

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

Genotyping Report

Report Date for this Batch: 10 September 2013

FMDV type A

Country: Mongolia

Period: 2013

No. of samples: 5

BATCH: WRLFMD/2013/00018



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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 WRLFMD Ref No: MOG/1/2013 Batch No: WRLFMD/2013/00018 Sender Ref: A/MOG/1/2013 Location: Sagsai Soum, Bayan-Ulgii province, Mongolia Date collected: 05/07/2013 Date received by WRLFMD: 19/08/2013 Date received for sequencing: 04/09/2013 Species: Yak (<i>Bos grunniens</i>) Material used: BTy1 21/08/2013 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 10/09/2013 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Sea-97 Sequence filename: MOG13-01.SEQ Date sequence last updated: 09/09/2013 No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636 Total no. of comparisons: 1675 Min. no. of nt for comparison: 600 Total turn-around time: 22 days Sequencing time: 6 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/2/2013	MOG13-02	636	636	0	100.00	0.00	ASIA	Sea-97
2	A/MOG/4/2013	MOG13-04	636	636	0	100.00	0.00	ASIA	Sea-97
3	A/MOG/2013 (ARRIAH)	MOG13-AA	636	635	0	99.84	0.16	ASIA	Sea-97
4	A/MOG/3/2013	MOG13-03	636	635	0	99.84	0.16	ASIA	Sea-97
5	A/MOG/5/2013	MOG13-05	636	635	0	99.84	0.16	ASIA	Sea-97
6	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	632	0	99.37	0.63	ASIA	Sea-97
7	A/Amur/2/RUS/2013 (ARRIAH)	RUS13-AH	636	631	0	99.21	0.79	ASIA	Sea-97
8	A/GDMM-CHA-2013-S (LVRI)	CHA13-AA	636	631	0	99.21	0.79	ASIA	Sea-97
9	A/Zabaikalsky/RUS/2013 (ARRIAH)	RUS13-AA	636	631	0	99.21	0.79	ASIA	Sea-97
10	A/Amur/3/RUS/2013 (ARRIAH)	RUS13-AI	636	630	0	99.06	0.94	ASIA	Sea-97
Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
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1	A/TAI/7/2003 (HQ116312)	TAI03-07	636	595	0	93.55	6.45	ASIA	Sea-97
2	A/TAI/2/97 (EF208778)	TAI97-02	636	573	0	90.09	9.91	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	523	0	82.23	17.77	ASIA	A22
5	A/IRN/2/87 (EF208770)	IRN87-02	633	517	0	81.67	18.33	ASIA	Iran-87
6	A/IRN/78/2009	IRN09-78	636	515	0	80.97	19.03	ASIA	Iran-05 ^{FAR-09}
7	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	515	0	80.97	19.03	ASIA	A15
8	A/IRN/125/2010	IRN10125	636	514	0	80.82	19.18	ASIA	Iran-05 ^{SIS-10}
9	A/TUR/1/2008	TUR08-01	636	514	0	80.82	19.18	ASIA	Iran-05 ^{ARD-07}
10	A/GHA/16/73 (KF561698)	GHA73-16	633	511	0	80.73	19.27	AFRICA	G-VI

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: A WRLFMD Ref No: MOG/2/2013 Batch No: WRLFMD/2013/00018 Sender Ref: A/MOG/5/2013 Location: Sagsai Soum, Bayan-Ulgii province, Mongolia Date collected: 03/07/2013 Date received by WRLFMD: 19/08/2013 Date received for sequencing: 04/09/2013 Species: Yak (<i>Bos grunniens</i>) Material used: BTy1 21/08/2013 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 10/09/2013 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Sea-97 Sequence filename: MOG13-02.SEQ Date sequence last updated: 09/09/2013 No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636 Total no. of comparisons: 1675 Min. no. of nt for comparison: 600 Total turn-around time: 22 days Sequencing time: 6 days
Comments:	

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2	A/MOG/4/2013	MOG13-04	636	636	0	100.00	0.00	ASIA	Sea-97
3	A/MOG/2013 (ARRIAH)	MOG13-AA	636	635	0	99.84	0.16	ASIA	Sea-97
4	A/MOG/3/2013	MOG13-03	636	635	0	99.84	0.16	ASIA	Sea-97
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6	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	632	0	99.37	0.63	ASIA	Sea-97
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3	A/TAI/118/87* (EF208777)	TAI87-AD	636	556	0	87.42	12.58	ASIA	Thai-87
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6	A/IRN/78/2009	IRN09-78	636	515	0	80.97	19.03	ASIA	Iran-05 ^{FAR-09}
7	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	515	0	80.97	19.03	ASIA	A15
8	A/IRN/125/2010	IRN10125	636	514	0	80.82	19.18	ASIA	Iran-05 ^{SIS-10}
9	A/TUR/1/2008	TUR08-01	636	514	0	80.82	19.18	ASIA	Iran-05 ^{ARD-07}
10	A/GHA/16/73 (KF561698)	GHA73-16	633	511	0	80.73	19.27	AFRICA	G-VI

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Serotype: A WRLFMD Ref No: MOG/3/2013 Batch No: WRLFMD/2013/00018 Sender Ref: A/MOG/9/2013 Location: Sagsai Soum, Bayan-Ulgii province, Mongolia Date collected: 03/07/2013 Date received by WRLFMD: 19/08/2013 Date received for sequencing: 04/09/2013 Species: Yak (<i>Bos grunniens</i>) Material used: BTy1 21/08/2013 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 10/09/2013 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Sea-97 Sequence filename: MOG13-03.SEQ Date sequence last updated: 09/09/2013 No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636 Total no. of comparisons: 1675 Min. no. of nt for comparison: 600 Total turn-around time: 22 days Sequencing time: 6 days
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2	A/MOG/5/2013	MOG13-05	636	636	0	100.00	0.00	ASIA	Sea-97
3	A/MOG/1/2013	MOG13-01	636	635	0	99.84	0.16	ASIA	Sea-97
4	A/MOG/2/2013	MOG13-02	636	635	0	99.84	0.16	ASIA	Sea-97
5	A/MOG/4/2013	MOG13-04	636	635	0	99.84	0.16	ASIA	Sea-97
6	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	633	0	99.53	0.47	ASIA	Sea-97
7	A/Amur/2/RUS/2013 (ARRIAH)	RUS13-AH	636	632	0	99.37	0.63	ASIA	Sea-97
8	A/GDMM-CHA-2013-S (LVRI)	CHA13-AA	636	632	0	99.37	0.63	ASIA	Sea-97
9	A/Zabaikalsky/RUS/2013 (ARRIAH)	RUS13-AA	636	632	0	99.37	0.63	ASIA	Sea-97
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3	A/TAI/118/87* (EF208777)	TAI87-AD	636	556	0	87.42	12.58	ASIA	Thai-87
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Report on FMDV A in Mongolia in 2013

Batch: WRLFMD/2013/00018

◆ 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,
10 September 2013

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Sea-97

ASIA

0.02