

FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

Report Date for this Batch: 21 August 2013

FMDV type A

Country: Mongolia

Period: 2013

No. of sequences: 1 (VP1)

Originator: [REDACTED] Federal Centre for Animal
Health (FGI ARRIAH), Yur'evets, Vladimir, 600900, Russia,
600900 Yur'evets.



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IAH-P-EP-MEG-FOR-005-3

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Serotype: A WRLFMD Ref No: MOG/2013 Batch No: WRLMEG/2013/00020 Sender Ref: A/MOG/2013 Location: Sar Bastay, Sagsai soum, Bayan-Ulgii, Mongolia Date collected: 04/07/2013 Date received by WRLFMD: 21/08/2013 Date received for sequencing: n/a Species: Cattle Material used: saliva Region sequenced: VP1 RT-PCR primers: not known	Report date: 21/08/2013 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Sea-97 Sequence filename: MOG13-AA.SEQ Date sequence last updated: 21/08/2013 No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636 Total no. of comparisons: 1666 Min. no. of nt for comparison: 600 Total turn-around time: 0 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	633	0	99.53	0.47	ASIA	Sea-97
2	A/Amur/2/RUS/2013 (ARRIAH)	RUS13-AH	636	632	0	99.37	0.63	ASIA	Sea-97
3	A/GDMM-CHA-2013-S (LVRI)	CHA13-AA	636	632	0	99.37	0.63	ASIA	Sea-97
4	A/Zabaikalsky/RUS/2013 (ARRIAH)	RUS13-AA	636	632	0	99.37	0.63	ASIA	Sea-97
5	A/Amur/3/RUS/2013 (ARRIAH)	RUS13-AI	636	631	0	99.21	0.79	ASIA	Sea-97
6	A/Amur/RUS/2013* (ARRIAH)	RUS13-AG	636	630	0	99.06	0.94	ASIA	Sea-97
7	A/QHXN-CHA-2013-B (LVRI)	CHA13-AB	636	630	0	99.06	0.94	ASIA	Sea-97
8	A/KAZ/1/2013* (ARRIAH)	KAZ13-AA	636	629	0	98.90	1.10	ASIA	Sea-97
9	A/TAI/15/2012	TAI12-15	636	628	0	98.74	1.26	ASIA	Sea-97
10	A/TAI/1/2011	TAI11-01	636	618	0	97.17	2.83	ASIA	Sea-97

Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/TAI/7/2003 (HQ116312)	TAI03-07	636	596	0	93.71	6.29	ASIA	Sea-97
2	A/TAI/2/97 (EF208778)	TAI97-02	636	574	0	90.25	9.75	ASIA	Sea-97
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	556	0	87.42	12.58	ASIA	Thai-87
4	A22/IRQ/64 (AY593763)	IRQ64--A	636	524	0	82.39	17.61	ASIA	A22
5	A/IRN/2/87 (EF208770)	IRN87-02	633	518	0	81.83	18.17	ASIA	Iran-87
6	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	516	0	81.13	18.87	ASIA	A15
7	A/IRN/78/2009	IRN09-78	636	515	0	80.97	19.03	ASIA	Iran-05 ^{FAR-09}
8	A/TUR/1/2008	TUR08-01	636	515	0	80.97	19.03	ASIA	Iran-05 ^{ARD-07}
9	A/GHA/16/73	GHA73-16	633	512	0	80.88	19.12	AFRICA	G-VI
10	A/IRN/125/2010	IRN10125	636	514	0	80.82	19.18	ASIA	Iran-05 ^{SIS-10}

nt, nucleotides

*. not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV A in Mongolia in 2013

Batch: WRLMEG/2013/00020

 indicates viruses in this batch

Software: MEGA 5.2

Analysis

Analysis ----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

Test of Phylogeny ----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment ----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 639

No Of Bootstrap Reps = 1000

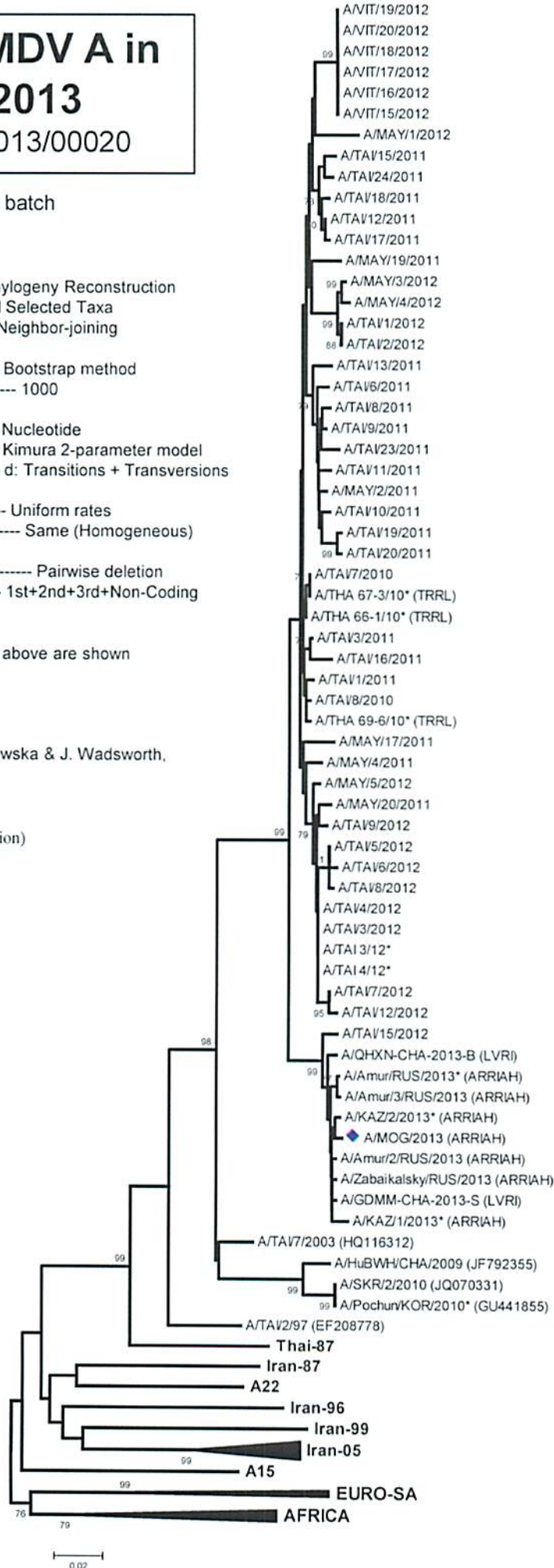
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, K. Bachanek-Bankowska & J. Wadsworth,
21 August 2013

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Sea-97

ASIA

0.02