

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

Genotyping Report

Report Date for this Batch: 8 November 2013

FMDV type A

Country: Mongolia

Period: 2013

No. of samples: 3

BATCH: WRLFMD/2013/00020



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: A	Report date: 07/11/2013
WRLFMD Ref No: MOG/11/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00020	Checked by: K. Bachanek-Bankowska
Sender Ref: A/MOG/15/2013	
Location: Not given, Mongolia	Topotype: ASIA
Date collected: 01/09/2013	Genotype/strain: Sea-97
Date received by WRLFMD: 28/10/2013	Sequence filename: MOG13-11.SEQ
Date received for sequencing: 05/11/2013	Date sequence last updated: 07/11/2013
Species: Cattle	No. of Nt determined: 636
Material used: BTy1 30/10/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 636
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1751
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 10 days
	Sequencing time: 2 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/MOG/12/2013	MOG13-12	636	636	0	100.00	0.00	ASIA	Sea-97
2	A/MOG/13/2013	MOG13-13	636	636	0	100.00	0.00	ASIA	Sea-97
3	A/Amur/2/RUS/2013 (ARRIAH)	RUS13-AH	636	632	0	99.37	0.63	ASIA	Sea-97
4	A/Amur/4/RUS/2013 (ARRIAH)	RUS13-AJ	636	632	0	99.37	0.63	ASIA	Sea-97
5	A/GDMM-CHA-2013-S (LVRI)	CHA13-AA	636	632	0	99.37	0.63	ASIA	Sea-97
6	A/Zabaikalsky/RUS/2013 (ARRIAH)	RUS13-AA	636	632	0	99.37	0.63	ASIA	Sea-97
7	A/Amur/3/RUS/2013 (ARRIAH)	RUS13-AI	636	631	0	99.21	0.79	ASIA	Sea-97
8	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	631	0	99.21	0.79	ASIA	Sea-97
9	A/Amur/RUS/2013* (ARRIAH)	RUS13-AG	636	630	0	99.06	0.94	ASIA	Sea-97
10	A/MOG/2013 (ARRIAH)	MOG13-AA	636	630	0	99.06	0.94	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	572	0	89.94	10.06	ASIA	Sea-97
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	554	0	87.11	12.89	ASIA	Thai-87
4	A22/IRQ/64 (AY593763)	IRQ64--A	636	525	0	82.55	17.45	ASIA	A ₂₂
5	A/IRN/2/87 (EF208770)	IRN87-02	633	522	0	82.46	17.54	ASIA	Iran-87
6	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	518	0	81.45	18.55	ASIA	A15
7	A/IRN/78/2009	IRN09-78	636	517	0	81.29	18.71	ASIA	Iran-05 ^{FAR-09}
8	A/IRN/1/96 (EF208771)	IRN96-01	635	515	1	81.10	18.90	ASIA	Iran-96
9	A/GHA/16/73 (KF561698)	GHA73-16	633	513	0	81.04	18.96	AFRICA	G-VI
10	A/BAR/6/2008 (FJ755010)	BAR08-06	636	515	0	80.97	19.03	ASIA	Iran-05 ^{BAR-08}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: A WRLFMD Ref No: MOG/12/2013 Batch No: WRLFMD/2013/00020 Sender Ref: A/MOG/18/2013 Location: Not given, Mongolia Date collected: 01/09/2013 Date received by WRLFMD: 28/10/2013 Date received for sequencing: 05/11/2013 Species: Cattle Material used: BTy1 30/10/2013 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 07/11/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ASIA Genotype/strain: Sea-97 Sequence filename: MOG13-12.SEQ Date sequence last updated: 07/11/2013 No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636 Total no. of comparisons: 1751 Min. no. of nt for comparison: 600 Total turn-around time: 10 days Sequencing time: 2 days
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Report on FMDV A in Mongolia in 2013

Batch: WRLFMD/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

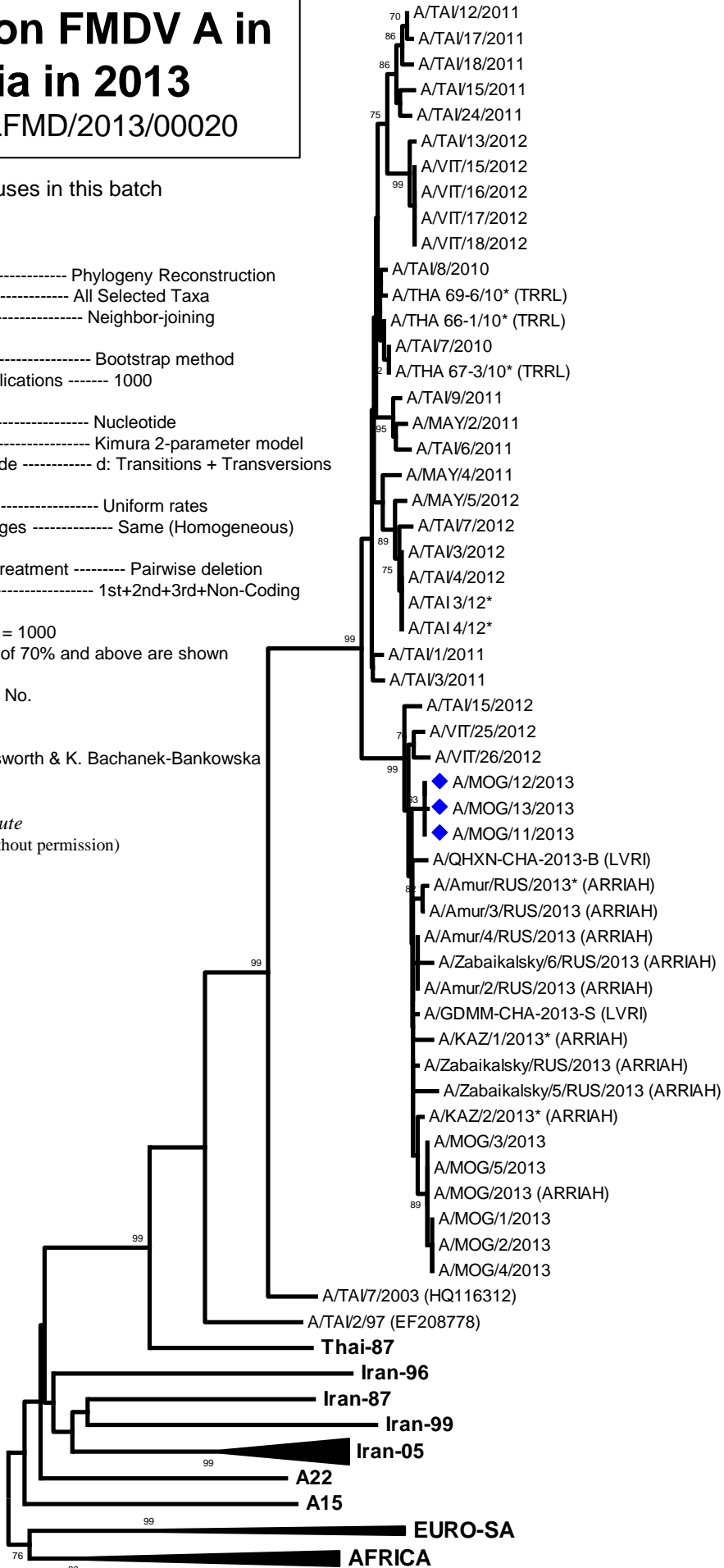
*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska

8 November 2013

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Sea-97

ASIA

0.02