

# WRLFMD Quarterly Report January to March 2018

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

Two outbreaks of FMD were reported on the 1<sup>st</sup> and 2<sup>nd</sup> of January 2018 in Guizhou Province. The first was reported as **FMD type A** and occurred in cattle, sheep and pigs; the second was due to **FMD type O** and occurred only in pigs. Two further outbreaks due to **FMD type O** were reported to have occurred on 10/01/2018 in the Ningxia Hui Autonomous Region (in cattle) and on 24/02/2018 in Henan Province (in sheep). A **FMDV type A** VP1 sequence was received from the Lanzhou Veterinary Research Institute, China and genotyping showed this to belong to the ASIA topotype Sea-97 lineage (see below).

### Hong Kong Special Administrative Region

**FMD type O** viruses were isolated from three samples (in a batch of 10) which had been collected from pigs between October and December 2017. Real-time RT-PCR identified a further virus positive sample in one of the other cell culture-negative samples. VP1 sequencing showed all four viruses to belong to the CATHAY topotype and to be closely related to other CATHAY viruses isolated earlier in 2017.

### Israel

Ten samples, collected from cattle in May and June 2017, were received on the 18/01/2018. **FMDV type O** was isolated from four samples and **FMDV type A** from six samples. VP1 sequencing showed the type O viruses to belong to the EA-3 topotype (closely related to previously characterised viruses from Israel, Palestine, Egypt and Ethiopia) and the type A viruses to the ASIA topotype (lineage G-VII).

### Mongolia

Between 07/09/2017 and 06/03/2018, 30 outbreaks of **FMD type O** were reported in cattle, sheep and goats in the following eastern provinces: Dornod, Dornogovi, Dundgovi, Govi-Sumber, Khentii, Sukhbaatar and Umnugovi. These were a continuation of outbreaks first reported in January 2017. Three samples, collected

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from cattle, were received in February 2018; one was collected in March 2015 from Khovd Bulgan, one from Sukhbaatar Erdenetsagaan (January 2017) and one from Dundgovi Gurvansaihan (November 2017). The sample from 2015 contained both FMDV types O (SEA/Mya-98) and A (ASIA/Sea-97), while the January and November 2017 samples were FMDV type O (ME-SA/PanAsia and ME-SA/Ind-2001, respectively).

## **Nepal**

An outbreak due to **FMD type Asia 1** (09/12/2017) was reported in cattle and buffalo in Gandaki Zone. A batch of 18 samples, collected from cattle in Bagmati, Gandaki and Narayani Zones during November and December 2017. **FMD type O** was isolated from three samples (Bagmati) and **FMD type Asia 1** from eight samples (Gandaki and Narayani). VP1 sequencing showed the type O viruses to belong to the ME-SA toposotype (Ind-2001 lineage) and the Asia 1 viruses to belong to a previously undescribed lineage. Colleagues at the PD-FMD (Mukteswar, India) reported that these sequences were distinct from all other Indian Asia 1 viruses recently characterised.

## **Palestinian Autonomous Territories**

Twelve samples, collected from cattle and sheep in the Gaza Strip in May, June and December 2017. **FMD type O** viruses were isolated from all 12 samples. VP1 sequencing revealed all to belong to the EA-3 toposotype and to be related to recent viruses from Israel, Egypt and Ethiopia.

## **Republic of Korea (South Korea)**

An outbreak due to **FMD type A** was reported on 26/03/2018 in pigs in Gyeonggi-Do. VP1 sequencing was performed at the Animal and Plant Quarantine Agency (APQA) and genotyping revealed that the virus belonged to the ASIA toposotype, Sea-97 lineage (see below).

## **Russian Federation**

Between 1<sup>st</sup> and 10<sup>th</sup> February 2018, five outbreaks due to **FMD type O** were reported in cattle in the Zabaykalsky Krai region. No genotyping has been reported.

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## 1.2. Africa

### Kenya

Seven samples, collected from cattle between November 2016 and November 2017, were received on 15/12/2017. Three **FMD type O** viruses were isolated in cell cultures, FMDV genome was detected (FMDV-GD) in two and two were NVD. RT-PCR and sequencing of one of the FMDV-GD samples revealed the presence of **FMD type SAT 1**. VP1 sequencing showed the type O viruses to belong to the EA-2 topotype (but distinct from previously characterised viruses) while the SAT 1 belonged to topotype I (and again distinct from previously characterised viruses).

### Mozambique

An outbreak of suspected **FMD** was reported to have occurred on 25/12/2017 in cattle in the Chicualacuala District, Gaza Province. On the 18/01/2017, a **FMDV type SAT 3** VP1 sequence was received from the OIE Sub-Saharan Africa Regional Reference laboratory (SSARRL) for FMD (Botswana Vaccine Institute). Genotyping showed the virus to belong to topotype I and to be distinct from other viruses in this topotype (see below).

### South Africa

On the 14-15/10/2017, three outbreaks due to **FMD type SAT 1** were reported in cattle in Greater Giyani, Limpopo. No genotyping has been reported.

### Tunisia

On the 23/02/2018, seven **FMDV type A** VP1 sequences were received from the Laboratoire de santé animale, UMR Virologie, INRA, Ecole Nationale Vétérinaire d'Alfort (ANSES) derived from sample collected in Tunisia during 2017. Genotyping showed them to belong to the AFRICA topotype, G-IV lineages and to be closely related to sequences from Algeria.

### Zambia

Between 27/06/2017 and 02/08/2017, three outbreaks of suspected **FMD** (as yet untyped) were reported in cattle in the North-Western province.

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## Zimbabwe

In January 2018, three outbreaks of suspected FMD were reported in cattle in Mashonaland West and Mashonaland East.

### 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/2018.htm](http://www.wrlfmd.org/fmd_genotyping/2018.htm).

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 January to March 2018 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 January to March 2018 (\* 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/2017/00031*	15/12/2017	Kenya	O	3	3	completed
WRLFMD/2017/00031*	15/12/2017	Kenya	SAT 1	1	1	completed
WRLFMD/2018/00002	17/01/2018	Hong Kong SAR	O	4	4	completed
WRLFMD/2018/00003	18/01/2018	Israel	O	4	4	completed
WRLFMD/2018/00003	18/01/2018	Israel	A	6	6	completed
WRLFMD/2018/00004	18/01/2018	Palestinian AT	O	12	12	completed
WRLFMD/2018/00005	26/01/2018	Nepal	O	3	3	completed
WRLFMD/2018/00005	26/01/2018	Nepal	Asia 1	8	8	completed
WRLFMD/2018/00006	05/02/2018	Mongolia	O	3	3	completed
WRLFMD/2018/00006	05/02/2018	Mongolia	A	1	1	completed
WRLFMD/2018/00007	12/03/2018	Iran	pending	n=25†		pending
WRLFMD/2018/00009	14/03/2018	Ethiopia	pending	n=28†		pending
<b>Total</b>				<b>45</b>	<b>45</b>	

\*, carried over from previous quarter.

†, not included in the totals.

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## 2. Detailed Analysis

Key for maps and trees:

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

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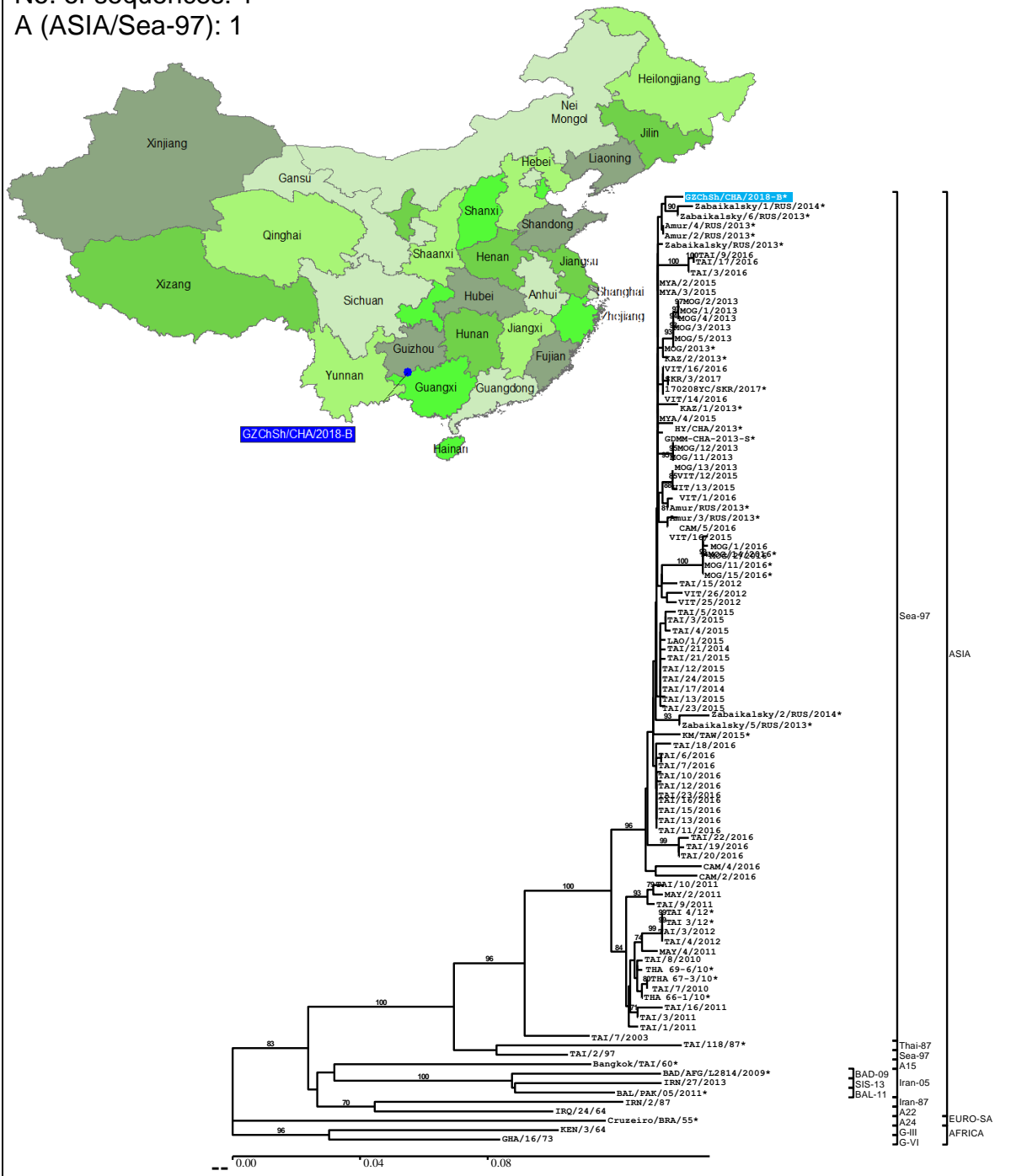
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## 2.1. ASIA

**China, People's Republic of**  
 Batch: WRLMEG/2018/00003  
 Submitted by: LVRI, PR China  
 Date received: 12/01/2018  
 No. of sequences: 1  
 A (ASIA/Sea-97): 1



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### Hong Kong SAR

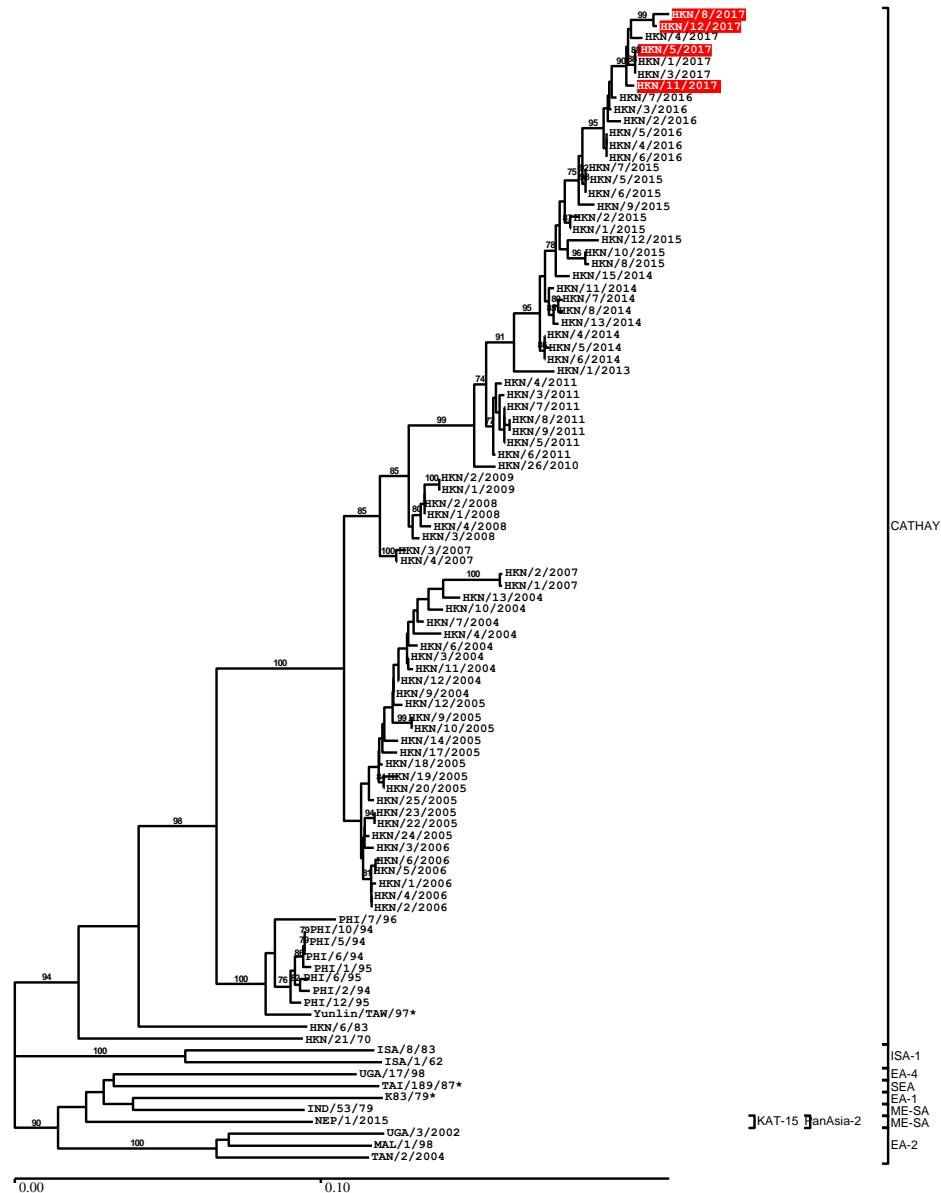
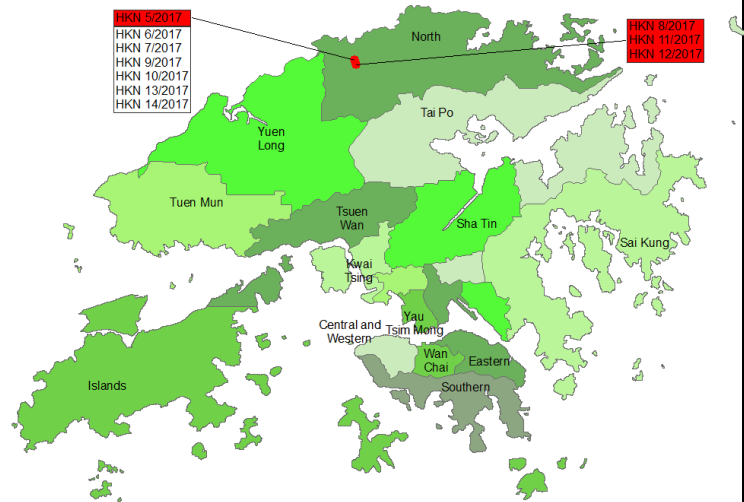
Batch: WRLFMD/2018/00002

Date received: 17/01/2018

No. of samples: 10

O (CATHAY): 4

NVD: 6



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### Israel

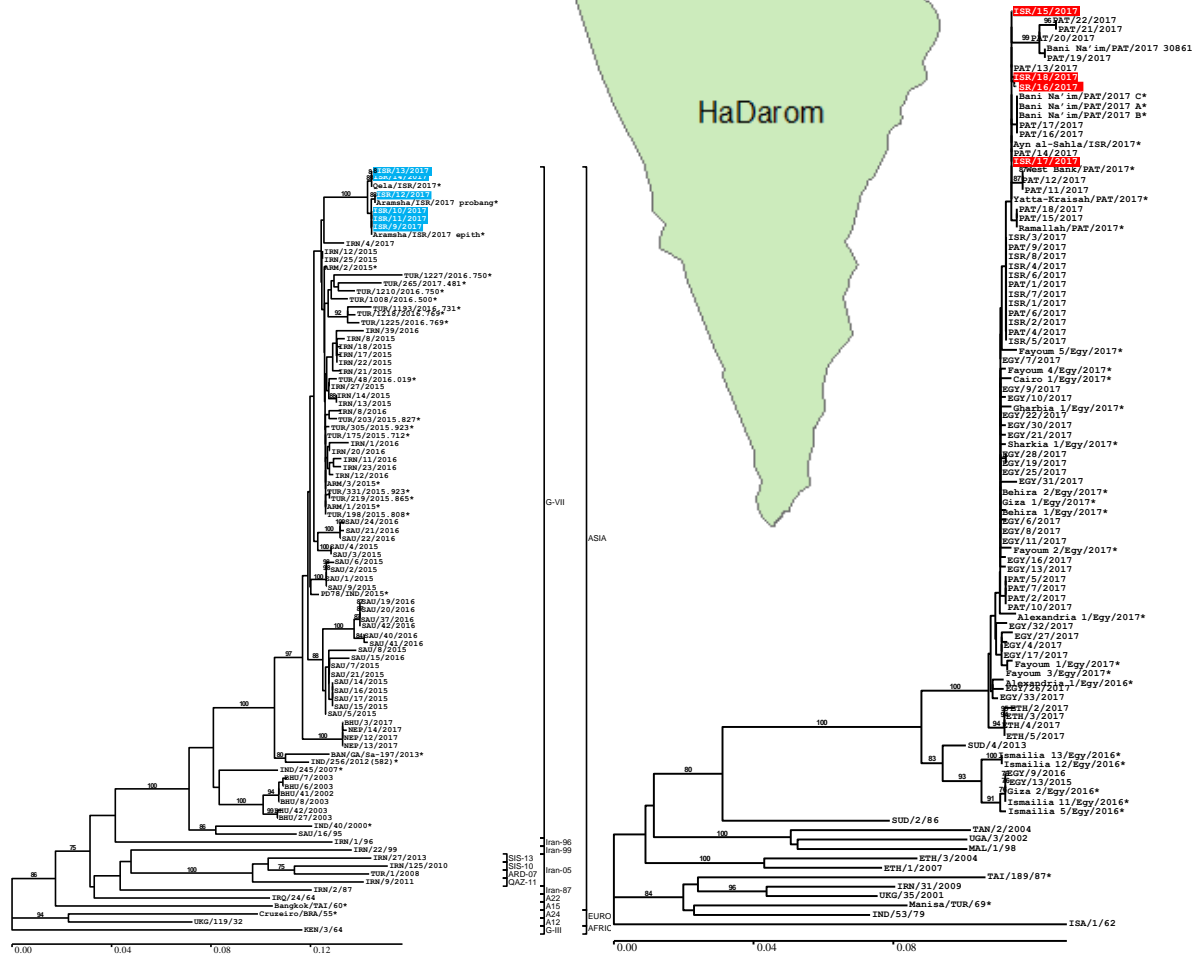
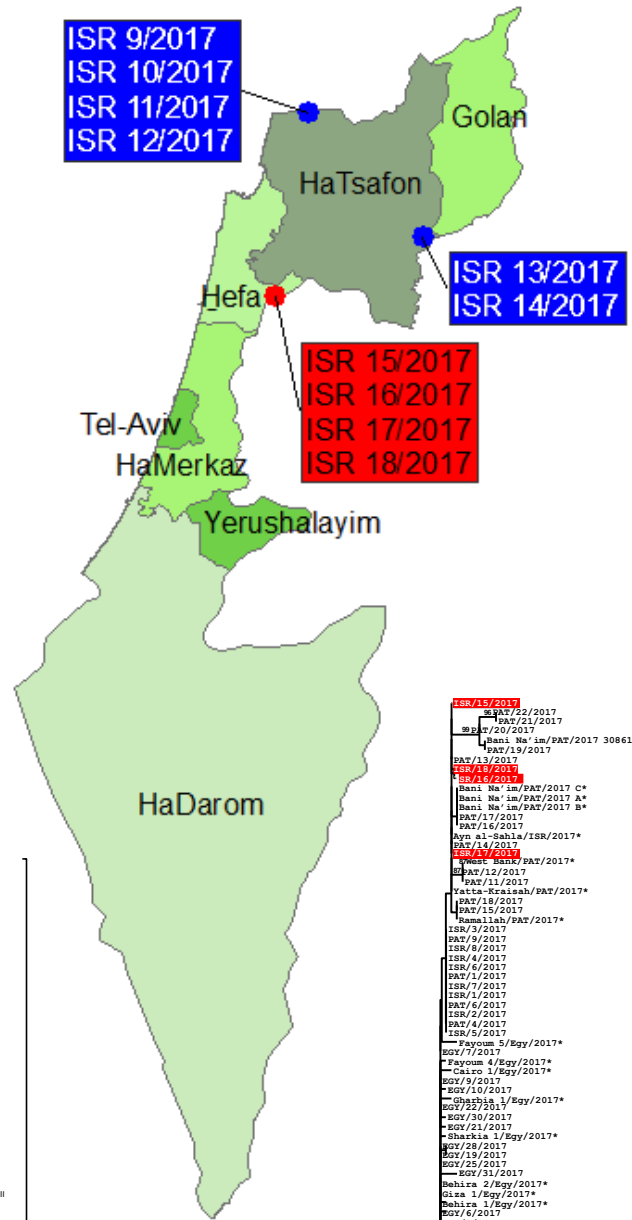
Batch: WRLFMD/2018/00003

Date received: 18/01/2018

No. of samples: 10

O (EA-3): 4

A (ASIA/G-VII): 6



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## Mongolia

Batch: WRLFMD/2018/00006

Date received: 05/02/2018

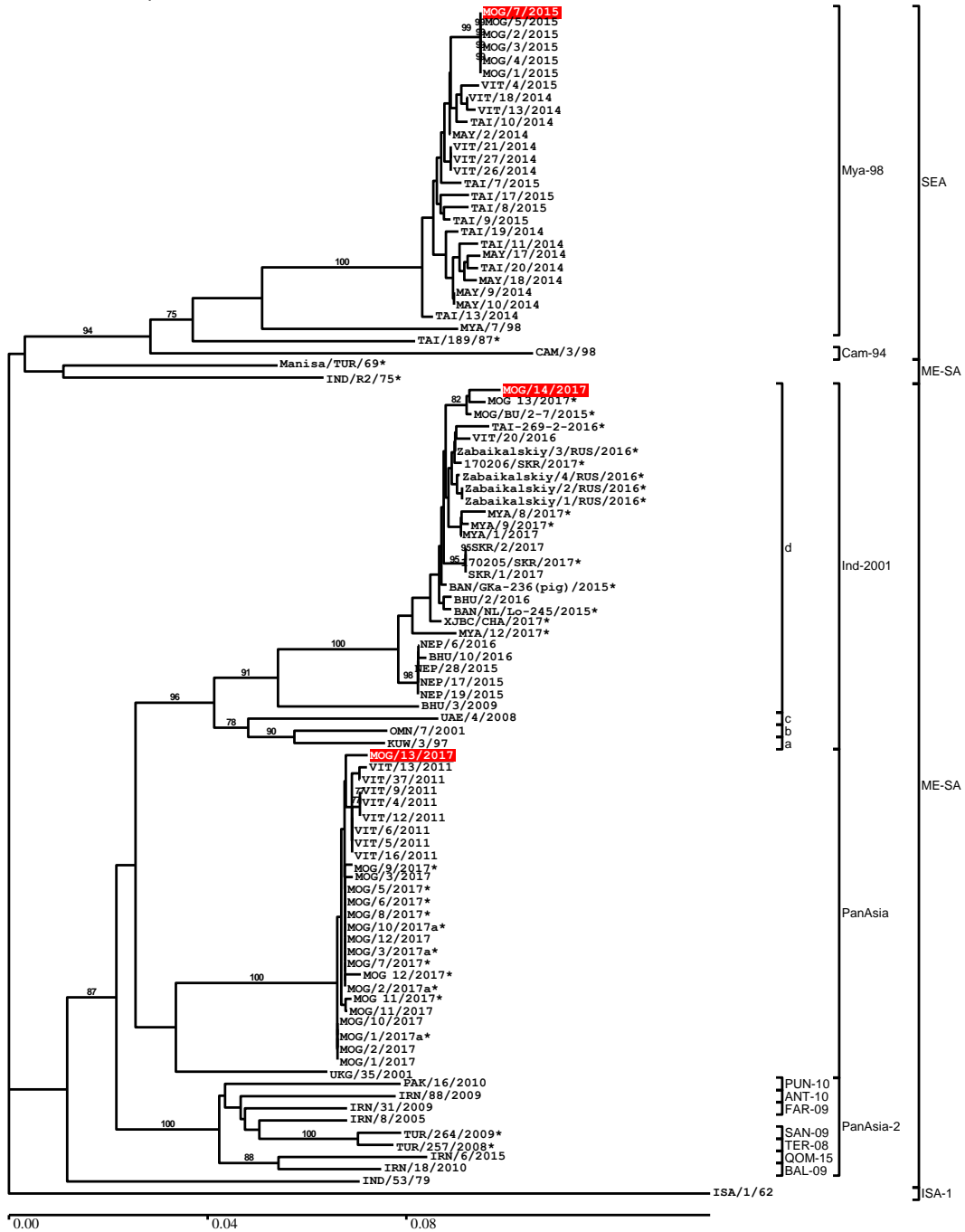
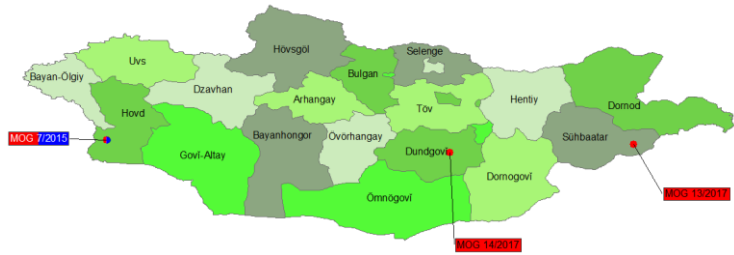
No. of samples: 3

O (SEA/Mya-98): 1

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

O (ME-SA/PanAsia): 1

A (ASIA/Sea-97): 1



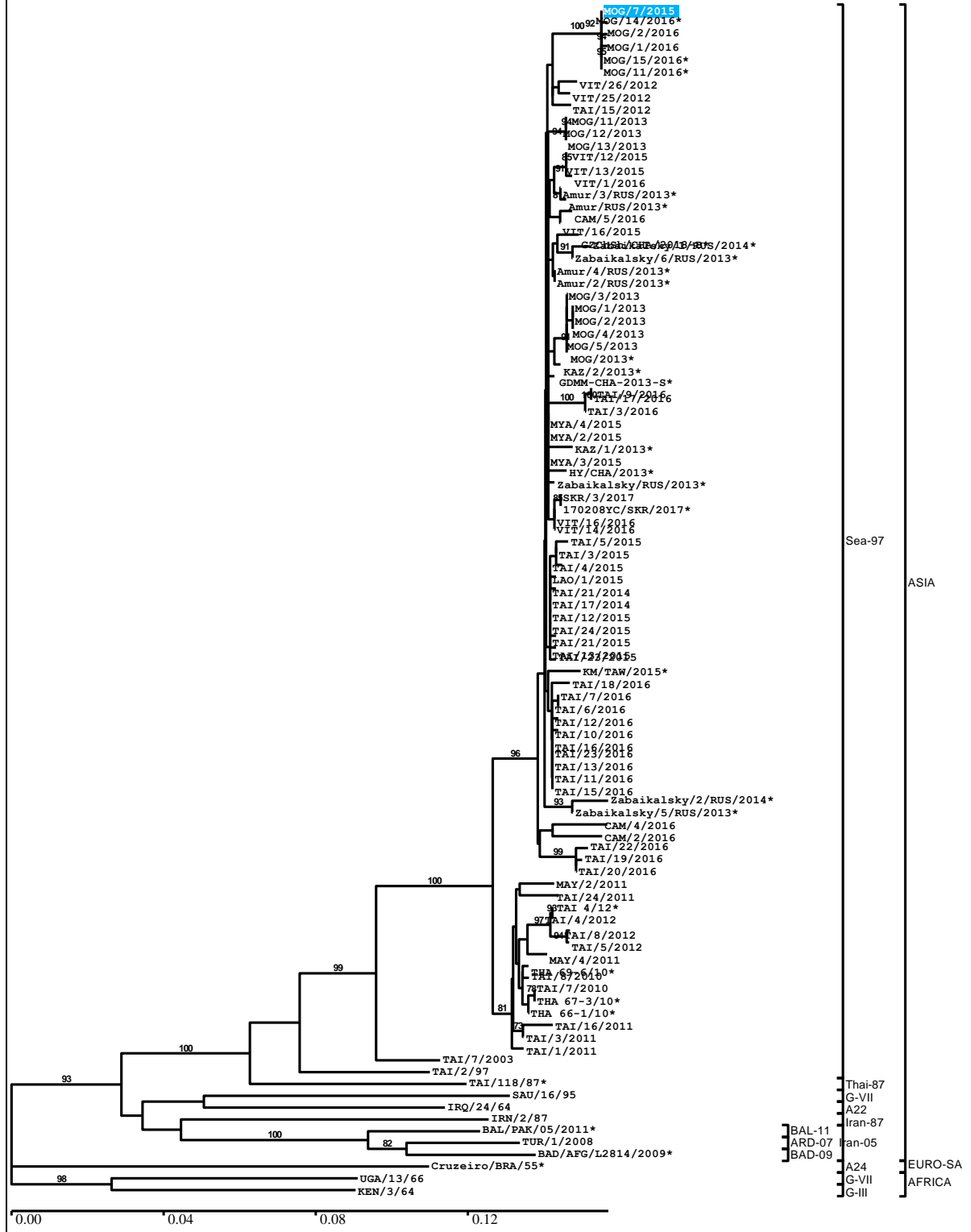
Mongolia Continued on next page

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# Mongolia continued



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# Nepal

Batch: WRLFMD/2018/00005

Date received: 26/01/2018

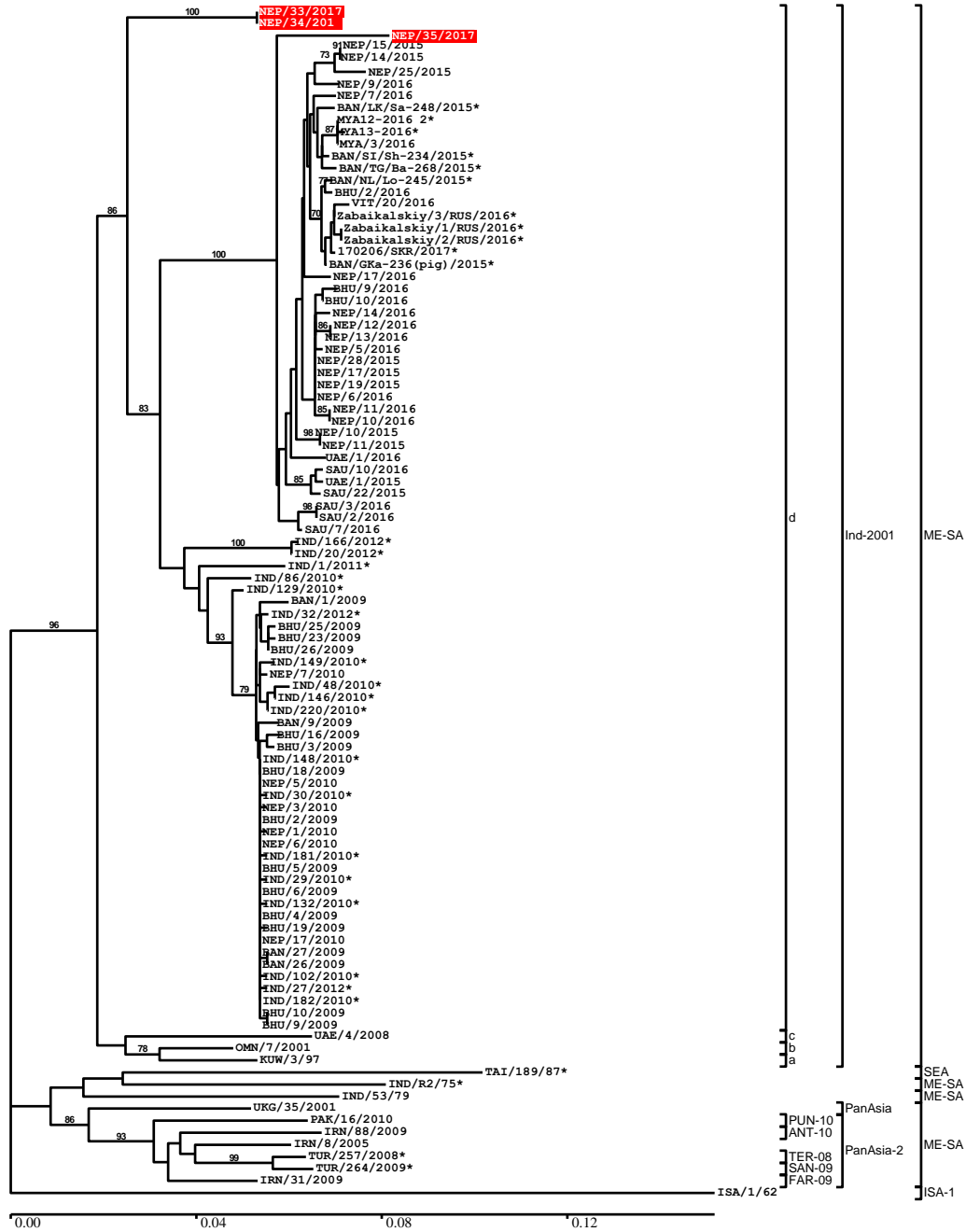
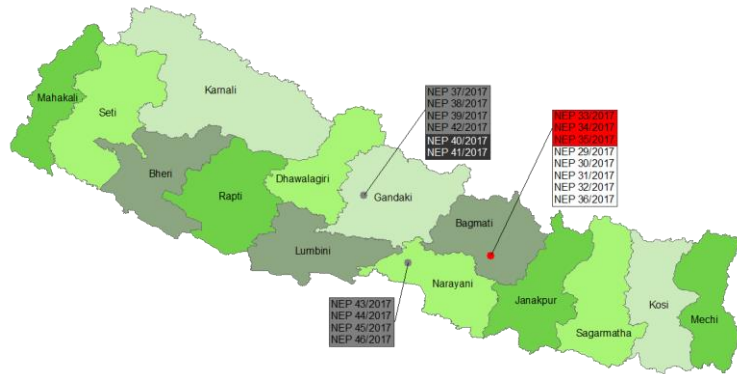
No. of samples: 18

O (ME-SA/Ind-2001): 3

Asia 1 (ASIA/unnamed): 8

FMDV-GD: 2

NVD: 5



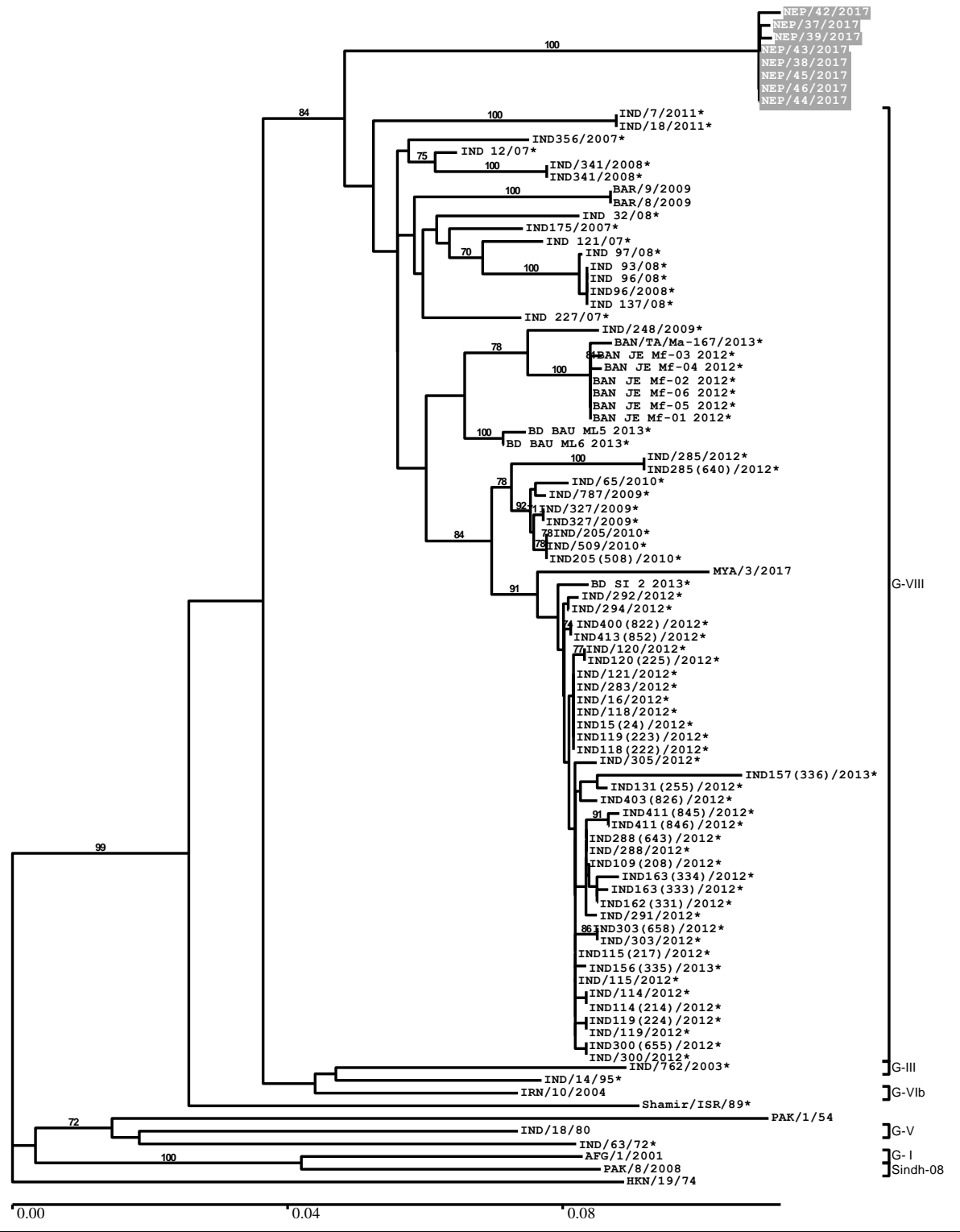
Nepal continued on next page

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# Nepal continued



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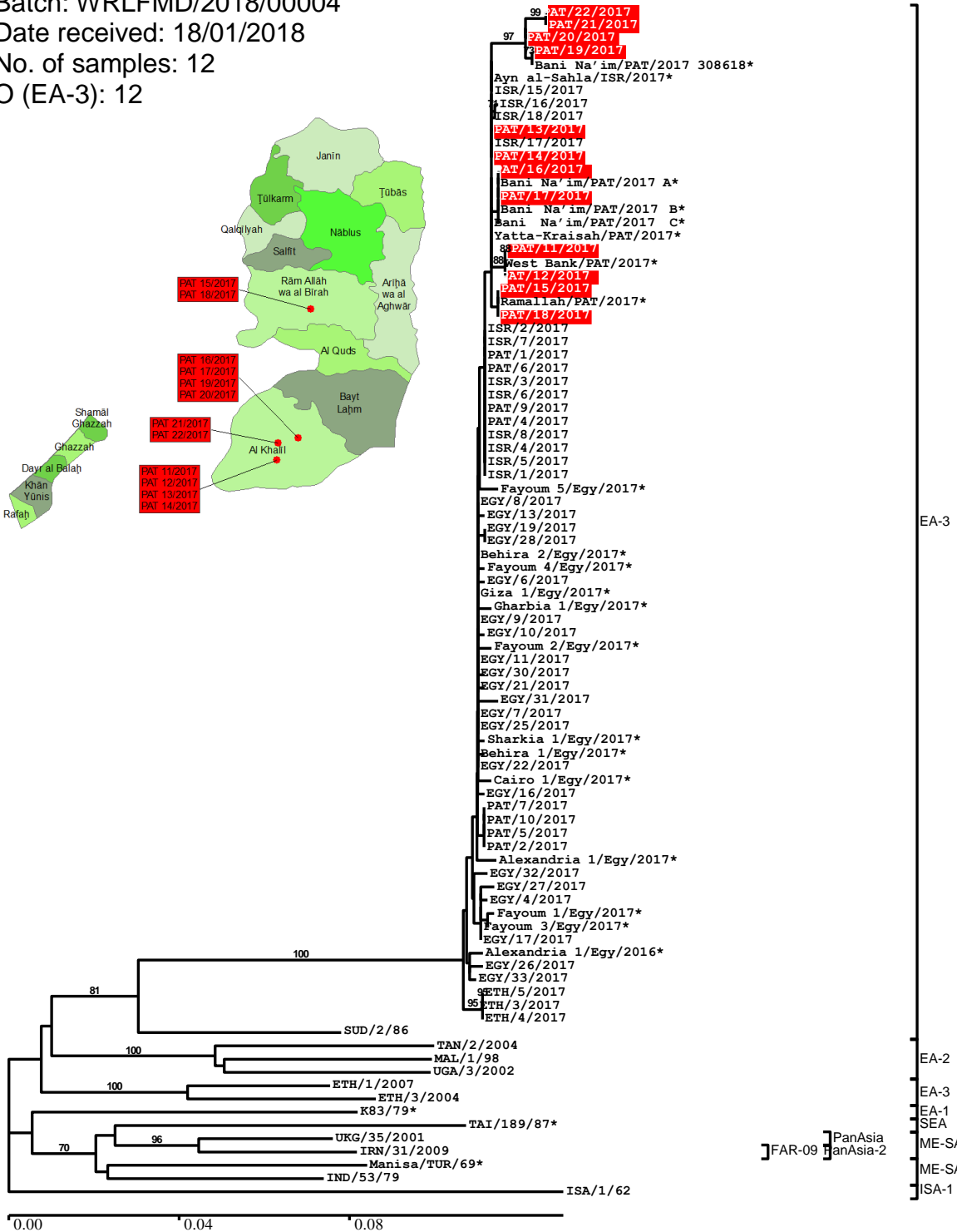
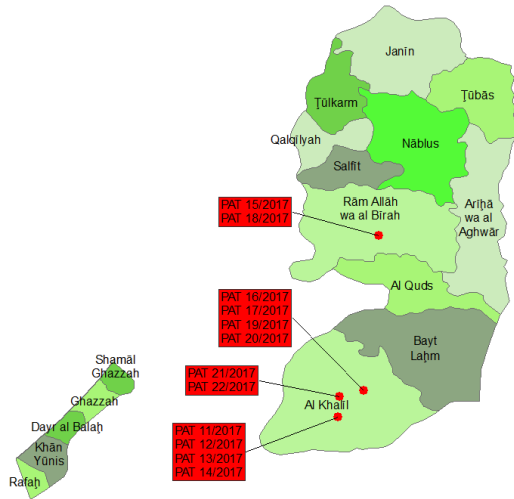
# Palestinian Autonomous Territories

Batch: WRLFMD/2018/00004

Date received: 18/01/2018

No. of samples: 12

O (EA-3): 12



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# Republic of Korea (South Korea)

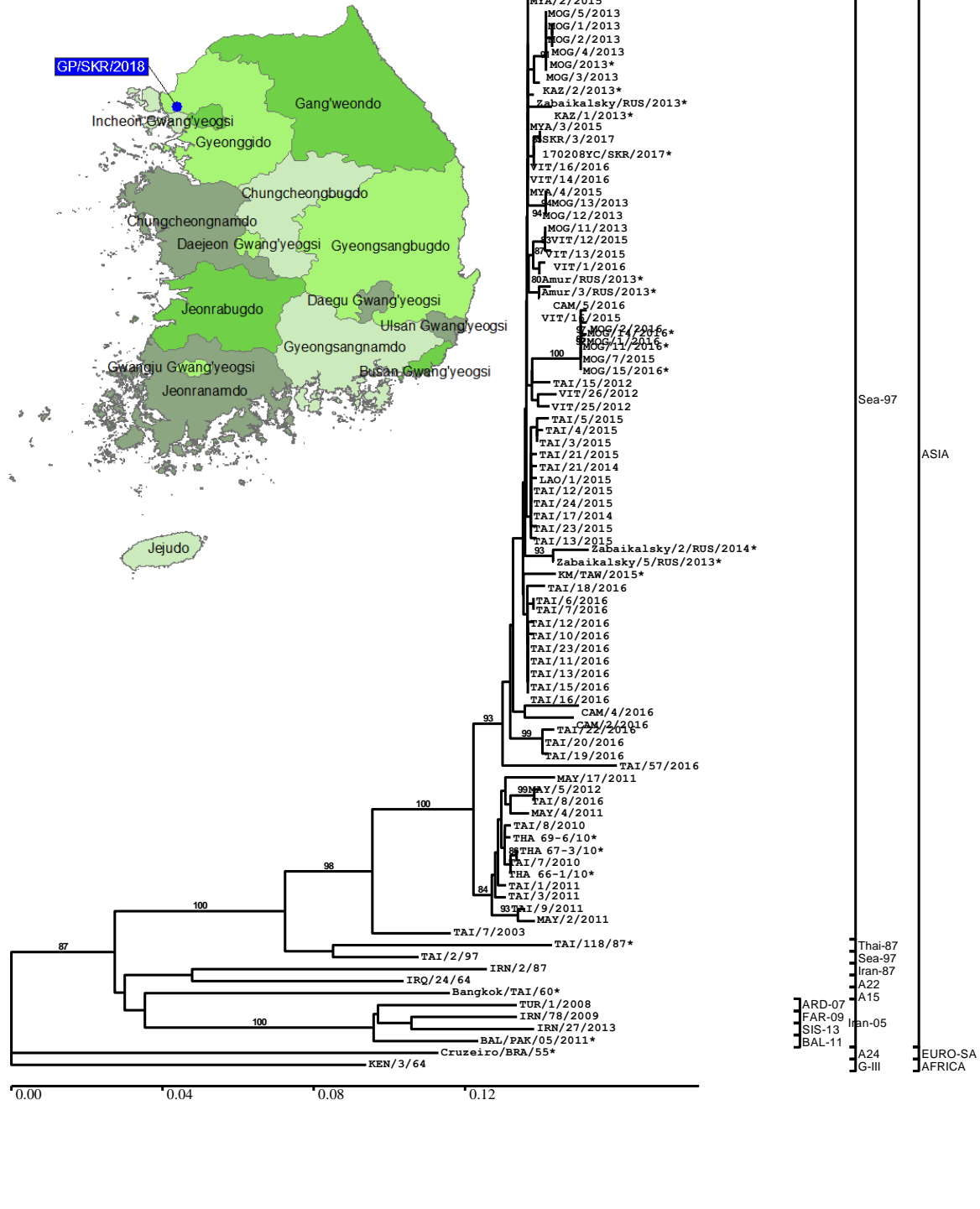
Batch: WRLMEG/2018/00008

Submitted by: APQA, ROK

Date received: 27/03/2018

No. of sequences: 1

A (ASIA/Sea-97): 1



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## 2.2. AFRICA

### Kenya

Batch: WRLFMD/2017/00031

Date received: 15/12/2017

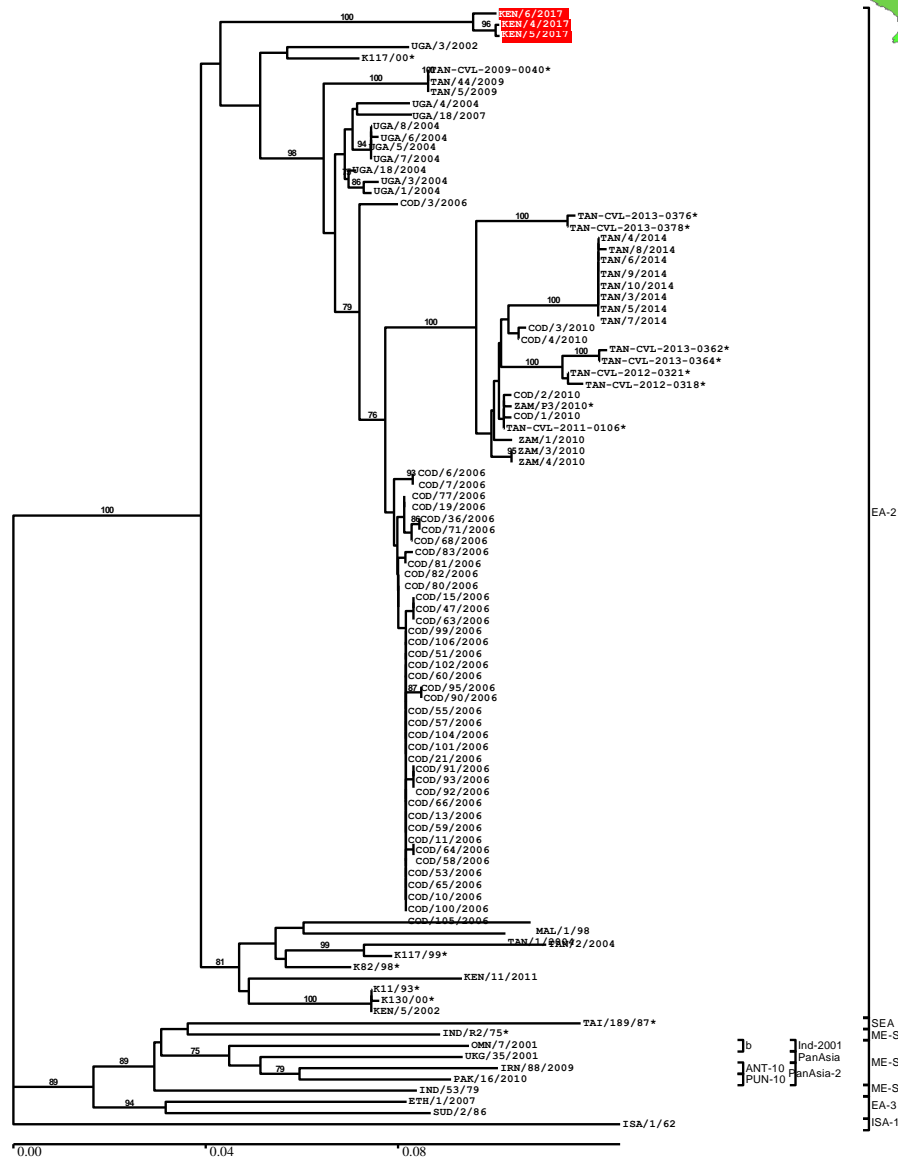
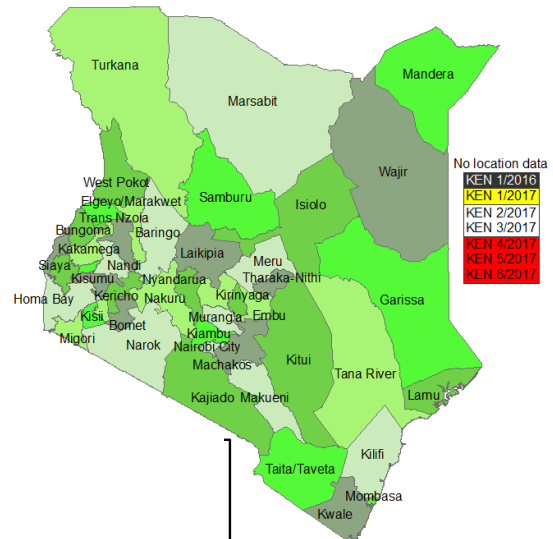
No. of samples: 7

O (EA-2): 3

SAT 1 (I): 1

FMDV-GD: 1

NVD: 2



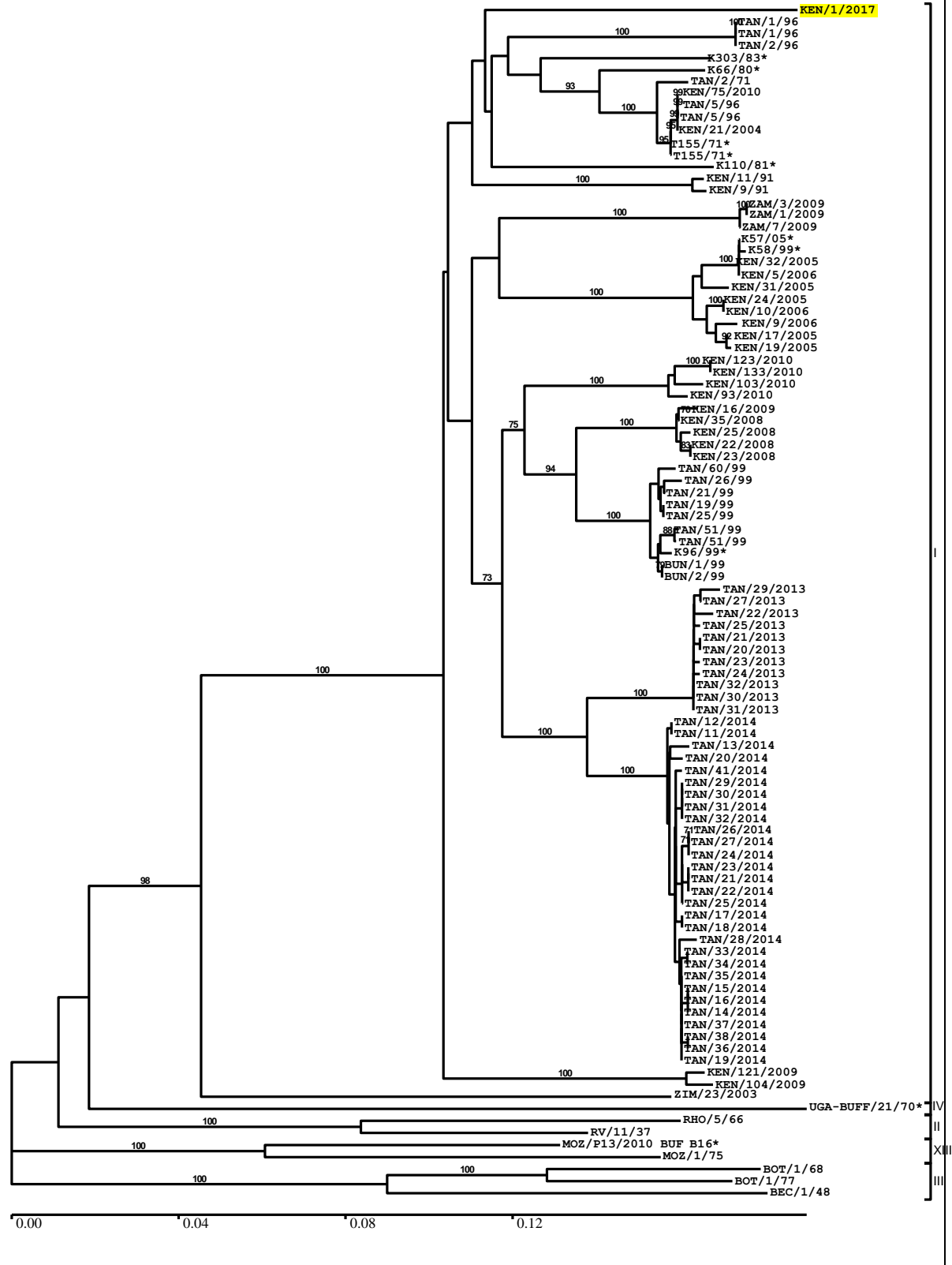
Kenya continued on next page

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### Kenya continued



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## Mozambique

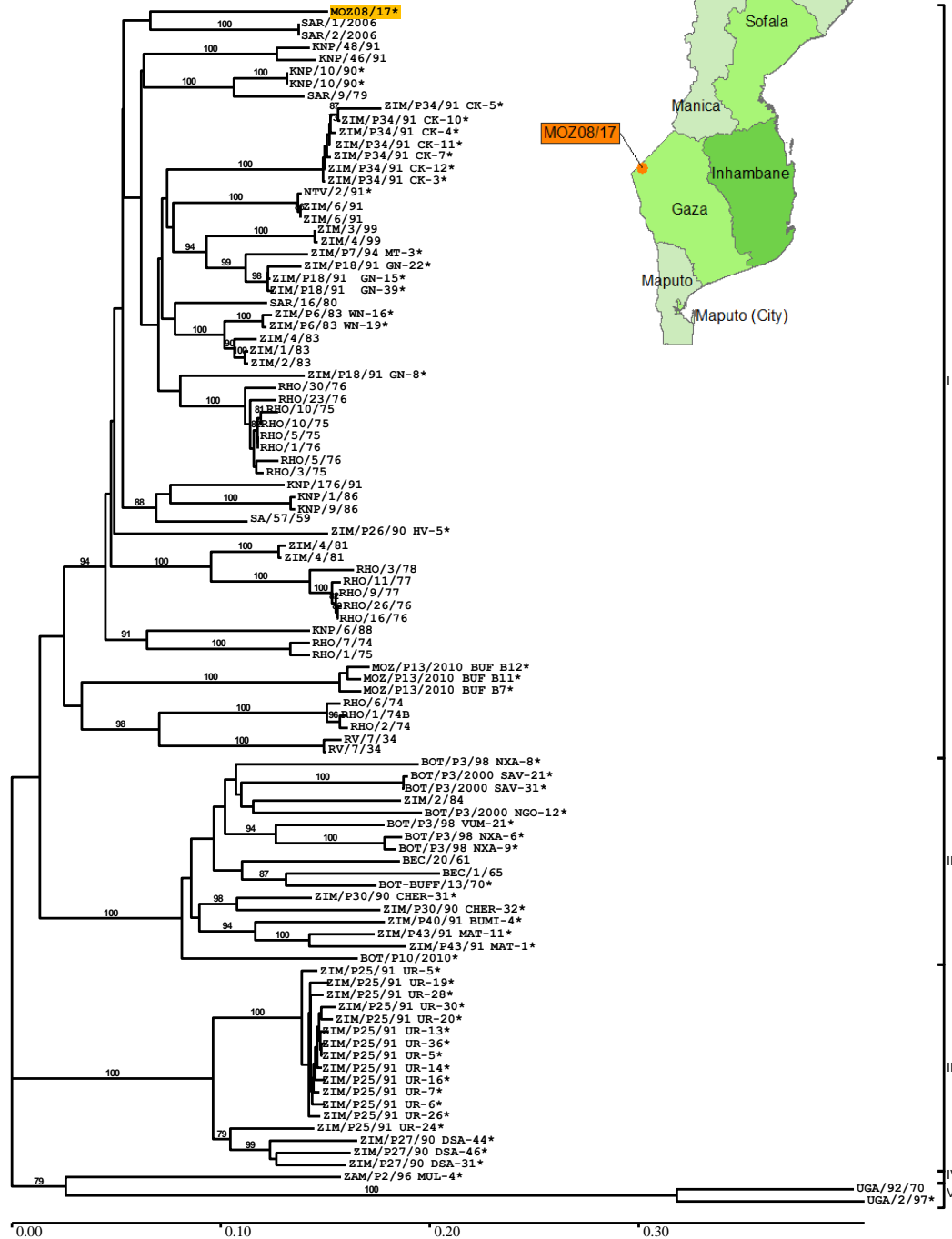
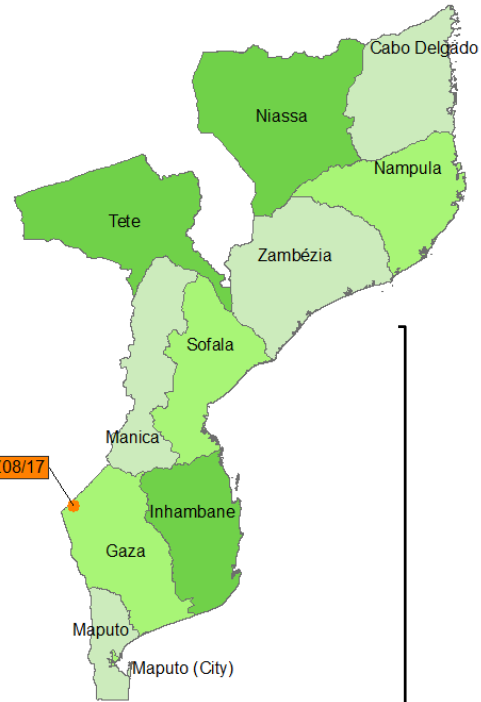
Batch: WRLMEG/2018/00005

Submitted by: SSARRL, BVI, Botswana

Date received: 18/01/2018

No. of sequences: 1

SAT3 (I): 1



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## Tunisia

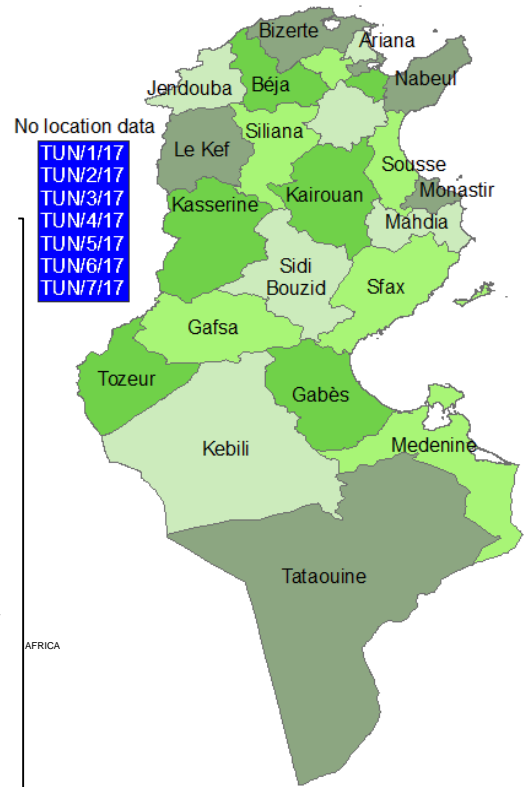
Batch: WRLMEG/2018/00006

Submitted by: ANSES

Date received: 23/02/2018

No. of sequences: 7

A (AFRICA/G-IV): 7



G-IV  
AFRICA  
G-V  
G-VI  
G-III  
G-I  
G-VII  
A24  
A12  
AS  
A22  
Sas-97  
EURO-SA  
ASIA

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### **3. Vaccine matching**

During this reporting period vaccine matching has been undertaken for 16 FMD virus field strains: serotypes O (n=11), A (n=3) and Asia-1 (n=2). These are samples from Israel, Kenya, Nepal, Palestinian Autonomous Territories, Pakistan and Sri Lanka.

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 (January to March 2018)

Country	Nº of samples	Virus isolation in cell culture/ELISA								No Virus Detected	RT-PCR for FMD (or SVD) virus (where appropriate)	
		FMD virus serotypes									Positive	Negative
		O	A	C	SAT 1	SAT 2	SAT 3	ASIA -1				
Hong Kong, SAR Of PRC	10	3	-	-	-	-	-	-	7	3	7	
Israel	10	4	6	-	-	-	-	-	-	1-	-	
Kenya	7	3	-	-	-	-	-	-	4	5	2	
Mongolia	3	3	1	-	-	-	-	-	-	3	-	
Nepal	18	3	-	-	-	-	-	8	7	13	5	
Palestinian Autonomous Territories	12	12	-	-	-	-	-	-	-	12	-	
Swaziland	3	-	-	-	-	-	-	-	3	-	3	
<b>TOTAL</b>	<b>63</b>	<b>28</b>	<b>7</b>	<b>-</b>	<b>-</b>	<b>-</b>	<b>-</b>	<b>8</b>	<b>21</b>	<b>36</b>	<b>17</b>	

\* One samples from Mongolia had a mixed serotype result of A and O.

#### 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® January-March

# 2018 January to March 2018

Country	WRL for FMD Sample Identification	Animal	Date of Collection	Results		
				VI/ELISA	RT-PCR	Final report
Hong Kong, SAR Of PRC	HKN 5/2017	PIG	09-Oct-17	NEG	POS	FMDV GD
	HKN 6/2017	PIG	09-Oct-17	NEG	NEG	NVD
	HKN 7/2017	PIG	09-Oct-17	NEG	NEG	NVD
	HKN 8/2017	PIG	30-Oct-17	O	NEG	O
	HKN 9/2017	PIG	30-Oct-17	NEG	NEG	NVD
	HKN 10/2017	PIG	30-Oct-17	NEG	NEG	NVD
	HKN 11/2017	PIG	09-Nov-17	O	POS	O
	HKN 12/2017	PIG	13-Nov-17	O	POS	O
	HKN 13/2017	PIG	04-Dec-17	NEG	NEG	NVD
	HKN 14/2017	PIG	04-Dec-17	NEG	NEG	NVD
Israel	ISR 9/2017	CATTLE	07-May-17	A	POS	A
	ISR 10/2017	CATTLE	07-May-17	A	POS	A
	ISR 11/2017	CATTLE	10-May-17	A	POS	A
	ISR 12/2017	CATTLE	10-May-17	A	POS	A
	ISR 13/2017	CATTLE	24-May-17	A	POS	A
	ISR 14/2017	CATTLE	26-May-17	A	POS	A
	ISR 15/2017	CATTLE	02-Jun-17	O	POS	O
	ISR 16/2017	CATTLE	02-Jun-17	O	POS	O
	ISR 17/2017	CATTLE	05-Jun-17	O	POS	O
ISR 18/2017	CATTLE	05-Jun-17	O	POS	O	
Kenya	KEN 1/2016	CATTLE	23-Nov-16	NEG	POS	FMDV GD
	KEN 1/2017	CATTLE	27-Jan-17	NEG	POS	FMDV GD
	KEN 2/2017	CATTLE	08-Feb-17	NEG	NEG	NVD
	KEN 3/2017	CATTLE	28-Mar-17	NEG	NEG	NVD
	KEN 4/2017	CATTLE	23-Aug-17	O	POS	O
	KEN 5/2017	CATTLE	04-Sep-17	O	POS	O
	KEN 6/2017	CATTLE	10-Nov-17	O	POS	O
Mongolia	MOG 7/2015	CATTLE	03-Mar-15	O & A	POS	O & A
	MOG 13/2017	CATTLE	28-Jan-17	O	POS	O
	MOG 14/2017	CATTLE	18-Nov-17	O	POS	O
Nepal	NEP 29/2017	CATTLE	16-Nov-17	NEG	NEG	NVD
	NEP 30/2017	CATTLE	16-Nov-17	NEG	NEG	NVD
	NEP 31/2017	CATTLE	16-Nov-17	NEG	NEG	NVD
	NEP 32/2017	CATTLE	16-Nov-17	NEG	NEG	NVD

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Country	WRL for FMD Sample Identification	Animal	Date of Collection	Results		
				VI/ELISA	RT-PCR	Final report
	NEP 33/2017	CATTLE	16-Nov-17	O	POS	O
	NEP 34/2017	CATTLE	16-Nov-17	O	POS	O
	NEP 35/2017	CATTLE	12-Dec-17	O	POS	O
	NEP 36/2017	CATTLE	12-Dec-17	NEG	NEG	NVD
	NEP 37/2017	CATTLE	19-Dec-17	ASIA-1	POS	ASIA-1
	NEP 38/2017	CATTLE	19-Dec-17	ASIA-1	POS	ASIA-1
	NEP 39/2017	CATTLE	19-Dec-17	ASIA-1	POS	ASIA-1
	NEP 40/2017	CATTLE	19-Dec-17	NEG	POS	FMDV GD
	NEP 41/2017	CATTLE	27-Dec-17	NEG	POS	FMDV GD
	NEP 42/2017	CATTLE	27-Dec-17	ASIA-1	POS	ASIA-1
	NEP 43/2017	CATTLE	27-Dec-17	ASIA-1	POS	ASIA-1
	NEP 44/2017	CATTLE	27-Dec-17	ASIA-1	POS	ASIA-1
	NEP 45/2017	CATTLE	27-Dec-17	ASIA-1	POS	ASIA-1
	NEP 46/2017	CATTLE	27-Dec-17	ASIA-1	POS	ASIA-1
Palestinian Autonomous Territories	PAT 11/2017	SHEEP	17-May-17	O	POS	O
	PAT 12/2017	SHEEP	25-May-17	O	POS	O
	PAT 13/2017	CATTLE	25-May-17	O	POS	O
	PAT 14/2017	CATTLE	27-May-17	O	POS	O
	PAT 15/2017	SHEEP	18-Jun-17	O	POS	O
	PAT 16/2017	SHEEP	18-Jun-17	O	POS	O
	PAT 17/2017	SHEEP	21-Jun-17	O	POS	O
	PAT 18/2017	SHEEP	22-Jun-17	O	POS	O
	PAT 19/2017	SHEEP	13-Dec-17	O	POS	O
	PAT 20/2017	SHEEP	16-Dec-17	O	POS	O
	PAT 21/2017	CATTLE	23-Dec-17	O	POS	O
	PAT 22/2017	CATTLE	29-Dec-17	O	POS	O
Swaziland	SWA 1/2018	BUFFALO	27-Feb-18	NEG	NEG	NVD
	SWA 2/2018	BUFFALO	27-Feb-18	NEG	NEG	NVD
	SWA 2/2018	BUFFALO	27-Feb-18	NEG	NEG	NVD
<b>TOTAL</b>		<b>63</b>				

### 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

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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 January to March 2018.

**Table 4: Vaccine matching studies for O FMDV by VNT**

Strain	Serotype	Topotype	Strain	O 3039	O1 Manisa	O/TUR/5/2009
ISR/15/2017	O	EA-3		0.52	0.47	0.58
ISR/18/2017	O	EA-3		0.62	0.42	0.50
KEN/4/2017	O	EA-2		0.25	0.41	0.56
KEN/6/2017	O	EA-2		0.32	0.41	0.50
NEP/33/2017	O	ME-SA	Ind-2001d	0.35	0.23	0.76
NEP/35/2017	O	ME-SA	Ind-2001d	0.35	0.26	0.56
PAK/10/2016	O	ME-SA	PanAsia-2 <sup>ANT-10</sup>	0.00	0.00	0.00
PAT/11/2017	O	EA-3		0.60	0.62	0.93
PAT/22/2017	O	EA-3		0.40	0.37	0.63
SRL/3/2017	O	ME-SA	Ind-2001d	0.49	0.71	0.66
SRL/7/2016	O	ME-SA	Ind-2001d	0.46	0.51	0.87

**Table 5: Vaccine matching studies for A FMDV by VNT**

Strain	Serotype	Topotype	Strain	A/IRN/05	A/TUR/20/06	A22 IRAQ
ISR/13/2017	A	ASIA	G-VII	0	0	0.24
ISR/9/2017	A	ASIA	G-VII	0	0	0.11
PAK/25/2016	A	ASIA	Iran-05 <sup>FAR-11</sup>	0.26	0.17	0.33

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

Strain	Serotype	Topotype	Strain	Asia 1 Shamir
NEP/42/2017	Asia-1	G-VIII		0.83
NEP/45/2017	Asia-1	G-VIII		0.51

**Abbreviations used in tables**

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

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## 5. Annex 2

Recent FMD Publications (January to March 2018) cited by Web of Science (Pirbright Institute papers and authors are highlighted in **BOLD AND GREY**)

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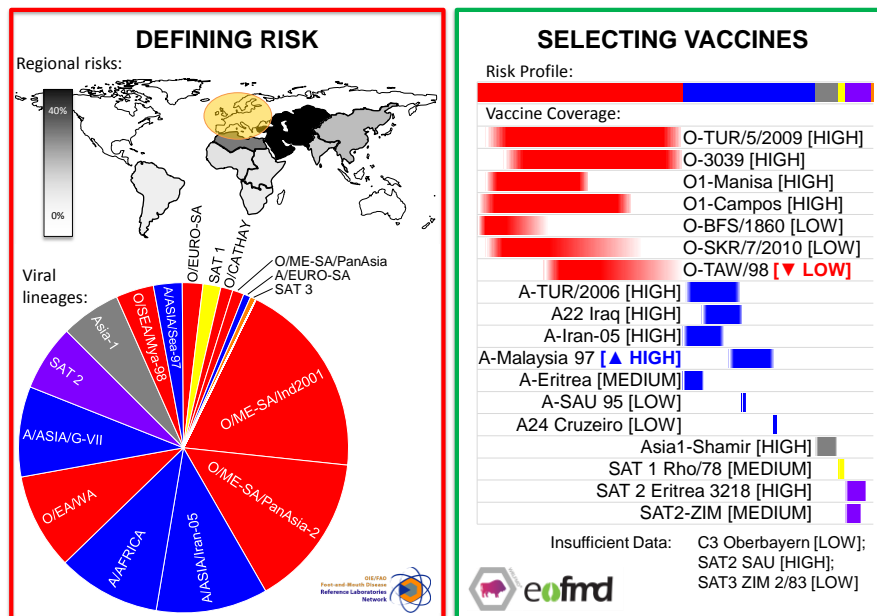
## 6. Annex 3

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

Lineage	West Eurasia	East Asia	North Africa	India and Southern Asia	East Africa	West and Central Africa	Southern Africa	South America
O/ME-SA/PanAsia-2	35	-	-	-	-	-	-	-
O/ME-SA/PanAsia	-	10	-	-	-	-	-	-
O/SEA/Mya-98	-	33	-	-	-	-	-	-
O/ME-SA/Ind2001	6	20	35	80	-	-	-	-
O/EA or O/WA	3	-	20	-	45	37	-	-
O/EURO-SA	-	-	-	-	-	-	-	74
O/CATHAY	-	10.5	-	-	-	-	-	-
A/ASIA/Sea-97	-	25	-	-	-	-	-	-
A/ASIA/Iran-05	25.5	-	-	-	-	-	-	-
A/ASIA/G-VII	17.5	-	-	16	-	-	-	-
A/AFRICA	-	-	35	-	24	25	-	-
A/EURO-SA	-	-	-	-	-	-	-	26
Asia-1	12.5	1.5	-	4	-	-	-	-
SAT 1	-	-	-	-	10	10	27	-
SAT 2	0.5	-	10	-	20	28	57	-
SAT 3	-	-	-	-	1	-	16	-
C	-	-	-	-	-	-	-	-

### Vaccine Antigen Prioritisation: Europe

March 2018



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

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

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