



INSTITUTE FOR ANIMAL HEALTH
Director: Professor Martin W. Shirley, PhD
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

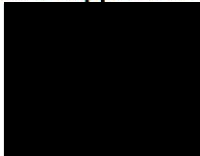
Lab Reference WRL Batch Number: WRLFMD/2010/00018
Sender Details: [REDACTED]
Date Received: [REDACTED]
Country of Origin: Iran
Date Reported: 21st May 2010

Dear Dr. Abdollah, Dr. Otard,

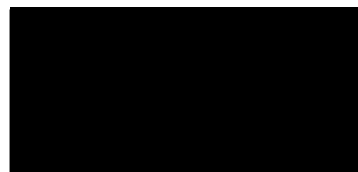
Re.: Serotype A.

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: 21/05/2010



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

Date: 20 May 2010

FMDV type A

Country: Iran

Period: 2010

No. of isolates: 1

BATCH: WRLFMD/2010/00018



The contents of this report are copyright and should not be reproduced without permission

© Institute for Animal Health

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: A WRLFMD Ref No: IRN/36/2010 Batch No: WRLFMD/2010/00018 Sender Ref: IR-89-6 Location: Sardasht, West Azerbaijan, Iran Date collected: 27/03/2010 Date received by WRLFMD: 21/04/2010 Date received for sequencing: 17/05/2010 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 20/05/2010 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Iran-05 ^{BAR-08} Sequence filename: IRN10-36.SEQ Date sequence last updated: 19/05/2010 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 1273 Min. no. of nt for comparison: 300 Total turn-around time: 29 days Sequencing time: 3 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/KUW/5/2009	KUW09-05	639	628	0	98.28	1.72	ASIA	Iran-05 ^{BAR-08}
2	A/IRN/2/2009	IRN09-02	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
3	A/IRN/21/2009	IRN09-21	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
4	A/IRN/22/2009	IRN09-22	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
5	A/IRN/29/2009	IRN09-29	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
6	A/IRQ/10/2009	IRQ09-10	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
7	A/IRQ/11/2009	IRQ09-11	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
8	A/IRQ/12/2009	IRQ09-12	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
9	A/IRQ/15/2009	IRQ09-15	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
10	A/IRQ/17/2009	IRQ09-17	639	627	0	98.12	1.88	ASIA	Iran-05 ^{BAR-08}
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/BAR/6/2008	BAR08-06	639	622	0	97.34	2.66	ASIA	Iran-05 ^{BAR-08}
2	A/AFG/6/2007	AFG07-06	639	612	0	95.77	4.23	ASIA	Iran-05 ^{AFG-07}
3	A/IRN/1/2005 (EF208769)	IRN05-01	639	603	0	94.37	5.63	ASIA	Iran-05
4	A/TUR/1/2008	TUR08-01	639	600	0	93.90	6.10	ASIA	Iran-05 ^{ARD-07}
5	A/TUR/33/2008	TUR08-33	639	594	0	92.96	7.04	ASIA	Iran-05 ^{EZM-07}
6	A/IRN/2/87 (EF208770)	IRN87-02	636	537	0	84.43	15.57	ASIA	Iran-87
7	A/TAI/118/87* (EF208777)	TAI87-AD	636	534	0	83.96	16.04	ASIA	Thai-87
8	A/IRN/22/99 (EF208772)	IRN99-22	636	533	0	83.81	16.19	ASIA	Iran-99
9	A/IRN/1/96 (EF208771)	IRN96-01	638	534	1	83.70	16.30	ASIA	Iran-96
10	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	530	0	82.94	17.06	ASIA	A ₁₅

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.1

© Institute for Animal Health

Report on FMDV A in Iran in 2010

Batch: WRLFMD/2010/00018

Software: MEGA 4.0
 No. of Taxa : 187
 Data File : n:\levd\meg\db\fmv\la\IRN2010b.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=21180)
 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, 20 May 2010

© Institute for Animal Health



0.02