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## **FMD Genotyping Report**

**Lab Reference WRL Batch Number:** WRLMEG/2012/00009  
**Country of Origin:** Kazakhstan  
**Date Reported:** 19<sup>th</sup> June 2012

Dear All,

Please find attached sequence analysis carried out on recent additions to GenBank. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

**Approved By:** 

**Official Stamp:** 

**Date:** 19/6/12

A UKAS accredited testing laboratory No. 4025.

To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: [gareth.shimmon@iah.ac.uk](mailto:gareth.shimmon@iah.ac.uk). IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

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

## Genotyping Report

Report Date for this Batch: 17 June 2012

FMDV type A

Country: Kazakhstan

Period: 2012

No. of sequences: 1

Originator: GenBank: submitted 12-Mar-2012 by Stochkov, V.,  
Orynbayev, M., Kerembayev, A., Musaeva, G. and  
Sultankulova, K., Ministry of Education and Science, Research  
Institute for Biological Safety Problems, Gvardeyskiy,  
Zhambyl oblast 080409, Kazakhstan.



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# FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: A WRLFMD Ref No: Mainkum/KAZ/02/2012* Batch No: WRLMEG/2012/00009 Sender Ref: Mainkum/02/2012 Location: Mainkum, Kazakhstan Date collected: 01/02/2012 Date received by WRLFMD: 17/06/2012 Date received for sequencing: n/a Species: Not Known Material used: not known Region sequenced: VP1 RT-PCR primers: not known	Report date: 17/06/2012 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Iran-05 <sup>HER-10</sup> Sequence filename: KAZ12-AC.SEQ Date sequence last updated: 17/06/2012 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 1410 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/KRG/11/2011* (JQ765587)	KRG11-AA	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
2	A/AFG/20/2011	AFG11-20	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
3	A/AFG/22/2011	AFG11-22	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
4	A/AFG/24/2011	AFG11-24	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
5	A/AFG/25/2011	AFG11-25	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
6	A/AFG/26/2011	AFG11-26	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
7	A/AFG/27/2011	AFG11-27	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
8	A/AFG/29/2011	AFG11-29	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
9	A/AFG/69/2011	AFG11-69	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
10	A/AFG/71/2011	AFG11-71	639	632	0	98.9	1.10	ASIA	Iran-05 <sup>HER-10</sup>
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/AFG/10/2010	AFG10-10	639	629	0	98.44	1.56	ASIA	Iran-05 <sup>HER-10</sup>
2	A/AFG/6/2007	AFG07-06	639	608	0	95.15	4.85	ASIA	Iran-05 <sup>AFG-07</sup>
3	A/IRN/78/2009	IRN09-78	639	600	0	93.90	6.10	ASIA	Iran-05 <sup>FAR-09</sup>
4	A/IRN/1/2005 (EF208769)	IRN05-01	639	599	0	93.74	6.26	ASIA	Iran-05
5	A/BAR/6/2008	BAR08-06	639	596	0	93.27	6.73	ASIA	Iran-05 <sup>BAR-08</sup>
6	A/TUR/1/2008	TUR08-01	639	594	0	92.96	7.04	ASIA	Iran-05 <sup>ARD-07</sup>
7	A/IRN/125/2010	IRN10125	639	592	0	92.64	7.36	ASIA	Iran-05 <sup>SIS-10</sup>
8	A/TUR/33/2008	TUR08-33	639	591	0	92.49	7.51	ASIA	Iran-05 <sup>EZM-07</sup>
9	A/IRN/9/2011	IRN11-09	639	584	0	91.39	8.61	ASIA	Iran-05 <sup>QAZ-11</sup>
10	A/IRN/9/2010	IRN10-09	639	580	0	90.77	9.23	ASIA	Iran-05 <sup>ESF-10</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# Report on FMDV A in Kazakhstan in 2012

Batch: WRLMEG/2012/00009

◆ indicates viruses in this batch

Software: MEGA 5.0

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

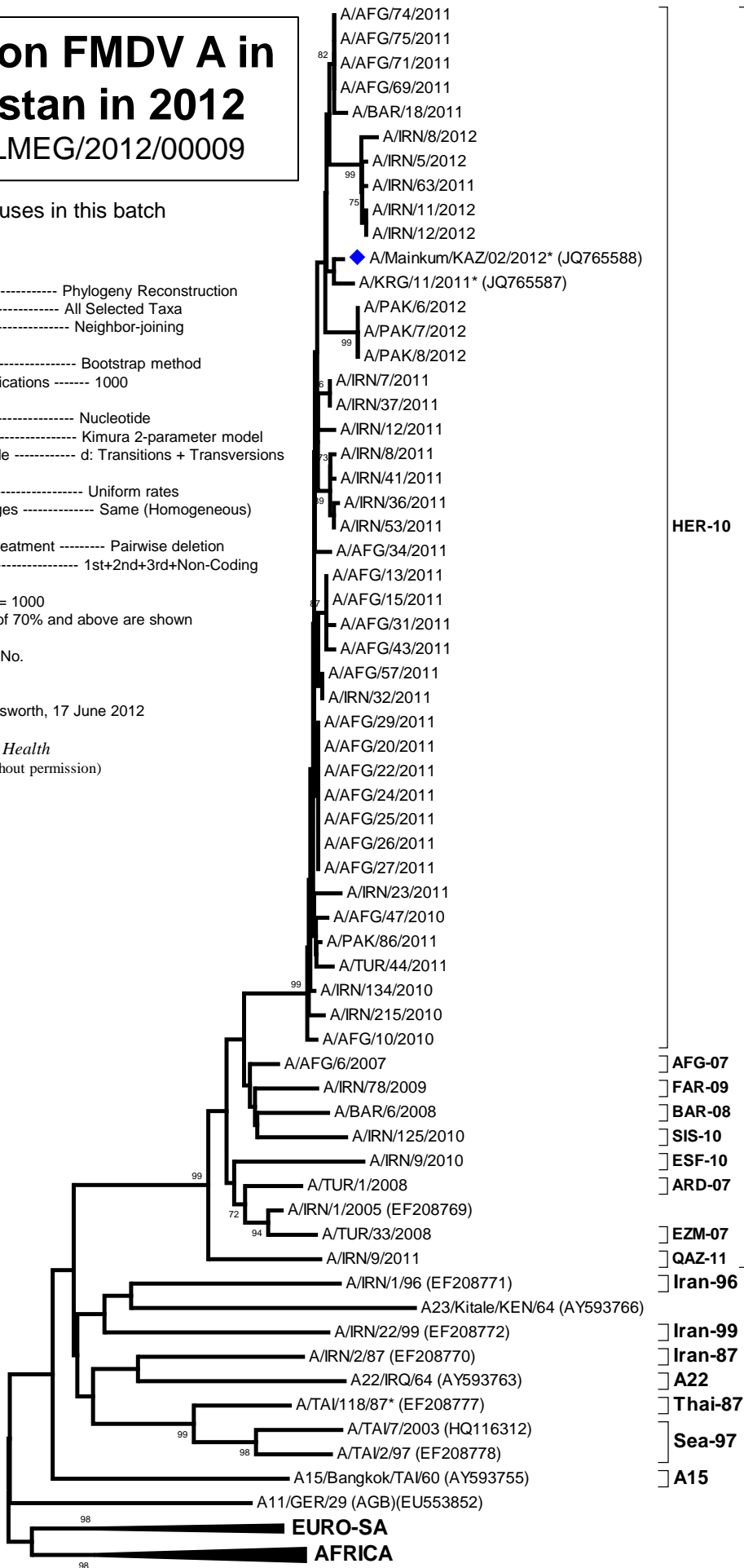
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 17 June 2012

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0.02