

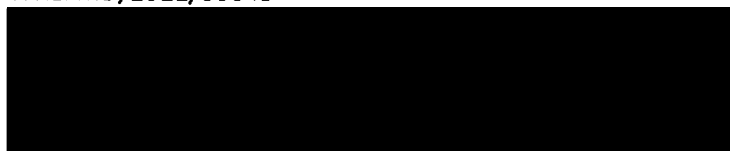


**INSTITUTE FOR ANIMAL HEALTH**  
Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath  
**PIRBRIGHT LABORATORY**  
Ash Road,  
Pirbright,  
Surrey,  
GU24 0NF  
Intn Tel: 00 44 1483 232441  
Tel: 01483 232441 Fax: 01483 232621

## **FMD Genotyping Report**

**Lab Reference WRL Batch Number:** WRLFMD/2011/00045

**Sender Details:**



**Date Received:** 3rd November 2011

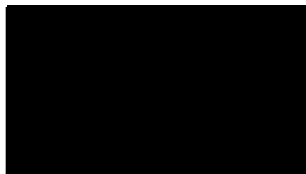
**Country of Origin:** Bahrain

**Date Reported:** 23rd November 2011

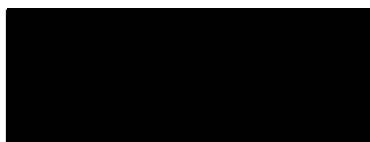
Dear Dr Shawq Al Mana'ei

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:**

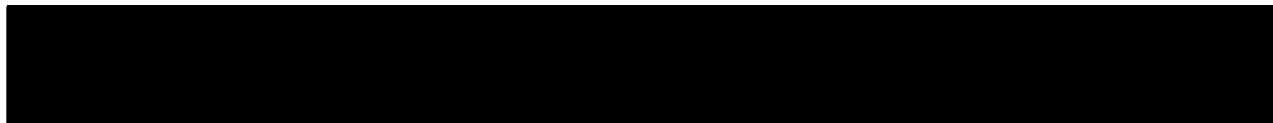


**Official Stamp:**



**Date:**

23/11/11



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: 11 November 2011

FMDV type A

Country: Bahrain

Period: 2011

No. of samples: 1

BATCH: WRLFMD/2011/00045



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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: 11/11/2011
WRLFMD Ref No: BAR/18/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2011/00045	Checked by: D.P. King
Sender Ref: 4	
Location: not given, Bahrain	Topotype: ASIA
Date collected: 12/10/2011	Genotype/strain: Iran-05 <sup>HER-10</sup>
Date received by WRLFMD: 03/11/2011	Sequence filename: BAR11-18.SEQ
Date received for sequencing: 09/11/2011	Date sequence last updated: 11/11/2011
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: A-1C612F/EUR-2B52R	Total no. of comparisons: 1354
	Min. no. of nt for comparison: 600
	Total turn-around time: 8 days
	Sequencing time: 2 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/AFG/20/2011	AFG11-20	639	630	0	98.59	1.41	ASIA	Iran-05 <sup>HER-10</sup>
2	A/AFG/22/2011	AFG11-22	639	630	0	98.59	1.41	ASIA	Iran-05 <sup>HER-10</sup>
3	A/AFG/24/2011	AFG11-24	639	630	0	98.59	1.41	ASIA	Iran-05 <sup>HER-10</sup>
4	A/AFG/25/2011	AFG11-25	639	630	0	98.59	1.41	ASIA	Iran-05 <sup>HER-10</sup>
5	A/AFG/26/2011	AFG11-26	639	630	0	98.59	1.41	ASIA	Iran-05 <sup>HER-10</sup>
6	A/AFG/27/2011	AFG11-27	639	630	0	98.59	1.41	ASIA	Iran-05 <sup>HER-10</sup>
7	A/AFG/29/2011	AFG11-29	639	630	0	98.59	1.41	ASIA	Iran-05 <sup>HER-10</sup>
8	A/IRN/12/2011	IRN11-12	639	630	0	98.59	1.41	ASIA	Iran-05 <sup>HER-10</sup>
9	A/AFG/57/2011	AFG11-57	639	629	0	98.44	1.56	ASIA	Iran-05 <sup>HER-10</sup>
10	A/IRN/134/2010	IRN10134	639	629	0	98.44	1.56	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	627	0	98.12	1.88	ASIA	Iran-05 <sup>HER-10</sup>
2	A/AFG/6/2007	AFG07-06	639	606	0	94.84	5.16	ASIA	Iran-05 <sup>AFG-07</sup>
3	A/IRN/1/2005 (EF208769)	IRN05-01	639	597	0	93.43	6.57	ASIA	Iran-05
4	A/IRN/78/2009	IRN09-78	639	596	0	93.27	6.73	ASIA	Iran-05 <sup>FAR-09</sup>
5	A/BAR/6/2008	BAR08-06	639	594	0	92.96	7.04	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	589	0	92.18	7.82	ASIA	Iran-05 <sup>EZM-07</sup>
9	A/IRN/9/2010	IRN10-09	639	582	0	91.08	8.92	ASIA	Iran-05 <sup>ESF-10</sup>
10	A/IRN/9/2011	IRN11-09	639	582	0	91.08	8.92	ASIA	Iran-05 <sup>QAZ-11</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# Report on FMDV A in Bahrain in 2011

Batch: WRLFMD/2011/00045

◆ indicates viruses in this batch

Software: MEGA 5.0

Analysis

----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 639

No Of Bootstrap Reps = 1000

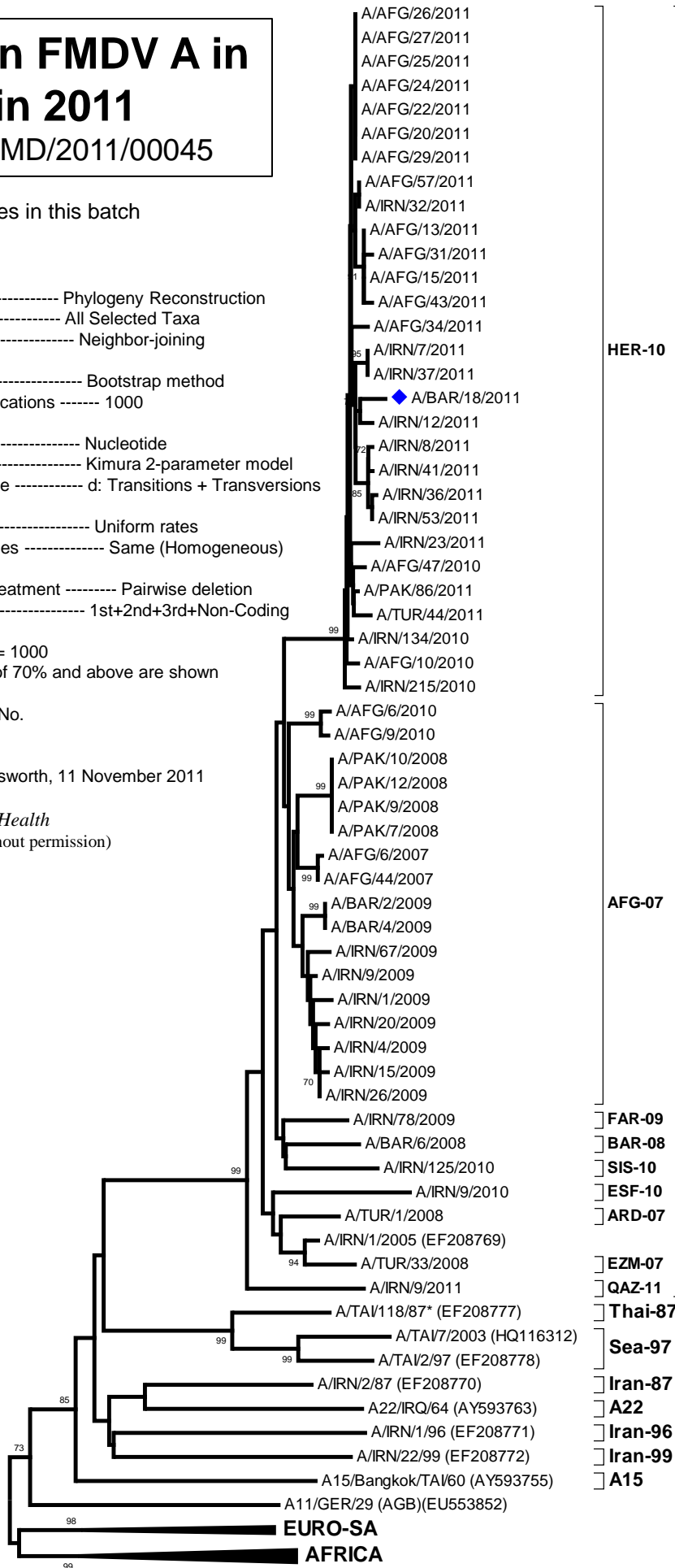
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 11 November 2011

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0.02