



INSTITUTE FOR ANIMAL HEALTH
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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00034
Sender Details: [REDACTED]
Date Received: 22nd June 2009
Country of Origin: Iran
Date Reported: 14th September 2009

Dear [REDACTED]

Re.: Serotype A results.

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: 14/09/09



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.byrom@bbsrc.ac.uk)

Molecular Epidemiology Report Form

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Serotype: A WRL Ref No: IRN/30/2009 Sender Ref: IR-51 Date collected: 10/04/2009 Date received by WRLFMD: 22/06/2009 Date received for sequencing: 07/07/2009 Species: CATTLE Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 02/09/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Iran-05 ^{AFG-07} Sequence filename: IRN09-30.SEQ Date sequence last updated: 17/07/2009 Total no. of comparisons: 1183 Min. no. of nt for comparison: 300 Total turn-around time: 72 days Sequencing time: 57 days																																																																																								
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Serotype: A WRL Ref No: IRN/32/2009 Sender Ref: IR-47 Date collected: 20/04/2009 Date received by WRLFMD: 22/06/2009 Date received for sequencing: 07/07/2009 Species: CATTLE Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 02/09/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Iran-05 ^{BAR-08} Sequence filename: IRN09-32.SEQ Date sequence last updated: 17/07/2009 Total no. of comparisons: 1183 Min. no. of nt for comparison: 300 Total turn-around time: 72 days Sequencing time: 57 days																																																																																								
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Molecular Epidemiology Report Form

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<p>Serotype: A WRL Ref No: IRN/37/2009 Sender Ref: IR-55 Date collected: 03/05/2009 Date received by WRLFMD: 22/06/2009 Date received for sequencing: 07/07/2009 Species: CATTLE Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639</p>	<p>Report date: 02/09/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Iran-05^{BAR-08} Sequence filename: IRN09-37.SEQ Date sequence last updated: 17/07/2009 Total no. of comparisons: 1183 Min. no. of nt for comparison: 300 Total turn-around time: 72 days Sequencing time: 57 days</p>																																																																																								
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Molecular Epidemiology Report Form

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Serotype: A WRL Ref No: IRN/39/2009 Sender Ref: IR-52 Date collected: 14/05/2009 Date received by WRLFMD: 22/06/2009 Date received for sequencing: 07/07/2009 Species: CATTLE Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 02/09/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Iran-05 ^{AFG-07} Sequence filename: IRN09-39.SEQ Date sequence last updated: 17/07/2009 Total no. of comparisons: 1183 Min. no. of nt for comparison: 300 Total turn-around time: 72 days Sequencing time: 57 days																																																																																								
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Serotype: A WRL Ref No: IRN/44/2009 Sender Ref: IR-50 Date collected: 01/01/2009 Date received by WRLFMD: 22/06/2009 Date received for sequencing: 07/07/2009 Species: UNKNOWN Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 02/09/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Iran-05 ^{AFG-07} Sequence filename: IRN09-44.SEQ Date sequence last updated: 17/07/2009 Total no. of comparisons: 1183 Min. no. of nt for comparison: 300 Total turn-around time: 72 days Sequencing time: 57 days
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Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/IRN/39/2009	IRN09-39	639	636	0	99.53	0.47
2	A/IRN/15/2009	IRN09-15	639	632	0	98.9	1.1
3	A/IRN/26/2009	IRN09-26	639	632	0	98.9	1.1
4	A/IRN/36/2009	IRN09-36	639	632	0	98.9	1.1
5	A/IRN/4/2009	IRN09-04	639	630	0	98.59	1.41
6	A/IRN/9/2009	IRN09-09	639	629	0	98.44	1.56
7	A/IRN/20/2009	IRN09-20	639	628	0	98.28	1.72
8	A/BAR/2/2009	BAR09-02	639	627	0	98.12	1.88
9	A/BAR/4/2009	BAR09-04	639	627	0	98.12	1.88
10	A/IRN/17/2009	IRN09-17	639	627	0	98.12	1.88

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/IRN/1/2005 (EF208769)	IRN05-01	639	608	0	95.15	4.85
2	A/IRN/2/87 (EF208770)	IRN87-02	636	537	0	84.43	15.57
3	A/SAU/41/91	SAU91-41	636	537	0	84.43	15.57
4	A/TAI/118/87* (EF208777)	TAI87-AD	636	532	0	83.65	16.35
5	A22/IRQ/24/64 (AJ251474)	IRQ64-24	639	534	0	83.57	16.43
6	A/IRN/22/99 (EF208772)	IRN99-22	636	528	0	83.02	16.98
7	A/SAU/23/86 (EU414536)	SAU86-23	639	530	0	82.94	17.06
8	A/TAI/2/97 (EF208778)	TAI97-02	636	523	0	82.23	17.77
9	A/IRN/1/96 (EF208771)	IRN96-01	638	523	1	81.97	18.03
10	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	639	511	0	79.97	20.03

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV A in Iran in 2009

Batch: WRLFMD/2009/00034

Software: MEGA 4.0

No. of Taxa : 170

Data File : n:\evd\meg\db\fmdva\IRN2009b.meg

Data Title : A Iran 2009

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, 2 September 2009

