

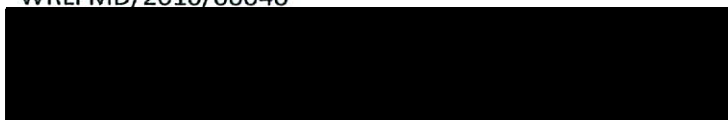


INSTITUTE FOR ANIMAL HEALTH
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GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00040

Sender Details:



Date Received: 17th November 2010

Country of Origin: Iran

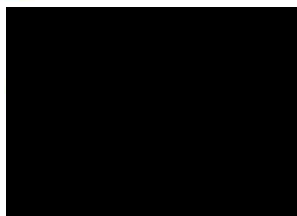
Date Reported: 8th December 2010

Dear Sir,

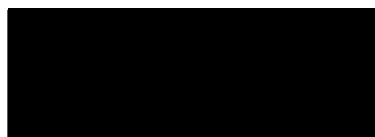
Re.: Serotype A

Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

Results Approved By:



Official Stamp:



Date:

8/12/10



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: elizabeth.wilson@bbsrc.ac.uk)

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

Genotyping Report

Report Date for this Batch: 30 November 2010

FMDV type A

Country: Iran

Period: 2010

No. of isolates: 1

BATCH: WRLFMD/2010/00040



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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: 30/11/2010
WRLFMD Ref No: IRN/215/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00040	Checked by: D.P. King
Sender Ref: IR-89-195	
Location: West Azerbaijan, Iran	Topotype: ASIA
Date collected: 10/10/2010	Genotype/strain: Iran-05 ^{AFG-07}
Date received by WRLFMD: 17/11/2010	Sequence filename: IRN10215.SEQ
Date received for sequencing: 25/11/2010	Date sequence last updated: 30/11/2010
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1185
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 13 days
	Sequencing time: 5 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/IRN/134/2010	IRN10134	639	634	0	99.22	0.78	ASIA	Iran-05 ^{AFG-07}
2	A/AFG/10/2010	AFG10-10	639	632	0	98.90	1.10	ASIA	Iran-05 ^{AFG-07}
3	A/AFG/47/2010	AFG10-47	639	632	0	98.90	1.10	ASIA	Iran-05 ^{AFG-07}
4	A/AFG/44/2007	AFG07-44	639	614	0	96.09	3.91	ASIA	Iran-05 ^{AFG-07}
5	A/IRN/9/2009	IRN09-09	639	614	0	96.09	3.91	ASIA	Iran-05 ^{AFG-07}
6	A/AFG/6/2007	AFG07-06	639	613	0	95.93	4.07	ASIA	Iran-05 ^{AFG-07}
7	A/IRN/26/2009	IRN09-26	639	613	0	95.93	4.07	ASIA	Iran-05 ^{AFG-07}
8	A/BAR/2/2009	BAR09-02	639	612	0	95.77	4.23	ASIA	Iran-05 ^{AFG-07}
9	A/BAR/4/2009	BAR09-04	639	612	0	95.77	4.23	ASIA	Iran-05 ^{AFG-07}
10	A/AFG/6/2010	AFG10-06	639	611	0	95.62	4.38	ASIA	Iran-05 ^{AFG-07}
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/6/2007	AFG07-06	639	613	0	95.93	4.07	ASIA	Iran-05 ^{AFG-07}
2	A/IRN/1/2005 (EF208769)	IRN05-01	639	604	0	94.52	5.48	ASIA	Iran-05
3	A/BAR/6/2008	BAR08-06	639	601	0	94.05	5.95	ASIA	Iran-05 ^{BAR-08}
4	A/TUR/1/2008	TUR08-01	639	601	0	94.05	5.95	ASIA	Iran-05 ^{ARD-07}
5	A/TUR/33/2008	TUR08-33	639	598	0	93.58	6.42	ASIA	Iran-05 ^{EZM-07}
6	A/TAI/118/87* (EF208777)	TAI87-AD	636	534	0	83.96	16.04	ASIA	Thai-87
7	A/IRN/2/87 (EF208770)	IRN87-02	636	532	0	83.65	16.35	ASIA	Iran-87
8	A/IRN/22/99 (EF208772)	IRN99-22	636	529	0	83.18	16.82	ASIA	Iran-99
9	A/TAI/2/97 (EF208778)	TAI97-02	636	527	0	82.86	17.14	ASIA	Thai-97
10	A/TAI/7/2003	TAI03-07	636	527	0	82.86	17.14	ASIA	Thai-03

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.11

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Report on FMDV A in Iran in 2010

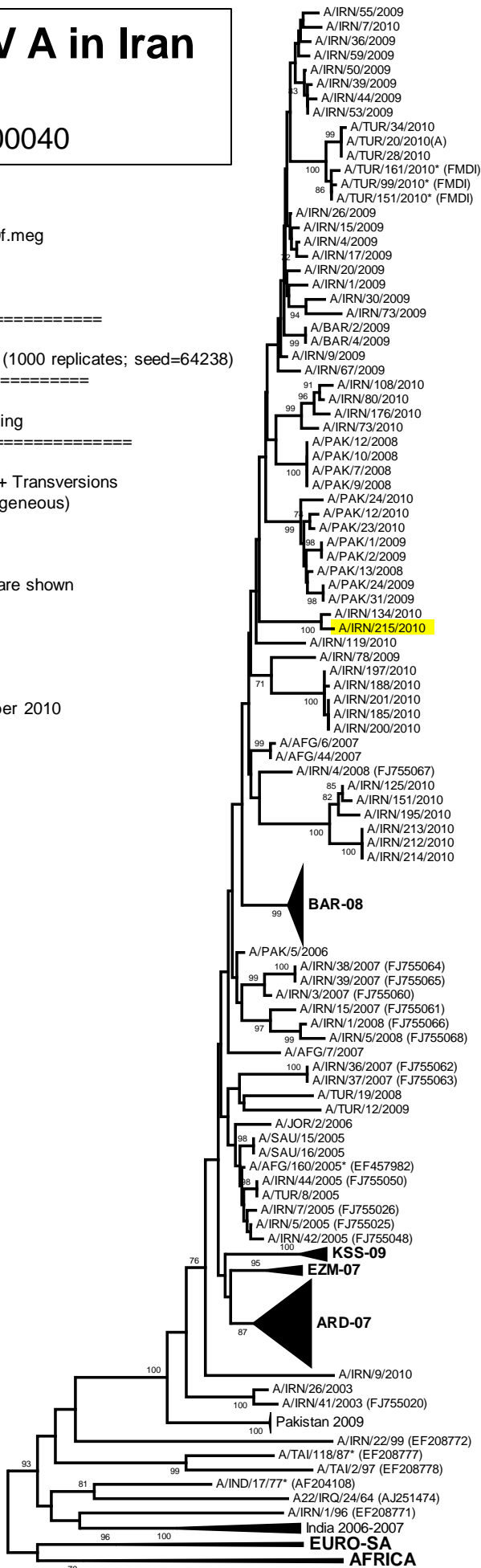
Batch: WRLFMD/2010/00040

Software: MEGA 4.0
 No. of Taxa : 209
 Data File : n:\evd\meg\db\fmvd\A\IRN2010f.meg
 Data Title : A Iran 2010
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)
 Include Sites : =====
 ->Gaps/Missing Data : Pairwise Deletion
 ->Codon Positions : 1st+2nd+3rd+Noncoding
 Substitution Model : =====
 ->Model : Nucleotide: Kimura 2-parameter
 ->Substitutions to Include : d: Transitions + Transversions
 ->Pattern among Lineages : Same (Homogeneous)
 ->Rates among sites : Uniform rates
 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, 30 November 2010

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AFG-07

Iran-05

ASIA

BAR-08

KSS-09

EZM-07

ARD-07

0.02