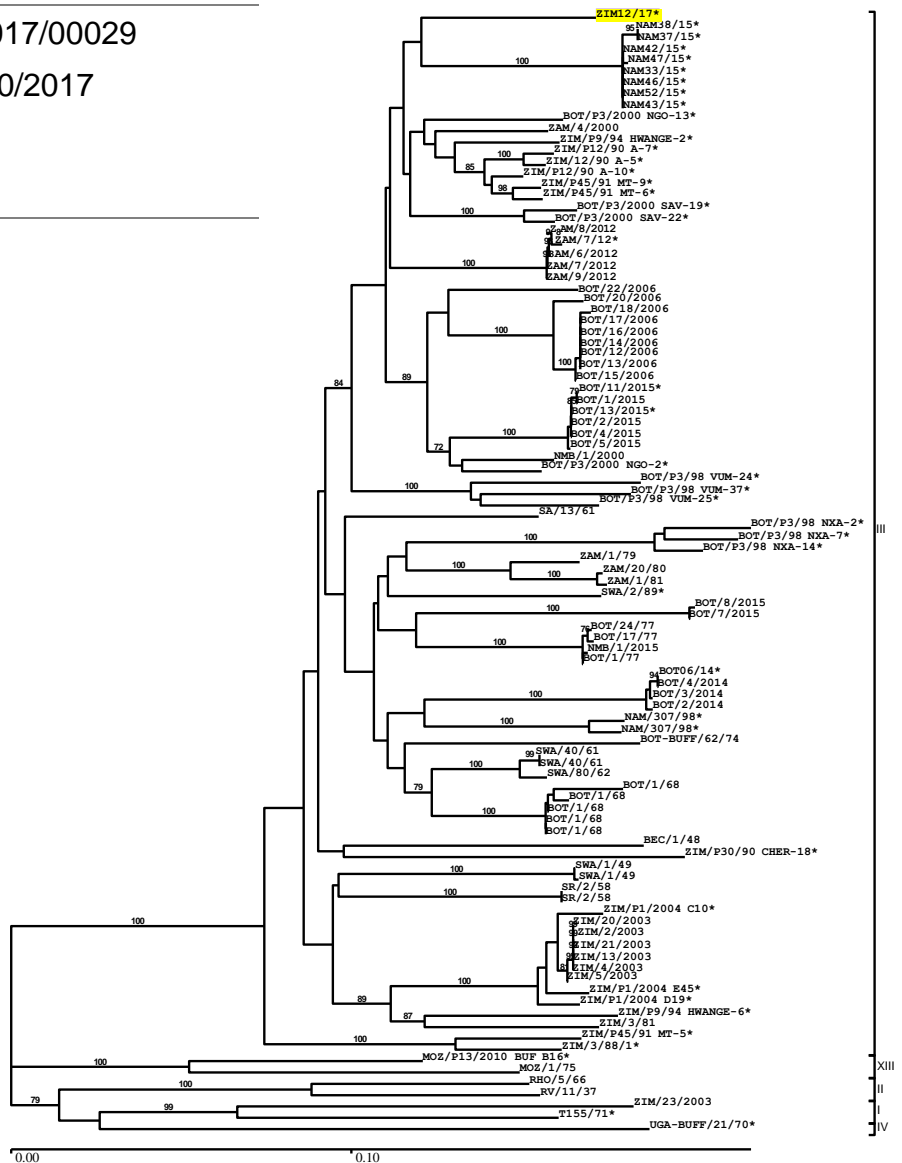


Batch: WRLFMD/2017/00029

Date received: 19/10/2017

No. of samples: 1

SAT 2 (II): 1



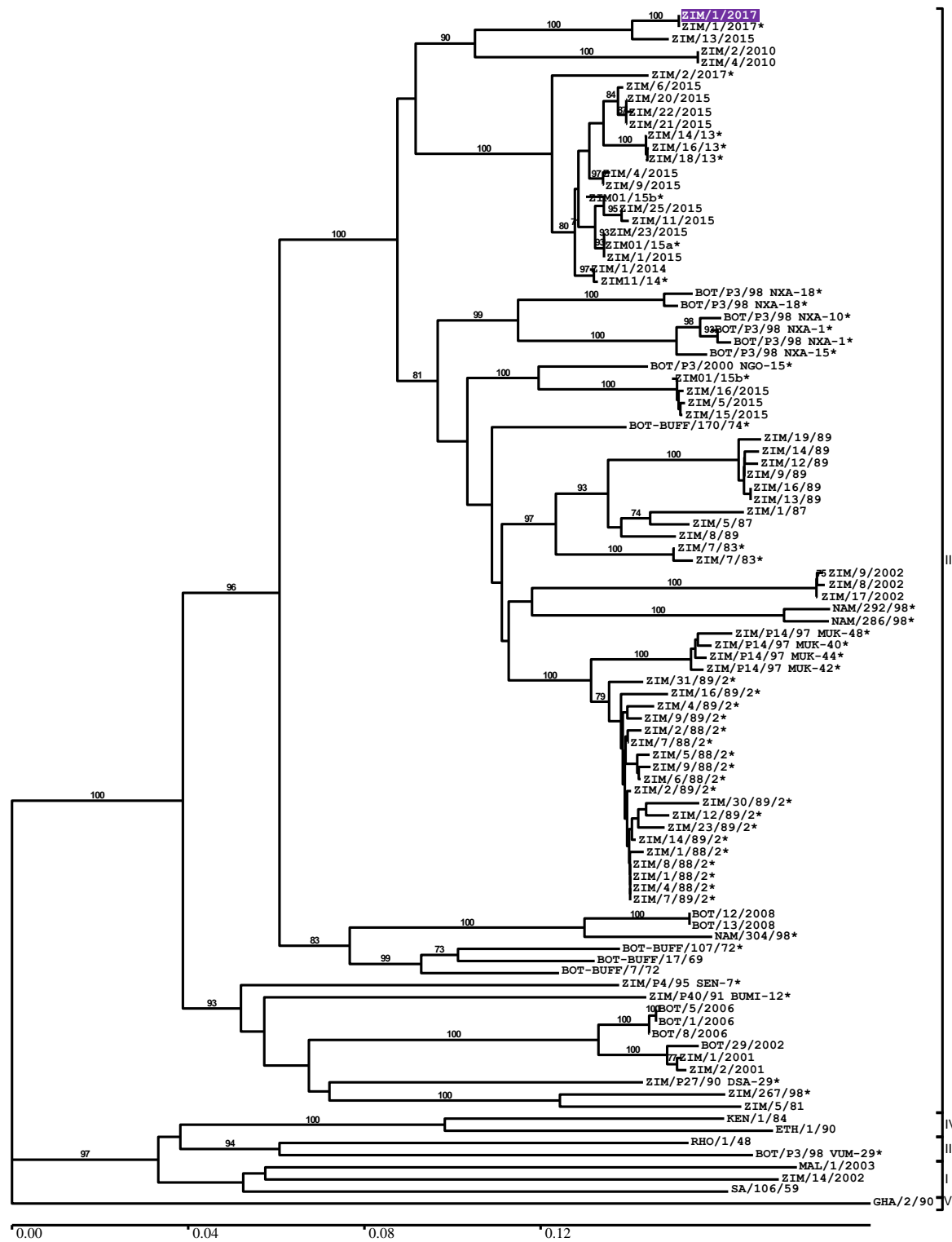
Zimbabwe continued on next page

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3. Vaccine matching

During this reporting period vaccine matching has been undertaken for 23 FMD virus field strains: serotypes O (n=11), A (n=5), Asia-1 (n=3), SAT 1 (n=1), SAT 2 (n=2) and SAT 3 (n=1). These are samples from Afghanistan, Bhutan, Botswana, Egypt, Ghana, Hong Kong (SAR of PRC), Malawi, Pakistan, Zambia and Zimbabwe

For individual data see Annex 1, section 4.3 (Antigenic Characterisation).

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4. Annex 1

4.1. Summary of Submissions

Table 2: Summary of samples collected and received to WRLFMD (October to December 2017)

Country	Nº of samples	Virus isolation in cell culture/ELISA								RT-PCR for FMD (or SVD)		
		FMD virus serotypes								virus (where appropriate)		
		O	A	C	SAT 1	SAT 2	SAT 3	ASIA -1	No Virus Detected	Positive	Negative	
Botswana	1	-	-	-	-	1	-	-	-	-	1	-
Ghana	2	1	-	-	-	-	-	-	-	1	1	1
Hong Kong, SAR of PRC	4	3	-	-	-	-	-	-	-	1	2	2
Malawi	1	-	-	-	1	-	-	-	-	-	-	1
Namibia	2	-	-	-	-	-	-	-	-	2	-	2
Sri Lanka	20	11	-	-	-	-	-	-	-	9	10	10
Uganda	2	1	-	-	-	-	-	-	-	1	1	1
Zambia	1	-	-	-	-	-	1	-	-	-	1	-
Zimbabwe	1	-	-	-	-	1	-	-	-	-	1	-
Carried over from previous quarterly report:												
Pakistan	45	14*	11	-	-	-	-	22*	4	44	1	1
TOTAL	79	30	11	-	1	2	1	11	18	61	18	18

* Six samples from Pakistan had a mixed serotype result of A and Asia-1.

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

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4.2. Clinical Samples

Table 3: Clinical sample diagnostics made by the WRLFMD® October to December 2017

Country	WRL for FMD Sample Identification	Animal	Date of Collection	Results		
				VI/ELISA	RT-PCR	Final report
BOTSWANA	BOT 1/2017	CATTLE	23-Sep-17	SAT 2	POS	SAT 2
GHANA	GHA 1/2016	CATTLE	01-Jan-16	O	POS	O
	GHA 2/2016	CATTLE	01-Jan-16	NEG	NEG	NVD
HONG KONG, SAR OF PRC	HKN 1/2017	PIG	11-Sep-17	O	POS	O
	HKN 2/2017	PIG	11-Sep-17	NEG	NEG	NVD
	HKN 3/2017	PIG	11-Sep-17	O	POS	O
	HKN 4/2017	PIG	14-Sep-17	O	NEG	O
MALAWI	MAL 1/2016	CATTLE	13-Jun-16	SAT 1	NEG	SAT 1
NAMIBIA	NMB 1/2017	CATTLE	27-Jul-17	NEG	NEG	NVD
	NMB 2/2017	CATTLE	27-Jul-17	NEG	NEG	NVD
SRI LANKA	SRL 36/2014	CATTLE	22-Dec-14	NEG	NEG	NVD
	SRL 1/2015	CATTLE	15-Dec-15	O	POS	O
	SRL 1/2016	CATTLE	15-Mar-16	NEG	NEG	NVD
	SRL 2/2016	CATTLE	15-Mar-16	NEG	NEG	NVD
	SRL 3/2016	CATTLE	21-Mar-16	NEG	POS	FMDV GD
	SRL 4/2016	CATTLE	02-Jun-16	O	POS	O
	SRL 5/2016	CATTLE	02-Jun-16	O	POS	O
	SRL 6/2016	CATTLE	02-Jun-16	O	NEG	O
	SRL 7/2016	CATTLE	14-Jun-16	O	POS	O
	SRL 8/2016	CATTLE	15-Jun-16	NEG	NEG	NVD
	SRL 9/2016	CATTLE	15-Jun-16	O	NEG	O
	SRL 10/2016	CATTLE	15-Jun-16	O	NEG	O
	SRL 11/2016	CATTLE	16-Jun-16	O	POS	O
	SRL 12/2016	CATTLE	16-Jun-16	O	POS	O
	SRL 13/2016	CATTLE	23-Jun-16	NEG	POS	FMDV GD
	SRL 14/2016	CATTLE	23-Jun-16	NEG	NEG	NVD
SRL 15/2016	CATTLE	26-Dec-16	O	POS	O	
SRL 1/2017	CATTLE	16-Aug-17	NEG	NEG	NVD	
SRL 2/2017	CATTLE	16-Aug-17	NEG	NEG	NVD	
SRL 3/2017	CATTLE	08-Sep-17	O	POS	O	
UGANDA	UGA 1/2017	CATTLE	23-May-17	O	NEG	O
	UGA 2/2017	CATTLE	23-May-17	NEG	POS	FMDV GD
ZAMBIA	ZAM 1/2017	CATTLE	18-May-17	SAT 3	POS	SAT 3
ZIMBABWE	ZIM 1/2017	CATTLE	01-Jan-17	SAT 2	POS	SAT 2
TOTAL		41				

Carried over from previous quarterly report:

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Country	WRL for FMD Sample Identification	Animal	Date of Collection	Results		
				VI/ELISA	RT-PCR	Final report
PAKISTAN	PAK 1/2016	CATTLE	10-Jan-16	ASIA-1	POS	ASIA-1
	PAK 2/2016	BUFFALO	10-Jan-16	O	POS	O
	PAK 3/2016	CATTLE	12-Jan-16	A	POS	A
	PAK 4/2016	CATTLE	03-Feb-16	O	POS	O
	PAK 5/2016	BUFFALO	12-Feb-16	ASIA-1	POS	ASIA-1
	PAK 6/2016	BUFFALO	05-Mar-16	O	POS	O
	PAK 7/2016	CATTLE	09-Mar-16	O	POS	O
	PAK 8/2016	BUFFALO	06-May-16	A, ASIA-1	POS	A, ASIA-1
	PAK 9/2016	CATTLE	08-May-16	ASIA-1	POS	ASIA-1
	PAK 10/2016	CATTLE	12-May-16	O	POS	O
	PAK 11/2016	BUFFALO	06-Jun-16	O	POS	O
	PAK 12/2016	CATTLE	09-Jul-16	NEG	NEG	NVD
	PAK 13/2016	BUFFALO	11-Aug-16	A, ASIA-1	POS	A, ASIA-1
	PAK 14/2016	BUFFALO	06-Sep-16	ASIA-1	POS	ASIA-1
	PAK 15/2016	CATTLE	08-Sep-16	O	POS	O
	PAK 16/2016	CATTLE	08-Sep-16	A	POS	A
	PAK 17/2016	CATTLE	12-Sep-16	ASIA-1	POS	ASIA-1
	PAK 18/2016	CATTLE	10-Oct-16	ASIA-1	POS	ASIA-1
	PAK 19/2016	CATTLE	16-Oct-16	NEG	POS	FMDV GD
	PAK 20/2016	BUFFALO	09-Nov-16	A, ASIA-1	POS	A, ASIA-1
	PAK 21/2016	CATTLE	11-Nov-16	O	POS	O
	PAK 22/2016	CATTLE	11-Nov-16	A, ASIA-1	POS	A, ASIA-1
	PAK 23/2016	CATTLE	09-Dec-16	ASIA-1	POS	ASIA-1
	PAK 24/2016	CATTLE	11-Dec-16	O	POS	O
	PAK 25/2016	BUFFALO	12-Dec-16	A	POS	A
	PAK 26/2016	CATTLE	12-Dec-16	O	POS	O
	PAK 27/2016	CATTLE	12-Dec-16	ASIA-1	POS	ASIA-1
	PAK 28/2016	CATTLE	22-Dec-16	NEG	POS	FMDV GD
	PAK 1/2017	BUFFALO	12-Jan-17	ASIA-1	POS	ASIA-1
	PAK 2/2017	CATTLE	19-Jan-17	A	POS	A
	PAK 3/2017	CATTLE	01-Feb-17	A, ASIA-1	POS	A, ASIA-1
	PAK 4/2017	BUFFALO	02-Feb-17	O	POS	O
	PAK 5/2017	BUFFALO	02-Feb-17	A, ASIA-1	POS	A, ASIA-1
	PAK 6/2017	CATTLE	03-Feb-17	ASIA-1	POS	ASIA-1
	PAK 7/2017	CATTLE	03-Feb-17	ASIA-1	POS	ASIA-1
	PAK 8/2017	CATTLE	03-Feb-17	O	POS	O
	PAK 9/2017	BUFFALO	03-Feb-17	ASIA-1	POS	ASIA-1
	PAK 10/2017	BUFFALO	04-Feb-17	NEG	POS	FMDV GD
	PAK 11/2017	BUFFALO	15-Feb-17	ASIA-1	POS	ASIA-1
	PAK 12/2017	CATTLE	03-Mar-17	A	POS	A
	PAK 13/2017	CATTLE	04-Mar-17	O	POS	O

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Country	WRL for FMD Sample Identification	Animal	Date of Collection	Results		
				VI/ELISA	RT-PCR	Final report
	PAK 14/2017	CATTLE	11-Mar-17	O	POS	O
	PAK 15/2017	CATTLE	05-Apr-17	ASIA-1	POS	ASIA-1
	PAK 16/2017	CATTLE	02-Aug-17	ASIA-1	POS	ASIA-1
	PAK 17/2017	BUFFALO	02-Sep-17	ASIA-1	POS	ASIA-1
TOTAL		45				

Abbreviations used in table

FMD(V)	Foot-and-mouth disease (virus)
FMDV GD	Genome detected
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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4.3. Antigenic Characterisation

Antigenic characterisation of FMD field isolates by matching with vaccine strains by 2dmVNT from October to December 2017.

Table 4: Vaccine matching studies for O FMDV by VNT

Strain	Serotype	Topotype	Strain	O 3039	O1 Manisa	O/TUR/5/2009
O/AFG/23/2017	O	ME-SA	PanAsia-2	0.46	0.72	0.74
O/AFG/34/2017	O	ME-SA	PanAsia-2	0.41	0.63	0.69
O/BHU/14/2017	O	ME-SA	Ind-2001	0.40	0.66	0.58
O/BHU/5/2017	O	ME-SA	Ind-2001	0.43	0.36	0.81
O/EGY/10/2017	O	EA-3	-	0.47	0.33	0.78
O/EGY/26/2017	O	EA-3	-	0.33	0.30	0.54
O/GHA/1/2016	O	WA	-	0.19	0.20	0.29
O/HKN/1/2017	O	CATHAY	-	0	0.12	0
O/HKN/3/2017	O	CATHAY	-	0.18	0.14	0.09
O/PAK/14/2017	O	ME-SA	PanAsia-2	0.62	0.32	0.48
O/PAK/4/2017	O	ME-SA	PanAsia-2	0	0.1	0

Table 5: Vaccine matching studies for A FMDV by VNT

Strain	Serotype	Topotype	Strain	A/IRN/05	A/TUR/20/06	A22 IRAQ
A/AFG/11/2017	A	ASIA	Iran-05	0.20	0.18	0.23
A/AFG/25/2017	A	ASIA	Iran-05	0.26	0.18	0.30
A/BHU/3/2017	A	ASIA	G-VII	0	0	0.11
A/PAK/12/2017	A	ASIA	Iran-05	0.54	0.25	0.63
A/PAK/2/2017	A	ASIA	Iran-05	0.37	0.20	0.46

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Table 6: Vaccine matching studies for Asia-1 FMDV by VNT

Strain	Serotype	Topotype	Strain	Asia 1 Shamir
Asia 1/AFG/22/2017	Asia 1	Asia	Sindh-08	0.37
Asia 1/PAK/17/2017	Asia 1	Asia	Sindh-08	0.41
Asia 1/PAK/6/2017	Asia 1	Asia	Sindh-08	0.23

Table 7: Vaccine matching studies for SAT 1 FMDV by VNT

Strain	Serotype	Topotype	Strain	SAT 1/RHO
SAT 1/MAL/1/2016	SAT 1	I	-	0.15

Table 8: Vaccine matching studies for SAT 2 FMDV by VNT

Strain	Serotype	Topotype	Strain	SAT 2 ERI	SAT 2 ZIM
SAT 2/BOT/1/2017	SAT 2	III	-	0.69	0.33
SAT 2/ZIM/1/2017	SAT 2	II	-	0.59	0.40

Table 9: Vaccine matching studies for SAT3 FMDV by VNT

Strain	Serotype	Topotype	Strain	SAT 3 ZIM
SAT 3/ZAM/1/2017	SAT 3	II	-	0.10

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Abbreviations used in tables

M	Vaccine Match <i>$r_1 = \geq 0.3$. 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.</i>
N	No Vaccine Match <i>$r_1 = < 0.3$. Suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect</i>
B	Borderline <i>Any r_1 values between 0.28 to 0.32</i>
NT	Not tested against this vaccine

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5. Annex 2

Recent FMD Publications (July to September 2017) cited by Web of Science (Pirbright Institute papers and authors are highlighted in **BOLD AND GREY**)

1. Ahmed, Z., S.J. Pauszek, A. **Ludi**, M. LaRocco, E.U.H. Khan, M. Afzal, M.J. Arshed, U. Farooq, J. Arzt, M. Bertram, B. Brito, K. Naeem, M. Abubakar, and L.L. Rodriguez (2017). Genetic diversity and comparison of diagnostic tests for characterization of *Foot-and-mouth disease virus* strains from Pakistan 2008-2012. *Transboundary and Emerging Diseases*.
2. Alam, M.A., M.R. Amin, T.K. Paul, and M.K. Rizon (2016). Clinically detection of Foot-and-mouth disease at Kapasia upazila under Gazipur district in Bangladesh. *Journal of the Bangladesh Agricultural University*, **14**(2): 185-190.
3. Ali, M.R., A.S.M. Rubayet-UI-Alam, M. Al-Amin, U. Huzzat, M.A. Siddique, M. Samina, S. Munawar, and M.A. Hossain (2017). Complete genome sequence of the circulatory *Foot-and-Mouth Disease Virus* serotype Asia1 in Bangladesh. *Genome Announcements*, **5**(43): e01135-17.
4. Audarya, S.D., B. Pattnaik, A. Sanyal, and J.K. Mohapatra (2017). TOLL like receptor 7 messenger ribonucleic acid expression levels in dairy animals in an outbreak of Foot-and-mouth disease. *Buffalo Bulletin*, **36**(3): 489-495.
5. Avci, O., S. Yavru, and M. Sevik (2017). Changes in serum biochemical values in adult cattle with Foot-and-Mouth Disease. *International Journal of Veterinary Science*, **6**(3): 174-177.
6. Baba Sheikh, M.O., P.M.A. Rashid, A.S. Marouf, Z.H. Raheem, and S.C. Janga (2017). Phylogenic analysis of serotype Asia1 *Foot-and-Mouth Disease Virus* from Sulaimani/Iraq using VP1 protein: heterogeneity with vaccine strain As1/Shamir/89. *Iranian Journal of Veterinary Research*, **18**(3): 212-215.
7. Babangida, D., A.A. Ibrahim, F.O. Oladayo, A.A. Magaji, B.R. Alkali, and A.H. Jibril (2017). Sero survey of *Foot-and-Mouth Disease Virus* infection in cattle crossing some major Border States in northwestern Nigeria. *Folia Veterinaria*, **61**(3): 12-18.
8. Bhatt, M., J.K. Mohapatra, L.K. Pandey, N.N. Mohanty, B. Das, B.R. Prusty, and B. Pattnaik (2017). Mutational analysis of *Foot-and-mouth disease virus* nonstructural polyprotein 3AB-coding region to design a negative marker virus. *Virus Research*, **243**: 36-43.
9. Cha, C.-N., B.J. Lee, E.-K. Park, C.-Y. Yoo, S. Kim, and H.-J. Lee (2017). Effects of dietary acetaminophen and vitamin C supplement on serum cortisol and tumor necrosis factor- α concentrations in pigs vaccinated with Foot-and-mouth disease vaccine. *Korean Journal of Veterinary Research*, **57**(3): 197-200.
10. Cui, C., L. Huang, J. Li, X. Zou, Y. Zhu, L. Xie, Q. Zhao, L. Yang, and W. Liu (2016). Establishment of chemiluminescent enzyme immunoassay for detecting antibodies against *Foot-and-mouth disease virus* serotype O in swine. *Sheng wu gong cheng xue bao*, **32**(11): 1519-1530.

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11. Ebrahim, F.O., A.M. Fellah, A. Elzagheid, N.S. Enattah, F. Karem, F. Abosrer, K. Mostafa, O. Alwaer, A. Hassan, M. Farhat, A. Bredan, and N. Elmarzugi (2017). Seroprevalence of Foot-and-mouth disease, Bluetongue disease and Camel brucellosis in animals imported into Libya. *Alexandria Journal of Veterinary Sciences*, **54**(1): 97-100.
12. Ehizibolo, D.O., A. Haegeman, A.R. De Vleeschauwer, J.U. Umoh, H.M. Kazeem, E.C. Okolocha, S. Van Borm, and K. De Clercq (2017). Detection and Molecular Characterization of Foot-and-Mouth Disease Viruses from Outbreaks in Some States of Northern Nigeria 2013-2015. *Transboundary and Emerging Diseases*, **64**(6): 1979-1990.
13. Ehizibolo, D.O., A. Haegeman, A.R. De Vleeschauwer, J.U. Umoh, H.M. Kazeem, E.C. Okolocha, S. Van Borm, and K. De Clercq (2017). *Foot-and-Mouth Disease Virus* serotype SAT1 in cattle, Nigeria. *Transboundary and Emerging Diseases*, **64**(3): 683-690.
14. Fang, H., B. Yuan, L. Han, X. Xin, H. Wang, F. Yu, C. Zheng, and C. Shen (2017). Single-cell analysis reveals the relevance of *Foot-and-Mouth Disease Virus* persistence to emopamil-binding protein gene expression in host cells. *Archives of Virology*, **162**(12): 3791-3802.
15. Gunasekera, U.C., A. Sivasothy, N. Wedasingha, S. Thayaparan, B. Rotewewa, M. Muralithas, M.P.O. Baumann, and V. Punyapornwithaya (2017). Analyzing the Foot-and-Mouth Disease outbreak as from 2008 to 2014 in cattle and buffaloes in Sri Lanka. *Preventive Veterinary Medicine*, **148**: 78-88.
16. Herod, M.R., **S. Gold, L. Lasecka-Dykes, C. Wright**, J.C. Ward, T.C. McLean, S. Forrest, **T. Jackson, T.J. Tuthill**, D.J. Rowlands, and N.J. Stonehouse (2017). Genetic economy in picornaviruses: *Foot-and-mouth disease virus* replication exploits alternative precursor cleavage pathways. *PLoS Pathogens*, **13**(10): e1006666-e1006666.
17. Horsington, J., C. Beascoechea Perez, E. Maradei, S. Galdo Novo, J.L. Gonzales, N.B. Singanallur, P. Bonastre, and W. Vosloo (2017). Protective effects of high -potency FMDV O-1 Manisa monovalent vaccine in cattle challenged with FMDV O/SKR/2010 at 7 or 4 days post vaccination. *Vaccine*, **35**(38): 5179-5185.
18. Hou, L., J. Chen, X. Qiao, X. Yu, J. Hou, Q. Zheng, and J. Li (2017). Design and immunogenicity evaluation for the bacteria-like particle vaccine against swine type O *Foot-and-mouth disease virus*. *Sheng wu gong cheng xue bao*, **33**(2): 217-227.
19. Kim, A.-Y., D. Tark, H. Kim, J.-S. Kim, J.-M. Lee, M. Kwon, S. Bae, B. Kim, and Y.-J. Ko (2017). Determination of optimal age for single vaccination of growing pigs with Foot-and-mouth disease bivalent vaccine in South Korea. *The Journal of Veterinary Medical Science*.
20. Kjar, J. and G.J. Belsham (2017). Selection of functional 2A sequences within *Foot-and-mouth disease virus*; requirements for the NPGP motif with a distinct codon bias. *RNA (New York, N. Y.)*.
21. Kloc, A., F. Diaz-San Segundo, E.A. Schafer, D.K. Rai, M. Kenney, T. de Los Santos, and E. Rieder (2017). *Foot-and-mouth disease virus* 5'-terminal S

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- fragment is required for replication and modulation of the innate immune response in host cells. *Virology*, **512**: 132-143.
22. Kompas, T., H. Pham Van, N. Hoa Thi Minh, I. East, S. Roche, and G. Garner (2017). Optimal surveillance against Foot-and-mouth disease: the case of bulk milk testing in Australia. *Australian Journal of Agricultural and Resource Economics*, **61**(4): 515-538.
 23. Kumar, A., V. Singh, T. Pongen, S.B. Hazarika, and A. Mitra (2017). Normal reference ranges of oxidative markers in mithun population and their alterations during the Foot-and-mouth disease. *Indian Journal of Animal Sciences*, **87**(9): 1087-1089.
 24. Li, F., R. Yan, Z. Wu, F. Ban, Z. Ma, X. Zhao, Q. Li, H. Zhang, X. Zhang, and L. Gao (2017). Preparation and identification of monoclonal antibodies against VP1 protein of *Foot-and-mouth disease virus* O serotype. *Zhongguo Shouyi Kexue*, **47**(7): 831-837.
 25. Li, K., H. Bao, G. Wei, D. Li, Y. Chen, Y. Fu, Y. Cao, P. Li, P. Sun, X. Bai, X. Ma, J. Zhang, Z. Lu, and Z. Liu (2017). Molecular vaccine prepared by fusion of XCL1 to the multi-epitope protein of *Foot-and-mouth disease virus* enhances the specific humoral immune response in cattle. *Applied Microbiology and Biotechnology*, **101**(21): 7889-7900.
 26. Liu, H., Q. Xue, Q. Zeng, Z. Zhu, and H. Zheng (2017). The Kinase STK3 Interacts with the Viral Structural Protein VP1 and Inhibits *Foot-and-Mouth Disease Virus* Replication. *Biomed Research International*.
 27. Liu, X., J. Lv, Y. Fang, P. Zhou, Y. Lu, L. Pan, Z. Zhang, J. Ma, Y. Zhang, and Y. Wang (2017). Expression and Immunogenicity of Two Recombinant Fusion Proteins Comprising *Foot-and-Mouth Disease Virus* Structural Protein VP1 and DC-SIGN-Binding Glycoproteins. *Biomed Research International*.
 28. **Logan, G., J. Newman, C.F. Wright, L. Lasecka-Dykes, D.T. Haydon, E.M. Cottam, and T.J. Tuthill** (2017). Deep sequencing of *Foot-and-mouth disease virus* reveals RNA sequences involved in genome packaging. *Journal of Virology*.
 29. Mahmoud, M.A.E., M.K. Elbayoumy, D. Sedky, and S. Ahmed (2017). Serological investigation of some important RNA viruses affecting sheep and goats in Giza and Beni-Suef governorates in Egypt. *Veterinary World*, **10**(10): 1161-1166.
 30. Malik, N., A. Kotecha, **S. Gold, A. Asfor**, J. Ren, J.T. Huiskonen, **T.J. Tuthill**, E.E. Fry, and D.I. Stuart (2017). Structures of *Foot-and-mouth disease virus* pentamers: Insight into capsid dissociation and unexpected pentamer reassociation. *PLoS Pathogens*, **13**(9): e1006607-e1006607.
 31. Mansoor, M.K., A.H. Al-Rawahi, H.A. El-Tahir, B. Al-Faraei, M.H. Hussain, M.N. Asi, I. Al-Hussani, and S. Sabar (2017). Concurrent vaccination of goats with Foot-and-mouth disease (FMD) and Peste des petits ruminants (PPR) booster vaccines. *Tropical Animal Health and Production*.
 32. Merhan, O., K. Bozukluhan, S. Kiziltepe, and H.I. Gokce (2017). Investigation of Levels of Haptoglobin, Serum Amyloid A, Ceruloplasmin and Albumin in Cattle with Foot-and-Mouth Disease. *Israel Journal of Veterinary Medicine*, **72**(4): 14-17.

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33. **Nelson, N., D.J. Paton, S. Gubbins, C. Colenutt, E. Brown, S. Hodgson, and J.L. Gonzales** (2017). Predicting the Ability of Preclinical Diagnosis To Improve Control of Farm-to-Farm Foot-and-Mouth Disease Transmission in Cattle (vol 55, pg 1671, 2017). *Journal of Clinical Microbiology*, **55**(10): 3146-3146.
34. Puckette, M., B.A. Clark, J.D. Smith, T. Turecek, E. Martel, L. Gabbert, M. Pisano, W. Hurtle, J.M. Pacheco, J. Barrera, J.G. Neilan, and M. Rasmussen (2017). *Foot-and-Mouth Disease (FMD) Virus 3C Protease Mutant L127P: Implications for FMD Vaccine Development. Journal of Virology*, **91**(22).
35. Rasheed, N.A., P.M.M. Sharif, and D.T. Barwari (2017). Geographic Distribution of Foot and Mouth Disease (FMD) in Sheep in Duhok Governorate, Iraq by using GIS. *Research Journal of Pharmaceutical Biological and Chemical Sciences*, **8**(2): 1386-1395.
36. Relmy, A., A. Romey, K. Gorna, S. Blaise-Boisseau, E. Laloy, D. Meenowa, K. Samoisy, R. Harena, R. Ram, J. Aboo, E. Cardinale, C. Sailleau, S. Lecollinet, S. Zientara, and K.L. Bakkali (2017). Animal health crisis in the Indian Ocean: *Foot-and-mouth disease virus* in Mauritius and Rodrigues in 2016. *Epidemiologie et Sante Animale*, (71): 117-127.
37. Rout, M., D. Bhattacharya, B.R. Prusty, N. Chatterjee, A.K. Bera, J. Doley, S. Deori, D. Medhi, J. Bam, S. Hanah, S.M. Deb, and B. Pattnaik (2017). *Foot-and-mouth disease virus* infection-specific nonstructural protein antibodies detected in populations of mithun (*Bos frontalis*), yak (*Bos grunniens*) and their hybrids maintained in farms and villages of Arunachal Pradesh, India. *Indian Journal of Animal Sciences*, **87**(9): 1090-1091.
38. Sanchez, J.A.C., J.V. Bagunu, R.P. Alili, and L.C. Cruz (2017). Cloning of the 2B region from Foot-and-Mouth Disease viral genome as a potential external positive control for FMD detection. *Tropical Agriculture and Development*, **61**(2): 94-98.
39. Sheikh, M.O.B., P.M.A. Rashid, A.S. Marouf, Z.H. Raheem, and S.C. Janga (2017). Phylogenetic analysis of serotype Asia1 *Foot-and-Mouth Disease Virus* from Sulaimani/Iraq using VP1 protein: heterogeneity with vaccine strain As1/Shamir/89. *Iranian Journal of Veterinary Research*, **18**(3): 212-215.
40. Sieng, S., S.W. Walkden-Brown, and J. Kerr (2016). Variation in storage temperatures for Foot-and-mouth vaccine in Cambodia. *International Journal of Environmental and Rural Development*, **7**(2): 24-31.
41. Singh, A.P., R. Singh, T. Singh, and S.K. Yadav (2017). Randomised field trial to evaluate serological response after Foot-and-Mouth Disease vaccination in Uttar Pradesh, India. *Indian Journal of Animal Sciences*, **87**(12): 1485-1487.
42. Soltan, M.A., A.H. Negmaldin, M.M. El-Diasty, S.M.G. Mansour, M.A. Elbadry, and R.P. Wilkes (2017). Molecular characterization of circulating *Foot-and-mouth disease virus* (FMDV) serotype O topotype EA-3 and serotype A (African topotype) genotype IV in Egypt, 2016. *Veterinary Microbiology*, **208**: 89-93.
43. Soria, I., V. Quattrocchi, C. Langellotti, M. Gammella, S. Digiaco, B. Garcia de la Torre, D. Andreu, **M. Montoya**, F. Sobrino, E. Blanco, and P. Zamorano (2017). Dendrimeric peptides can confer protection against *Foot-and-mouth disease virus* in cattle. *Plos One*, **12**(9).

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44. Stenfeldt, C., M. Eschbaumer, G.R. Smoliga, L.L. Rodriguez, J. Zhu, and J. Arzt (2017). Clearance of a persistent *picornavirus* infection is associated with enhanced pro-apoptotic and cellular immune responses. *Scientific Reports*, **7**.
45. Sun, X., B. Zhang, Q. Zhang, K. He, and X. Zhang (2017). Adjuvant effects of flagellin from non-pathogenic *E. coli* on FMDV. *Scientia Agricultura Sinica*, **50**(9): 1714-1722.
46. Ularanu, H.G., J.O. Ibu, **B.A. Wood**, J.N. Abenga, D.D. Lazarus, Y.S. Wungak, **N.J. Knowles**, **J. Wadsworth**, **V. Mioulet**, **D.P. King**, D. Shamaki, and M.I. Adah (2017). Characterization of Foot-and-Mouth Disease Viruses Collected in Nigeria Between 2007 and 2014: Evidence for Epidemiological Links Between West and East Africa. *Transboundary and Emerging Diseases*, **64**(6): 1867-1876.
47. Vandebussche, F., E. Mathijs, H.G. Ularanu, D.O. Ehizibolo, A. Haegeman, D. Lefebvre, D.D. Lazarus, Y.S. Wungak, A.R.d. Vleeschauwer, S.v. Borm, and K.d. Clercq (2017). Complete genome sequences of four Foot-and-Mouth Disease Viruses of serotype South African territories 1 (SAT 1), topotype X, isolated from cattle in Nigeria in 2015. *Genome Announcements*, **5**(42): e01065-17.
48. Yang, B., M. Wang, W. Liu, Z. Xu, H. Wang, D. Yang, W. Ma, G. Zhou, and L. Yu (2017). Identification of a serotype-independent linear epitope of *Foot-and-Mouth Disease Virus*. *Archives of Virology*, **162**(12): 3875-3880.
49. Yang, S., J. Yang, Y. Sun, F. Peng, S. Zhang, Y. Liu, M. Teng, D. Zhao, S. Chai, and G. Zhang (2017). A rapid immunochromatographic strip for neutralizing antibodies detection of *Foot-and-Mouth Disease Virus* serotype O. *RSC Advances*, **7**(76): 48095-48101.
50. Younus, I., M. Ashraf, A. Fatima, I. Altaf, and A. Javeed (2017). Evaluation of cytotoxic and antiviral activities of aqueous leaves extracts of different plants against *Foot-and-Mouth Disease Virus* infection in farming animals. *Pakistan Journal of Pharmaceutical Sciences*, **30**(6): 2167-2172.
51. Yuan, H., P. Li, X. Ma, Z. Lu, P. Sun, X. Bai, J. Zhang, H. Bao, Y. Cao, D. Li, Y. Fu, Y. Chen, Q. Bai, J. Zhang, and Z. Liu (2017). The pH stability of *Foot-and-Mouth Disease Virus*. *Virology Journal*, **14**.
52. Zhang, Z., L. Pan, Y. Ding, J. Lv, P. Zhou, Y. Fang, X. Liu, Y. Zhang, and Y. Wang (2017). eEF1G interaction with *Foot-and-mouth disease virus* nonstructural protein 2B: Identification by yeast two-hybrid system. *Microbial pathogenesis*.
53. 박유리, 임다래, 김혜령, 박민지, 김범석, 김원일, 홍창호, 김성년, and 박최규 (2017). Evaluation of efficacy of a commercial vaccine stress-relieving agent to reduce the adverse effects of Foot-and-mouth disease vaccination site in pig. *Korean Journal of Veterinary Service*, **40**(3): 177-185.

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6. Annex 3

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

December 2017:

Note: Virus strains are NOT listed in order of importance

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

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

*Recent *in vitro* data from WRLFMD for serotype A viruses highlights an apparent gap in vaccines supplied by international manufacturers for this viral lineage.

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