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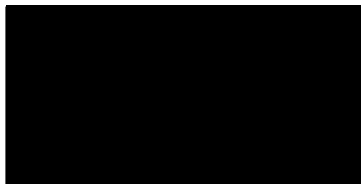
FMD Genotyping Report

Lab Reference WRL Batch Number: WRLMEG/2012/00009
Country of Origin: Kyrgyzstan
Date Reported: 19th June 2012

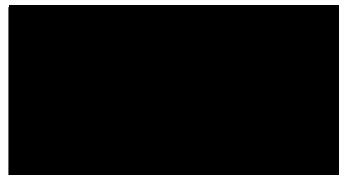
Dear All,

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. 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: Kyrgyzstan

Period: 2011

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

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

Page 1 of 1

Serotype: A	Report date: 17/06/2012
WRLFMD Ref No: KRG/11/2011*	Reported by: N.J. Knowles
Batch No: WRLMEG/2012/00009	Checked by: D.P. King
Sender Ref: Kirgizia/11/2011	
Location: not known, Kyrgyzstan	Topotype: ASIA
Date collected: 01/11/2011	Genotype/strain: Iran-05 ^{HER-10}
Date received by WRLFMD: 17/06/2012	Sequence filename: KRG11-AA.SEQ
Date received for sequencing: n/a	Date sequence last updated: 17/06/2012
Species: Not Known	No. of Nt determined: 639
Material used: not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not known	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/Mainkum/KAZ/02/2012* (JQ765588)	KAZ12-AC	639	632	0	98.90	1.10	ASIA	Iran-05 ^{HER-10}
2	A/AFG/69/2011	AFG11-69	639	631	0	98.75	1.25	ASIA	Iran-05 ^{HER-10}
3	A/AFG/71/2011	AFG11-71	639	631	0	98.75	1.25	ASIA	Iran-05 ^{HER-10}
4	A/AFG/74/2011	AFG11-74	639	631	0	98.75	1.25	ASIA	Iran-05 ^{HER-10}
5	A/AFG/75/2011	AFG11-75	639	631	0	98.75	1.25	ASIA	Iran-05 ^{HER-10}
6	A/AFG/20/2011	AFG11-20	639	629	0	98.44	1.56	ASIA	Iran-05 ^{HER-10}
7	A/AFG/22/2011	AFG11-22	639	629	0	98.44	1.56	ASIA	Iran-05 ^{HER-10}
8	A/AFG/24/2011	AFG11-24	639	629	0	98.44	1.56	ASIA	Iran-05 ^{HER-10}
9	A/AFG/25/2011	AFG11-25	639	629	0	98.44	1.56	ASIA	Iran-05 ^{HER-10}
10	A/AFG/26/2011	AFG11-26	639	629	0	98.44	1.56	ASIA	Iran-05 ^{HER-10}
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/AFG/10/2010	AFG10-10	639	626	0	97.97	2.03	ASIA	Iran-05 ^{HER-10}
2	A/AFG/6/2007	AFG07-06	639	607	0	94.99	5.01	ASIA	Iran-05 ^{AFG-07}
3	A/IRN/78/2009	IRN09-78	639	601	0	94.05	5.95	ASIA	Iran-05 ^{FAR-09}
4	A/BAR/6/2008	BAR08-06	639	599	0	93.74	6.26	ASIA	Iran-05 ^{BAR-08}
5	A/IRN/1/2005 (EF208769)	IRN05-01	639	598	0	93.58	6.42	ASIA	Iran-05
6	A/TUR/1/2008	TUR08-01	639	597	0	93.43	6.57	ASIA	Iran-05 ^{ARD-07}
7	A/IRN/125/2010	IRN10125	639	591	0	92.49	7.51	ASIA	Iran-05 ^{SIS-10}
8	A/TUR/33/2008	TUR08-33	639	590	0	92.33	7.67	ASIA	Iran-05 ^{EZM-07}
9	A/IRN/9/2011	IRN11-09	639	587	0	91.86	8.14	ASIA	Iran-05 ^{QAZ-11}
10	A/IRN/9/2010	IRN10-09	639	581	0	90.92	9.08	ASIA	Iran-05 ^{ESF-10}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV A in Kyrgyzstan in 2011

Batch: WRLMEG/2012/00009

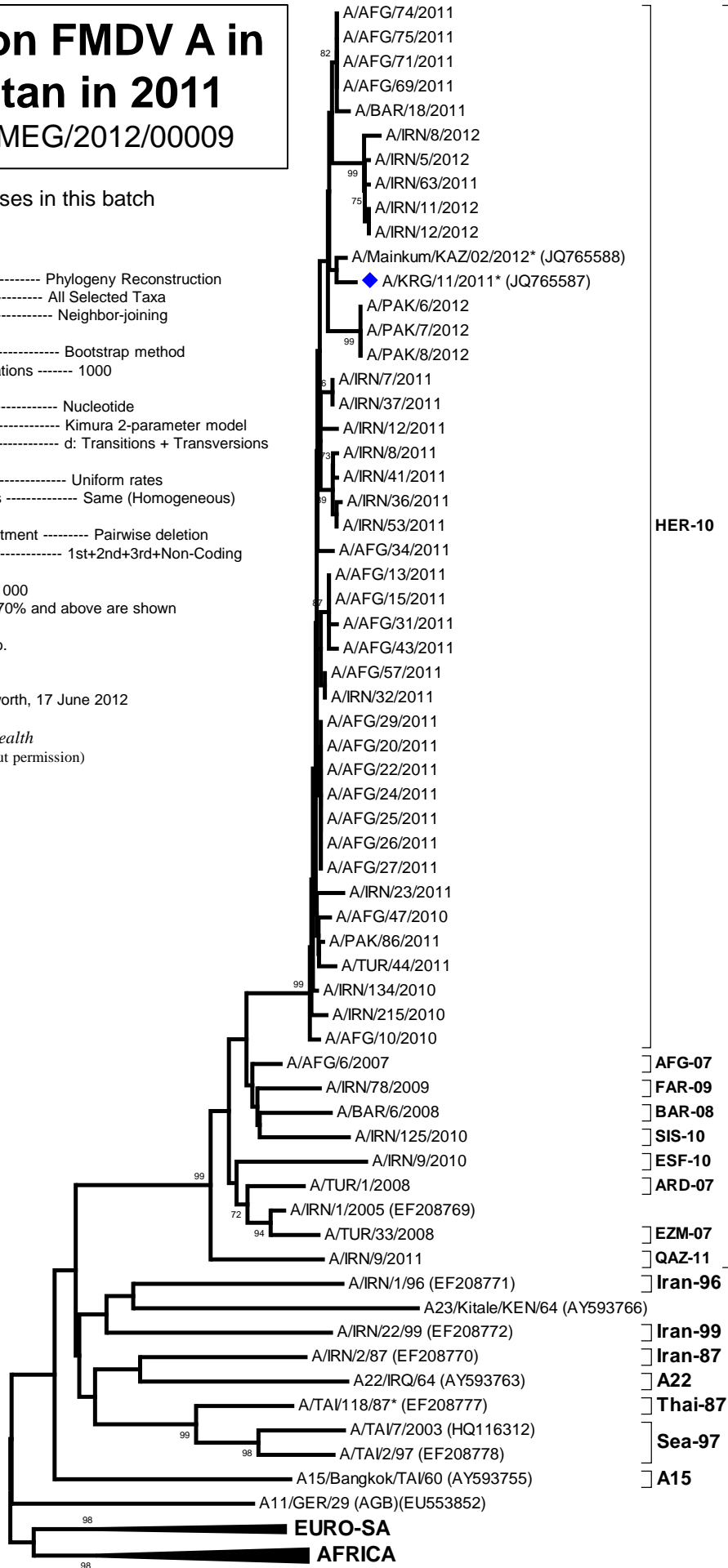
◆ indicates viruses in this batch

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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HER-10

Iran-05

ASIA

] AFG-07
] FAR-09
] BAR-08
] SIS-10
] ESF-10
] ARD-07

] EZM-07
] QAZ-11
] Iran-96

] Iran-99
] Iran-87
] A22

] Thai-87
] Sea-97

] A15

0.02