

WRLFMD Quarterly Report July to September 2019

Foot-and-Mouth Disease











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1. Summary of samples tested and reported FMD outbreaks

1.1. Global Overview of samples received and tested

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

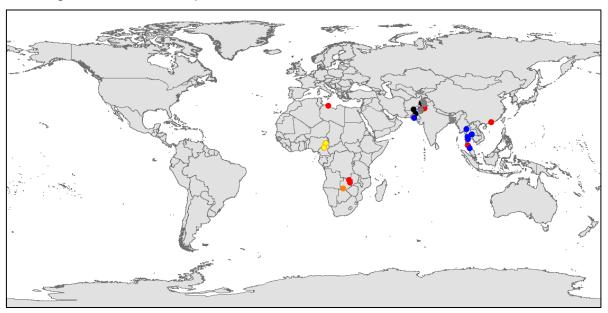


Figure 1: Samples tested by WRLFMD in this quarter (coloured spots define serotypes detected (O, A, C, Asia 1, SAT 1, SAT 2, SAT 3, untyped, negative)

1.2. Asia

Bangladesh

A new **FMDV Asia 1** lineage (named G-IX) has been described in cattle in Dhaka (24th January 2018) by workers at the University of Dhaka (DOI: 10.1101/604892). Two VP1 sequences were retrieved from GenBank (accession numbers MH457186 & MH457187). This lineage had previously been found in Nepal in 2017 (six virus isolates) by the WRLFMD (see below).



China, People's Republic of

A further outbreak of **FMD type O** was reported in cattle in the Xinjiang Autonomous Region on 13th July 2019. No genotyping has been reported.

Hong Kong SAR

Seven samples, collected from slaughterhouse pigs between March and May 2019 were received on 14th August 2019. **FMD type O** was identified in six samples and the VP1 sequence of five of these showed them to belong to the CATHAY topotype (see below).

Israel

A further outbreak of **FMD type O** was reported in cattle in Haifa on 13th July 2019. Strain identification was reported to the OIE as PanAsia-2.

Pakistan

A batch of 36 samples were received on 26th July 2019. **FMDV type O** was identified in 10 samples, **FMDV type A** in two samples and **FMDV type Asia 1** in 19 samples; FMDV genome was detected in four samples and one was NVD. Sequence analyses of the VP1 sequences revealed that eight of the type O viruses belonged to the ME-SA/PanAsia-2/ANT-10 sublineage while the other two (from cattle in Punjab province in January 2019) belonged to the ME-SA/Ind-2001e sublineage. **This is the first report of O-Ind-2001 in Pakistan.** A report to the OIE suggested that the same virus was present in cattle in Khyber Pakhtoon Khuwa province in April 2019. The type A viruses belonged to the ASIA/Iran-05/SIS-13 sublineage and the Asia 1 viruses belonged to ASIA/Sindh-08 lineage.

Thailand

A batch of 20 samples was received on the 11th September 2019. **FMDV type O** was identified in four samples and **FMDV type A** in the remaining 16. VP1 sequencing revealed that three of the type O viruses belonged to the ME-SA/Ind-2001e sublineage, while one belonged to the SEA/Mya-98 lineage. The 16 type A viruses all belonged to the ASIA/Sea-97 lineage.



1.3. Africa

Cameroon

FMDV type **SAT 1** was reported to have occurred for the first time in August/September 2016. VP1 sequences were determined at the PIADC for 15 samples collected at two locations in the North and Adamawa regions. VP1 sequences were retrieved from GenBank (accession numbers MK469979-MK469993). Phylogenetic analyses showed the viruses to belong to topotype X and to be closely relation to viruses from Nigeria sampled in 2015 and 2016 (see below). Subsequently, the complete genome sequences of four of the isolates were also deposited on GenBank (accession numbers MN275118-MN275121).

Libya

A single **FMDV type O** VP1 sequence was received from IZSLER on 12th August 2019. The sample had been collected from cattle in Misrata in May 2019. Phylogenetic analyse showed the virus to belong to the EA-3 topotype and to be closely related to viruses from Algeria, Morocco and Tunisia (see below).

Malawi

A further outbreak of **FMD type SAT 2** was reported to have occurred in cattle at Nkusabiyasi, Mchinji, Central (close to the border with Zambia) on 10th April 2019.

Morocco

In May 2019, five outbreaks due to **FMD type O** were reported in sheep and goats in the Fès-Meknès region. On 19th July 2019, a single outbreak was reported in cattle in the Souss-Massa region.

Namibia

Two outbreaks of **FMD type SAT 3** were reported in cattle at Katima-Mulilo, Kabwe North, Zambezi region. VP1 sequence data was received from the SSARRL (BVI) on 25th August 2019. Genotyping revealed that the viruses belonged to topotype II (see below).



South Africa

A single outbreak of **FMD type SAT 2** was reported to have occurred in cattle at Musina, Limpopo on 2nd September 2019. The outbreak occurred in South Africa's FMD Protection Zone. This virus is not related to the January 2019 FMD outbreak virus. The serotype was incorrectly reported as SAT 1 in the immediate notification, but later corrected and republished by the OIE on 19th September 2019.

Zambia

Between June and August 2019, 15 outbreaks due to **FMD type O** were reported in cattle in the Central, Copperbelt, Lusaka and Southern provinces. Three outbreaks in cattle in March and May 2019 in the Eastern province were reported to the OIE as type O but were actually **FMD type SAT 2** (F. Banda, personal communication, 2019). Genotyping was reported in the last Quarterly Report as topotype I. Two FMDV type O VP1 sequences were received from the SSARRL (BVI). They were from the Copperbelt and Central provinces (although no precise dates were given) and genotyping showed them to belong to the EA-2 topotype (see below).

Zimbabwe

A further outbreak due to **FMD type SAT1** was reported in cattle in Nkayi, Matabeleland North on 17th June 2019. No genotyping is available.

1.4. South America

No new outbreaks of FMD were reported in the continent.

1.5. Uncharacterised FMD viruses

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

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

Results from samples or sequences received at WRLFMD (status of samples being tested) are shown in Table 1 and a complete list of clinical sample diagnostics made by the WRLFMD from July to September 2019 is shown in Annex 1 (Summary of



Submissions). A record of all samples received by WRLFMD is shown in Annex 1 (Clinical Samples).

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

WRLFMD Batch No.	Date received	Country	Serotype	No. of samples	No. of sequences	Sequencing status
			0	10	10	completed
WRLFMD/2019/00028	26/07/2019	Pakistan	Α	2	2	completed
			Asia 1	19	19	completed
WRLFMD/2019/00029	14/08/2019	Hong Kong, S.A.R. of the P.R.C.	0	6	5	completed
WRLFMD/2019/00030	11/09/2019	Thailand	0	4	4	completed
VVKLFIVID/2019/00030	11/03/2019	mailanu	Α	16	16	completed
			Total	57	56	

Table 2: VP1 sequences submitted by other FMD Network laboratories to the WRLFMD from July to September 2019.

WRLFMD Batch No.	Date received	Country	Serotype	Date Collected	No. of sequences	Submitting laboratory
WRLMEG/2019/00038	09/08/2019	Zambia	0	2019	2	BVI
WRLMEG/2019/00039	12/08/2019	Libya	0	05/2019	1	IZSLER
WRLMEG/2019/00041	21/08/2019	Bangladesh	Asia 1	24/01/2018	2	UNIV- DHAKA
WRLMEG/2019/00042	25/08/2019	Namibia	SAT3	08/08/2019	2	BVI
WRLMEG/2019/00043	02/09/2019	Cameroon	SAT1	2016	15	PIADC
			Total		22	



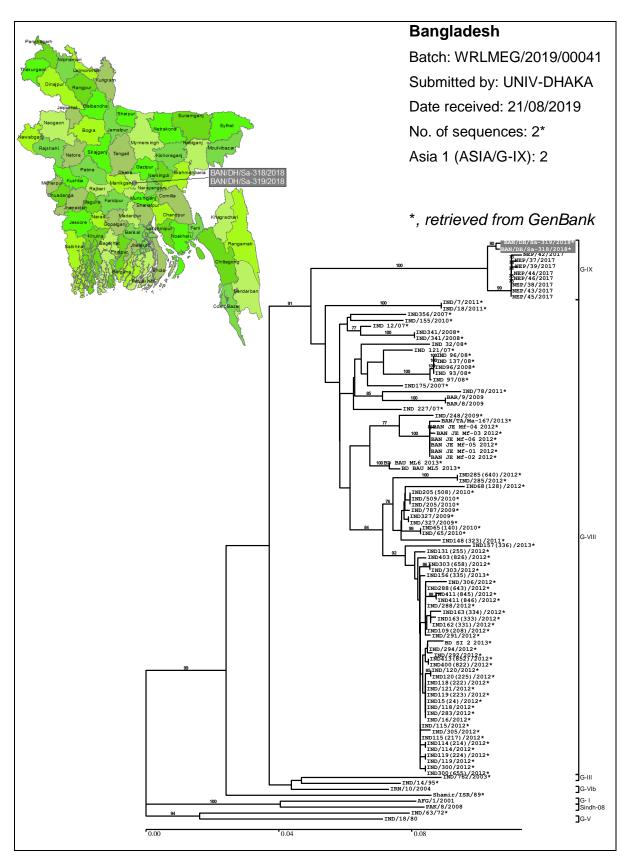
2. Detailed Analysis

Key for maps and trees:

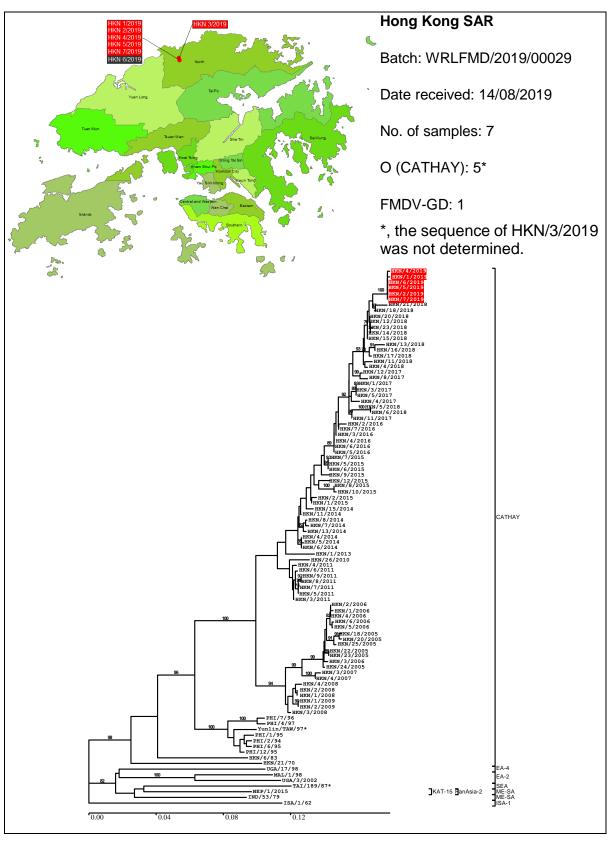
Serotype O	Serotype Asia-1	Serotype SAT 3
Serotype A	Serotype SAT 1	FMDV Genome Detected
Serotype C	Serotype SAT 2	No Virus Detected



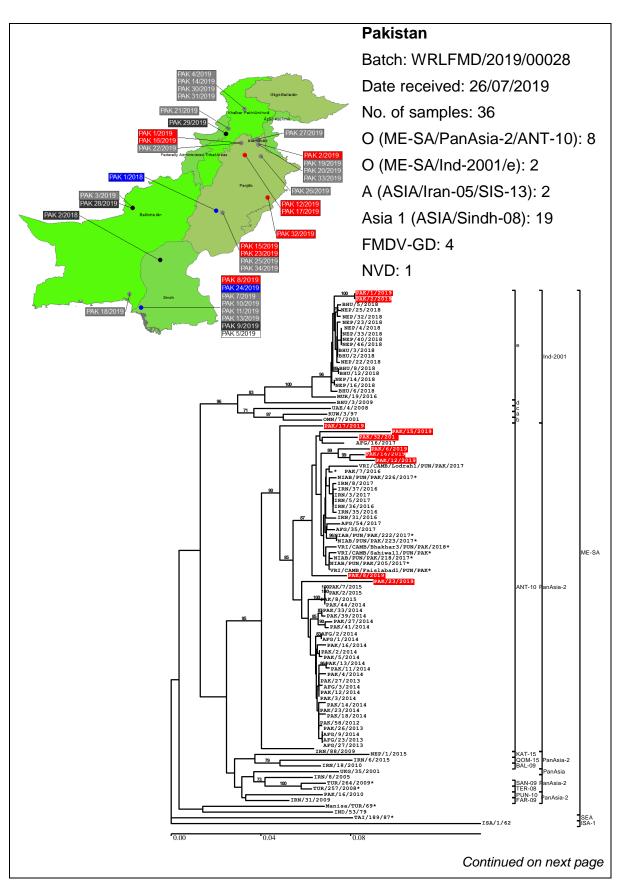
2.2. Asia



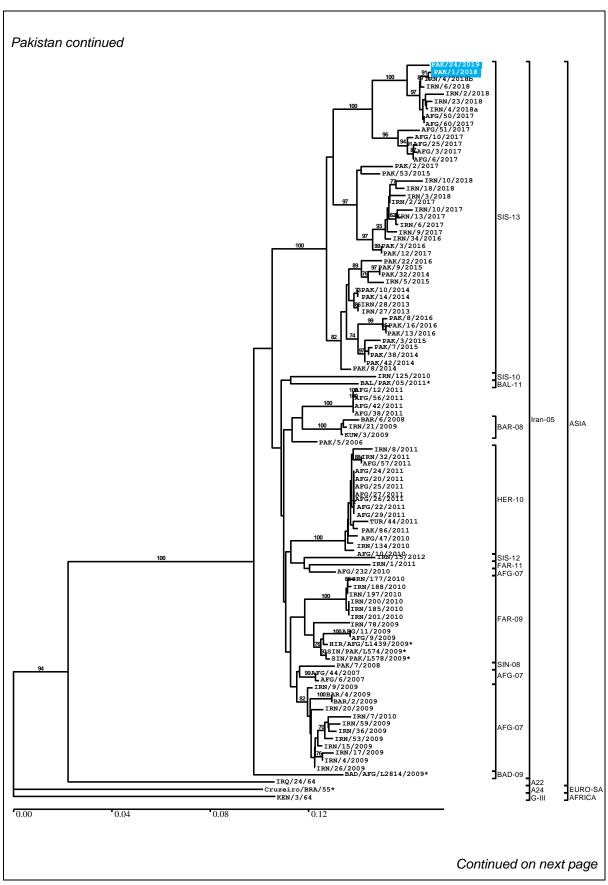




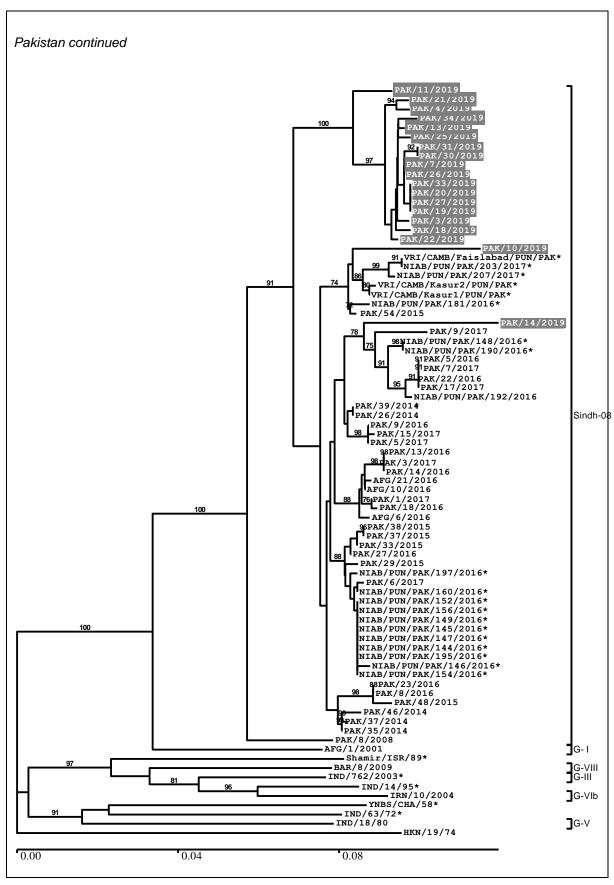




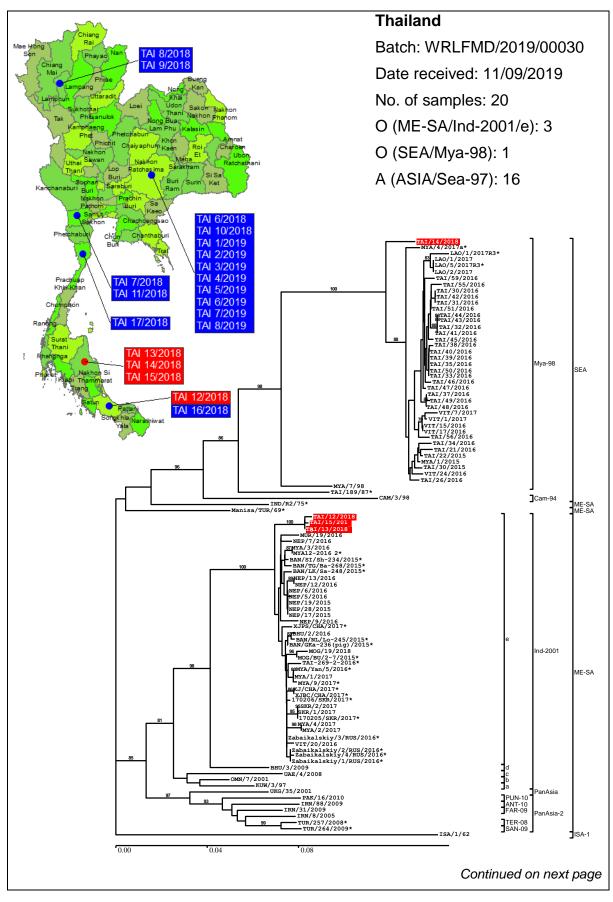




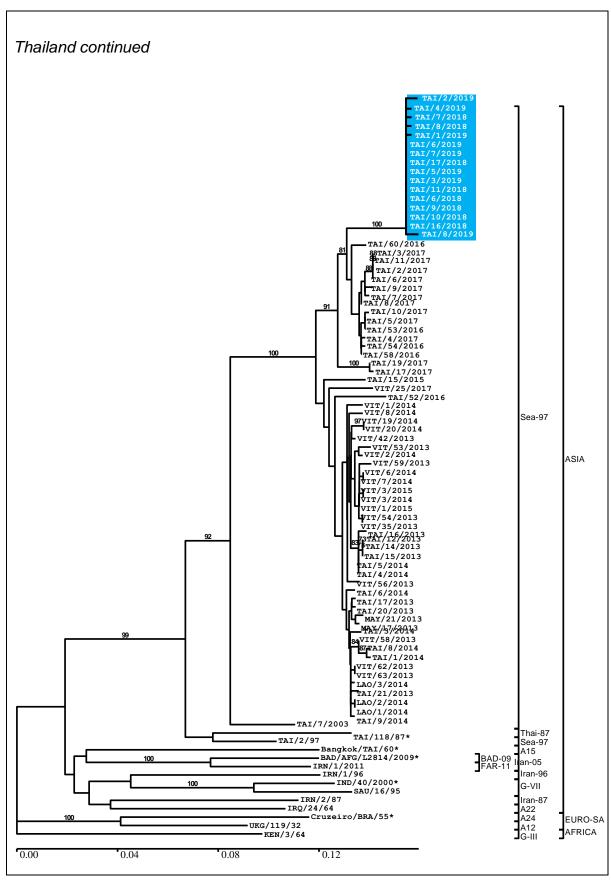






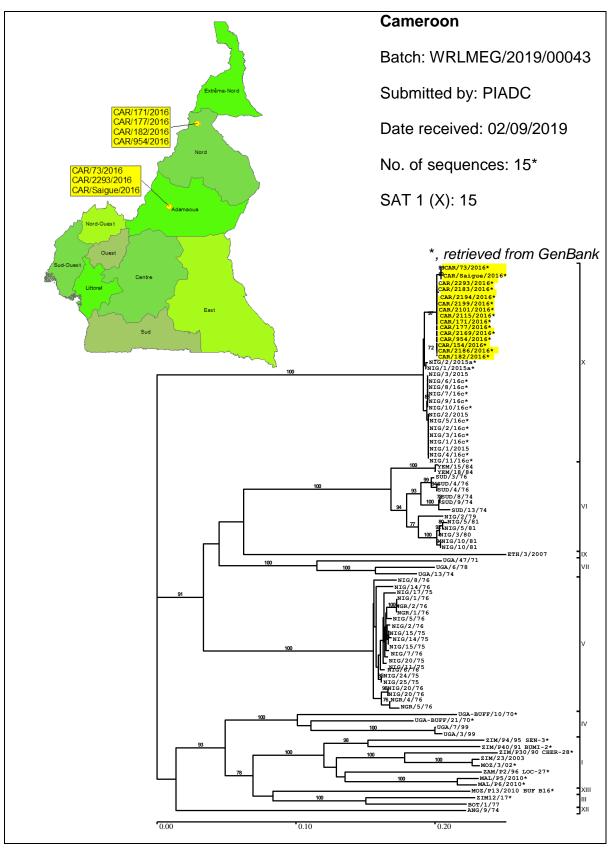




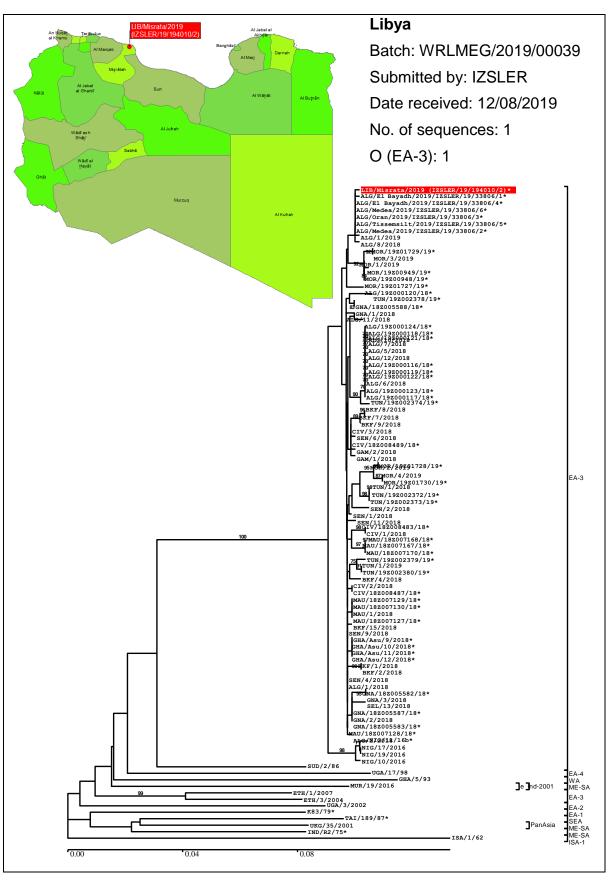




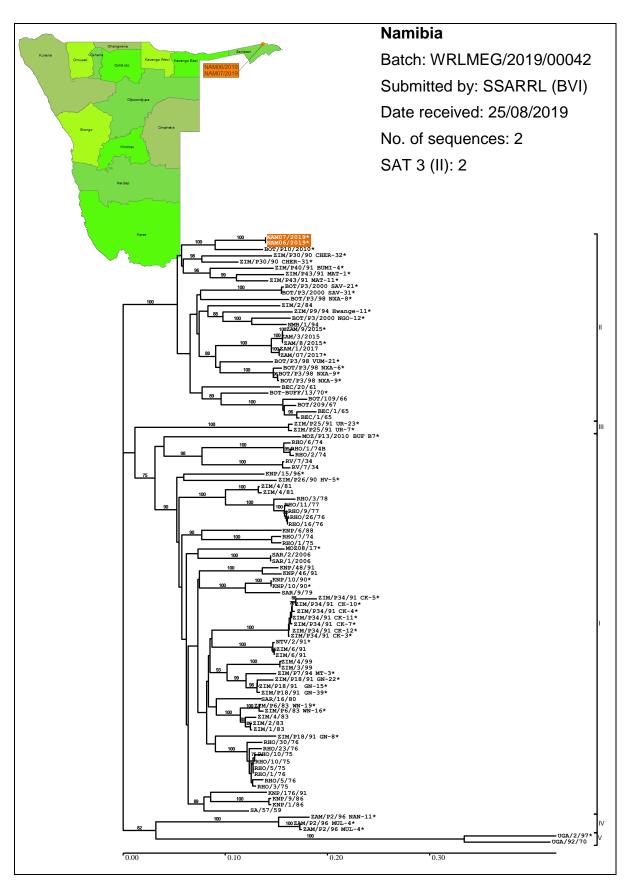
2.3. Africa



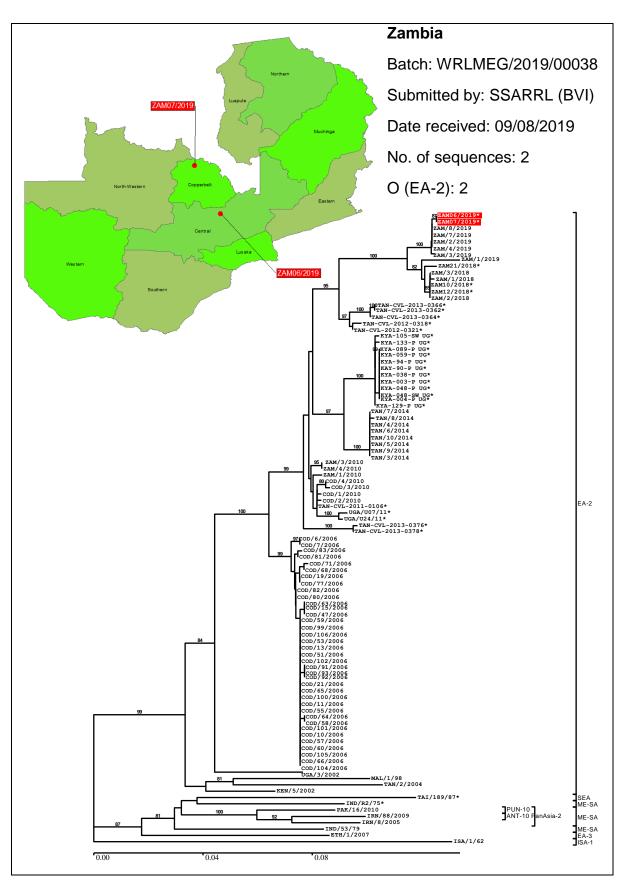














2.4. Vaccine matching

During this reporting period vaccine matching has been undertaken for 32 FMD virus field isolates.

Table 3: Summary of samples tested by vaccine matching.

Serotype	0	Α	С	Asia-1	SAT 1	SAT 2	SAT 3
Ethiopia	2	2					
Guinea	1						
Israel	2						
Mauritania	1						
Morocco	1						
Myanmar	1						
Nepal	2						
Pakistan	3	2		3			
Palestine, State of	2						
Tunisia	1						
Turkey	2	2					
Uganda	3	2					
Total	21	8	0	3	0	0	0

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



Annex 1: Sample data

2.5. Summary of Submissions

Table 4: Summary of samples collected and received to WRLFMD (July to September 2019)

		٧	irus is	olati	on in	cell c	ulture	/ELIS	Α		
Country	Nº of		FN	ID vi	rus se	rotyp	es		Virus ected		for FMD
	samples	0	A	С	SAT 1	SAT 2	SAT 3	ASIA -1	Z g	Positive	Negative
Hong Kong	7	6	-	-	-	-	-	-	-	-	7
Pakistan	36	10	2	-	-	-	-	19	5	35	1
Thailand	20	4	16	-	-	-	-	-	-	20	-
 TOTAL	63	20	18	-	-	-	-	19	5	55	8

Abbreviations used in table

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

2.6. Clinical Samples

Table 5: Clinical sample diagnostics made by the WRLFMD® July to September 2019

	Da	ite					Resu	lts
Country	Received	Reported	WRL for FMD Sample Identification	Animal	Date of Collection	VI/ELISA	RT-PCR	Final report
_		_	HKN 1/2019	PIG	28-Mar-19	0	NEG	0
Hana	61	19	HKN 2/2019	Pig	28-Mar-19	0	NEG	0
Hong Kong CAD	<u>,</u>	UB	HKN 3/2019	Pig	29-Apr-19	0	NEG	0
Kong, SAR of PRC	14-Aug-19	⋖	HKN 4/2019	Pig	29-Apr-19	0	NEG	0
OI PRC	14	28	HKN 5/2019	Pig	06-May-19	0	NEG	0
			HKN 6/2019	Pig	06-May-19	FMD	NEG	FMD



	Da	ate					Resu	ılts
Country	Received	Reported	WRL for FMD Sample Identification	Animal	Date of Collection	VI/ELISA	RT-PCR	Final report
			HKN 7/2019	Pig	06-May-19	0	NEG	0
			PAK 1/2018	Cattle	31-Jan-18	Α	POS	Α
			PAK 2/2018	Buffalo	21-Dec-18	NEG	POS	FMDV GD
			PAK 1/2019	Cattle	02-Jan-19	0	POS	Ο
			PAK 2/2019	Cattle	16-Jan-19	0	POS	0
			PAK 3/2019	Cattle	16-Jan-19	Asia-1	POS	Asia-1
			PAK 4/2019	Cattle	24-Jan-19	Asia-1	POS	Asia-1
			PAK 5/2019	Cattle	26-Jan-19	NEG	NEG	NVD
			PAK 6/2019	Buffalo	31-Jan-19	0	POS	0
			PAK 7/2019	Cattle	31-Jan-19	Asia-1	POS	Asia-1
			PAK 8/2019	Cattle	01-Feb-19	0	POS	0
			PAK 9/2019	Buffal0	03-Feb-19	NEG	POS	FMDV GD
			PAK 10/2019	Cattle	03-Feb-19	Asia-1	POS	Asia-1
			PAK 11/2019	Cattle	04-Feb-19	Asia-1	POS	Asia-1
			PAK 12/2019	Cattle	06-Feb-19	0	POS	0
			PAK 13/2019	Cattle	06-Feb-19	Asia-1	POS	Asia-1
			PAK 14/2019	Cattle	07-Feb-19	Asia-1	POS	Asia-1
	6	19	PAK 15/2019	Cattle	08-Feb-19	0	POS	0
Pakistan	26-Jul-19	07-Aug-19	PAK 16/2019	Cattle	14-Feb-19	0	POS	0
Fakisian)- -	-Ĭ	PAK 17/2019	Cattle	14-Feb-19	0	POS	0
	7	0	PAK 18/2019	Cattle	14-Feb-19	Asia-1	POS	Asia-1
			PAK 19/2019	Buffalo	19-Feb-19	Asia-1	POS	Asia-1
			PAK 20/2019	Buffalo	19-Feb-19	Asia-1	POS	Asia-1
			PAK 21/2019	Buffalo	19-Feb-19	Asia-1	POS	Asia-1
			PAK 22/2019	Cattle	26-Feb-19	Asia-1	POS	Asia-1
			PAK 23/2019	Cattle	27-Feb-19	0	POS	0
			PAK 24/2019	Cattle	27-Feb-19	Α	POS	Α
			PAK 25/2019	Cattle	07-Mar-19	Asia-1	POS	Asia-1
			PAK 26/2019	Cattle	13-Mar-19	Asia-1	POS	Asia-1
			PAK 27/2019	Cattle	14-Mar-19	Asia-1	POS	Asia-1
			PAK 28/2019	Cattle	14-Mar-19	NEG	POS	FMDV GD
			PAK 29/2019	Buffalo	19-Mar-19	NEG	POS	FMDV GD
			PAK 30/2019	Cattle	19-Mar-19	Asia-1	POS	ASIA-1
			PAK 31/2019	Cattle	19-Mar-19	Asia-1	POS	ASIA-1
			PAK 32/2019	Cattle	22-Mar-19	0	POS	0
			PAK 33/2019	Cattle	26-Mar-19	Asia-1	POS	ASIA-1
			PAK 34/2019	Cattle	16-Apr-19	Asia-1	POS	ASIA-1
	0	0	TAI 6/2018	Cattle	01-Nov-18	Α	POS	Α
	11-Sep-19	8-Sep-19	TAI 7/2018	Cattle	01-Nov-18	Α	POS	Α
Thailand	Sep	Sep	TAI 8/2018	Cattle	02-Nov-18	Α	POS	Α
	7-	18-	TAI 9/2018	Cattle	06-Nov-18	Α	POS	Α
			TAI 10/2018	Cattle	07-Nov-18	Α	POS	Α



	Da	ite					Resul	ts
Country	Received	Reported	WRL for FMD Sample Identification	Animal	Date of Collection	VI/ELISA	RT-PCR	Final report
			TAI 11/2018	Cattle	12-Nov-18	Α	POS	Α
			TAI 12/2018	Cattle	20-Nov-18	0	POS	0
			TAI 13/2018	Cattle	29-Nov-18	0	POS	0
			TAI 14/2018	Cattle	03-Dec-18	0	POS	0
			TAI 15/2018	Cattle	07-Dec-18	0	POS	0
			TAI 16/2018	Cattle	25-Dec-18	Α	POS	Α
			TAI 17/2018	Cattle	26-Dec-18	Α	POS	Α
			TAI 1/2019	Cattle	03-Jan-19	Α	POS	Α
			TAI 2/2019	Cattle	03-Jan-19	Α	POS	Α
			TAI 3/2019	Cattle	03-Jan-19	Α	POS	Α
			TAI 4/2019	Cattle	03-Jan-19	Α	POS	Α
			TAI 5/2019	Cattle	03-Jan-19	Α	POS	Α
			TAI 6/2019	Cattle	04-Jan-19	Α	POS	Α
			TAI 7/2019	Cattle	04-Jan-19	Α	POS	Α
			TAI 8/2019	Cattle	04-Jan-19	Α	POS	Α
			TOTAL	63				

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



2.7. Antigenic Characterisation

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

Abbreviations used in tables

NT	Not tested against this vaccine
В	Borderline Any r ₁ values between 0.28 to 0.32
N	No Vaccine Match $r_1 = < 0.3$. Suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect
М	Vaccine Match $r_1 = \ge 0.3$. 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.

Table 6: Vaccine matching studies for A FMDV by VNT

Strain	Serotype	Topotype	Lineage	A/IRN/05	A/ERI/3/98	A/TUR/20/06	A22 IRAQ	A/ASIA/GVII
UGA/28/2019	Α	AFRICA	G-I	0.05	0.15	0.15	0.14	0.00
UGA/42/2019	Α	AFRICA	G-I	0.06	0.28	0.17	0.17	0.00
ETH/85/2018	Α	AFRICA	G-IV	0.05		0	0	
ETH/19/2019	Α	AFRICA	G-IV	0.05		0	0	
TUR/01/2017	Α	ASIA	G-VII	0		0	0.15	0.85
TUR/13/2017	Α	ASIA	G-VII	0		0	0.17	0.78
PAK/01/2018	Α	ASIA	Iran-05	0.36		0.25	0.32	0
PAK/24/2019	Α	ASIA	Iran-05	0.49		0.59	0.48	0



Table 7: Vaccine matching studies for O FMDV by VNT

Strain	Serotype	Topotype	Lineage	O 3039	O1 Manisa	O/TUR/5/2009
UGA/06/2019	0	EA-2	-	0.55	0.31	0.68
UGA/10/2019	0	EA-2	-	0.10	0.09	0.28
UGA/21/2019	0	EA-2	-	0.59	0.32	0.66
ETH/09/2019	0	EA-3	-	0.76	0.52	0.71
ETH/73/2018	0	EA-3	-	0.50	0.29	1
GNA/03/2018	0	EA-3	-	0.55	0.40	0.50
MAU/01/2018	0	EA-3	-	0.79	0.22	0.47
MOR/01/2019	0	EA-3	-	0.62	0.48	0.87
TUN/01/2019	0	EA-3	-	0.51	0.46	0.47
NEP/01/2019	0	ME-SA	Ind-2001	0.71	0.38	0.85
NEP/07/2018	0	ME-SA	Ind-2001	0.40	0.40	0.89
PAK/01/2019	0	ME-SA	Ind-2001	0.78	0.59	0.69
ISR/12/2019	0	ME-SA	PanAsia-2	0.72	0.39	0.47
ISR/27/2019	0	ME-SA	PanAsia-2	0.62	0.44	0.50
PAK/12/2019	0	ME-SA	PanAsia-2	0.66	0.50	0.76
PAK/23/2019	0	ME-SA	PanAsia-2	0.79	0.45	0.51
PAT/03/2019	0	ME-SA	PanAsia-2	0.54	0.27	0.58
PAT/04/2019	0	ME-SA	PanAsia-2	0.81	0.36	0.56
TUR/04/2019	0	ME-SA	PanAsia-2	0.66	0.35	0.79
TUR/11/2018	0	ME-SA	PanAsia-2	0.66	0.35	0.79
MYA/01/2013	0	SEA	Mya-98	0.58	0.29	0.68



Table 8: Vaccine matching studies for Asia-1 FMDV by VNT

Strain	Serotype	Topotype	Lineage	Asia-1 Shamir
PAK 10/2019	Asia-1	ASIA	Sindh-08	0.35
PAK 11/2019	Asia-1	ASIA	Sindh-08	0.44
PAK 14/2019	Asia-1	ASIA	Sindh-08	0.34



Annex 2: FMD publications

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

- 1. Aghaei, A., M. Moghbeli, M. Kargar, S. Nazarian, and F. Kafilzadeh (2019). Cloning and expression of a novel synthetic gene containing VP1 and 3A in *Bacillus subtilis* as a vaccine candidate against *Foot-and-mouth disease virus*. *Biologicals*, **60**: 55-59.
- 2. Ahn, J., L. Cheng, and I.H. Kim (2019). Dietary *astragalus* membranaceus and *codonopsis pilosula* extracts supplementation increases growth performance and FMD antibody titers in growing-finishing pigs. *Journal of Animal Science*, **97**: 68-68.
- 3. Al-Hosary, A.A., A. El-Tanoby, A.F. Oreiby, Y.M. Hegazy, S.K. Abd-elghaffar, and M.H. Al-Gaabary (2019). Assessment of the efficacy of routine vaccination on the magnitude of Foot-and-mouth disease outbreak in Kafrelsheikh governorate, Delta Region, Egypt. *Journal of the Hellenic Veterinary Medical Society*, **70**(2): 1479-1486.
- 4. **Armson, B., J. Wadsworth**, T. Kibona, D. Mshanga, **V.L. Fowler**, **N.J. Knowles**, **V. Mioulet**, R. Reeve, **D.P. King**, **K. Bachanek-Bankowska**, and T. Lembo (2019). Opportunities for enhanced surveillance of Foot-and-mouth disease in endemic settings using milk samples. *Transboundary and Emerging Diseases*, **66**(3): 1405-1410.
- 5. Baazizi, R., N. Mimoune, M. El Mokhefi, M. Raza, A. Chahed, and T. Hussain (2019). Knowledge and behavior of cattle and sheep owners and herders regarding Foot-and-mouth disease in Northern Algeria. *Veterinary World*, **12**(8): 1285-1290.
- 6. Beemer, O., M. Remmenga, L. Gustafson, K. Johnson, D. Hsi, and M.C. Antognoli (2019). Assessing the value of PCR assays in oral fluid samples for detecting African swine fever, Classical swine fever, and Foot-and-mouth disease in US swine. *Plos One*, **14**(7): 16.
- 7. Beltran-Alcrudo, D., J.R. Falco, E. Raizman, and K. Dietze (2019). Transboundary spread of pig diseases: the role of international trade and travel. *BMC Veterinary Research*, **15**: 14.
- 8. Bertram, M.R., R.M. Palinski, R. Ranjan, J.K. Biswal, S.J. Pauszek, E.J. Hartwig, G.R. Smoliga, I.H. Fish, D. Vierra, S. Subramaniam, J.K. Mohapatra, B. Das, B. Pattnaik, and J. Arzt (2019). Genome sequences of 18 *Foot-and-mouth disease virus* outbreak strains of serotype O sublineage ind2001d from India, 2013 to 2014. *Microbiology Resource Announcements*, **8**(33): 3.
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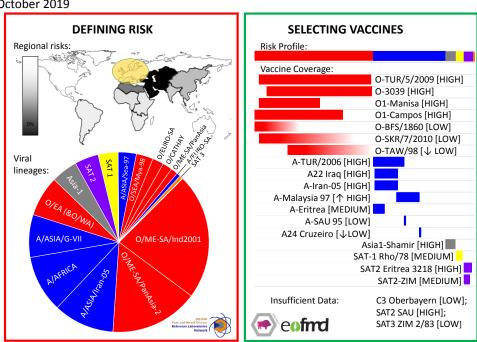
Annex 3: Vaccine Recommendations

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

Lineage	West Eurasia	East Asia	North Africa	India and Southern Asia	East Africa	West and Central Africa	Southern Africa	South America
O ME-SA PanAsia-2	35	-	-	-	-	-	-	-
O ME-SA PanAsia	-	10	-	-	-	-	-	-
O SEA Mya-98	-	33	-	-	-	-	-	-
O ME-SA Ind2001	6	20	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	-
С	-	-	-	-	-	-	-	-

Vaccine Antigen Prioritisation: Europe





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.



Annex 4: Brief round-up of WRLFMD activities

Proficiency test scheme organised by WRLFMD:

Phase XXXI: Feedback letters have been sent to those laboratories that participated in this phase of the proficiency test scheme.

Phase XXXII (available in early 2020): Sample panels (including "live" and inactivated samples for virology assays, and validated sera for FMDV-specific antibody tests) are currently being prepared at the WRLFMD. We anticipate that two panels will be prepared and dispatched to participating laboratories: Panel 1 (available as either "live" FMDV or inactivated FMDV) will test virological methods, while Panel 2 will evaluate serological assays. We are proposing that this proficiency test focuses on laboratory confirmation of FMDV virus infection using different laboratory methods, and that laboratories will be scored according to expectations defined by the PCP status of their country, or their international reference laboratory status (see Table below). Please contact WRLFMD if you have any comments on this proposal, or if you would like more information about participating in this phase of the proficiency test scheme.

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

	VIROLOG	Y (Panel 1)	SEROLOGY (Panel 2)			
Level	Minimum test requirements	Expected lab capability	Minimum test requirements	Expected lab capability		
PCP 0	-	n/a	NSP ELISA	Define infection history (FMDV+/-)		
PCP 1	either AgELISA or RT-PCR	FMD virus presentFMDV serotype	NSP ELISA	Define infection history (FMDV+/-)		
PCP 2	either AgELISA or RT-PCR	FMD virus presentFMDV serotype	NSP ELISA SP ELISA	 Define infectious status vaccination status serotype +/- PVM 		
PCP 3 PCP 4+	AgELISA rRT-PCR +/- sequencing +/- VI*	 FMD virus present FMDV serotype topotype, lineage 	NSP ELISA SP ELISA +/- VNT*	 Define infectious status vaccination status serotype +/- PVM 		
OIE/FAO Reference Laboratories	Enhanced genome sequencing*	 FMD virus present FMDV serotype topotype, lineage, and relationship between FMDV positive samples in panel 	NSP ELISA SP ELISA +/- VNT*	 Define infectious status vaccination status serotype PVM identify cross-reactivity 		

^{*} If able to receive the infectious panel



Residential Training Course:

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

Summary of Meetings attended by WRLFMD Scientists

- WRLFMD-Pirbright hosted colleagues from AU-PANVAC to initiate a new OIE Twinning project to develop vaccine QA/QC pipelines for Africa (July 2019)
- Second OIE/FAO GF-TADS FMD Roadmap meeting for West Africa (Dakar, Senegal) during 3rd-5th September 2019
- EuFMD Workshop in Bari, Italy to review coordinated approaches for the surveillance of FAST transboundary diseases (23rd – 25th September)

OIE/FAO FMD Reference Laboratory Network Activities

The framework agreement for the Network has been signed and circulated to all 15 laboratories (and partner organisations: OIE, FAO and EuFMD) and was included as a recent item in the OIE Bulletin (https://oiebulletin.com/?officiel=2019-1-oie-fao-fmd-reflab-network-en). Dates for this year's meeting have been agreed for w/c 2nd December 2019 and the meeting will be kindly hosted by Dr Park and colleagues from APQA, South Korea (please contact donald.king@pirbright.ac.uk for further information).