

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

## Genotyping Report

Report Date for this Batch: 21 August 2013

FMDV type A

Country: Russian Federation

Period: 2013

No. of sequences: 2 (VP1)

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



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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: A WRLFMD Ref No: Amur/2/RUS/2013 Batch No: WRLMEG/2013/00019 Sender Ref: A/Amur/2/RUS/2013 Location: Ust-Ivanovka, Blagoveschensk, Amurskaya oblast, Russia Date collected: 08/08/2013 Date received by WRLFMD: 21/08/2013 Date received for sequencing: n/a Species: Cattle Material used: epithelium Region sequenced: VPI 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: RUS13-AH.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/GDMM-CHA-2013-S (LVRI)	CHA13-AA	636	634	0	99.69	0.31	ASIA	Sea-97
2	A/Zabaikalsky/RUS/2013 (ARRIAH)	RUS13-AA	636	634	0	99.69	0.31	ASIA	Sea-97
3	A/Amur/3/RUS/2013 (ARRIAH)	RUS13-AI	636	633	0	99.53	0.47	ASIA	Sea-97
4	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	633	0	99.53	0.47	ASIA	Sea-97
5	A/Amur/RUS/2013* (ARRIAH)	RUS13-AG	636	632	0	99.37	0.63	ASIA	Sea-97
6	A/MOG/2013 (ARRIAH)	MOG13-AA	636	632	0	99.37	0.63	ASIA	Sea-97
7	A/QHXN-CHA-2013-B (LVRI)	CHA13-AB	636	632	0	99.37	0.63	ASIA	Sea-97
8	A/KAZ/1/2013* (ARRIAH)	KAZ13-AA	636	631	0	99.21	0.79	ASIA	Sea-97
9	A/TAI/15/2012	TAI12-15	636	630	0	99.06	0.94	ASIA	Sea-97
10	A/TAI/1/2011	TAI11-01	636	620	0	97.48	2.52	ASIA	Sea-97

### Most Closely Related Reference Viruses

(see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](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	558	0	87.74	12.26	ASIA	Thai-87
4	A22/IRQ/64 (AY593763)	IRQ64--A	636	525	0	82.55	17.45	ASIA	A <sub>22</sub>
5	A/IRN/2/87 (EF208770)	IRN87-02	633	519	0	81.99	18.01	ASIA	Iran-87
6	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	516	0	81.13	18.87	ASIA	A15
7	A/GHA/16/73	GHA73-16	633	513	0	81.04	18.96	AFRICA	G-VI
8	A/IRN/78/2009	IRN09-78	636	515	0	80.97	19.03	ASIA	Iran-05 <sup>FAR-09</sup>
9	A/TUR/1/2008	TUR08-01	636	514	0	80.82	19.18	ASIA	Iran-05 <sup>ARD-07</sup>
10	A/BAR/6/2008	BAR08-06	636	513	0	80.66	19.34	ASIA	Iran-05 <sup>BAR-08</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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

Page 1 of 1

Serotype: A WRLFMD Ref No: Amur/3/RUS/2013 Batch No: WRLMEG/2013/00019 Sender Ref: A/Amur/3/RUS/2013 Location: Krasnoe, Tambovskiy, Amurskaya oblast, Russia Date collected: 16/08/2013 Date received by WRLFMD: 21/08/2013 Date received for sequencing: n/a Species: Cattle Material used: epithelium 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: RUS13-A1.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
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Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/Amur/RUS/2013* (ARRIAH)	RUS13-AG	636	635	0	99.84	0.16	ASIA	Sea-97
2	A/Amur/2/RUS/2013 (ARRIAH)	RUS13-AH	636	633	0	99.53	0.47	ASIA	Sea-97
3	A/GDMM-CHA-2013-S (LVRI)	CHA13-AA	636	633	0	99.53	0.47	ASIA	Sea-97
4	A/Zabaikalsky/RUS/2013 (ARRIAH)	RUS13-AA	636	633	0	99.53	0.47	ASIA	Sea-97
5	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	632	0	99.37	0.63	ASIA	Sea-97
6	A/MOG/2013 (ARRIAH)	MOG13-AA	636	631	0	99.21	0.79	ASIA	Sea-97
7	A/QHXN-CHA-2013-B (LVRI)	CHA13-AB	636	631	0	99.21	0.79	ASIA	Sea-97
8	A/KAZ/1/2013* (ARRIAH)	KAZ13-AA	636	630	0	99.06	0.94	ASIA	Sea-97
9	A/TAI/15/2012	TAI12-15	636	629	0	98.90	1.10	ASIA	Sea-97
10	A/TAI/1/2011	TAI11-01	636	619	0	97.33	2.67	ASIA	Sea-97
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
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	595	0	93.55	6.45	ASIA	Sea-97
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3	A/TAI/118/87* (EF208777)	TAI87-AD	636	557	0	87.58	12.42	ASIA	Thai-87
4	A22/IRQ/64 (AY593763)	IRQ64--A	636	525	0	82.55	17.45	ASIA	A22
5	A/IRN/2/87 (EF208770)	IRN87-02	633	519	0	81.99	18.01	ASIA	Iran-87
6	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	517	0	81.29	18.71	ASIA	A15
7	A/IRN/78/2009	IRN09-78	636	515	0	80.97	19.03	ASIA	Iran-05 <sup>FAR-09</sup>
8	A/GHA/16/73	GHA73-16	633	512	0	80.88	19.12	AFRICA	G-VI
9	A/TUR/1/2008	TUR08-01	636	514	0	80.82	19.18	ASIA	Iran-05 <sup>ARD-07</sup>
10	A/BAR/6/2008	BAR08-06	636	513	0	80.66	19.34	ASIA	Iran-05 <sup>BAR-08</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# Report on FMDV A in the Russian Federation in 2013

Batch: WRLMEG/2013/00019

◆ 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

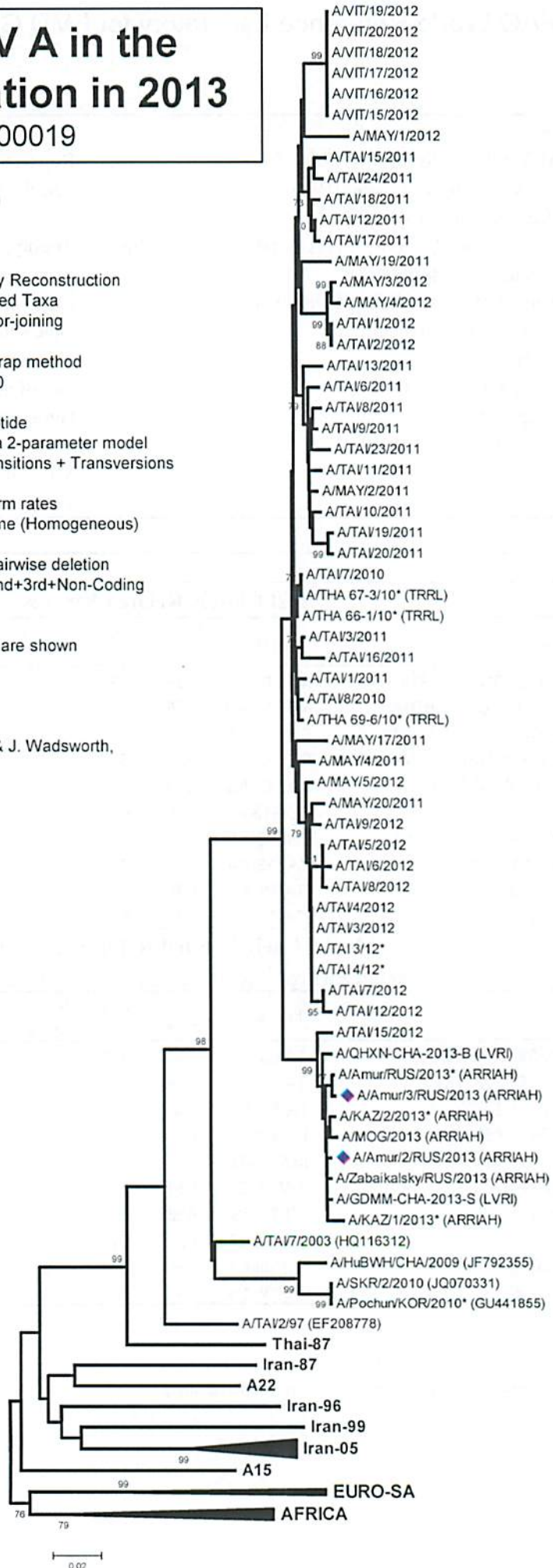
Only bootstrap values of 70% and above are shown

\*, 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