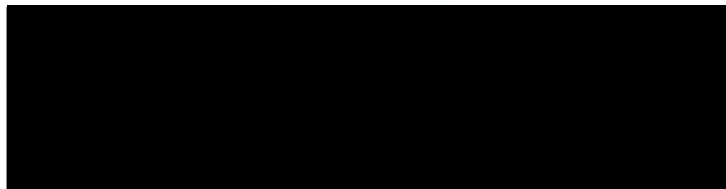




**INSTITUTE FOR ANIMAL HEALTH**  
Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath  
PIRBRIGHT LABORATORY  
Ash Road,  
Pirbright,  
Surrey,  
GU24 0NF  
Intn Tel: 00 44 1483 232441  
Tel: 01483 232441, Fax: 01483 232621

## FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00016  
Sender Details:

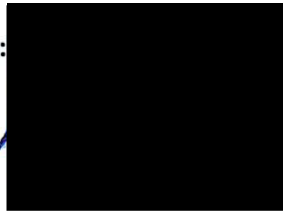


Date Received: 30<sup>th</sup> March 2012  
Country of Origin: BAHRAIN  
Date Reported: 8<sup>th</sup> May 2012

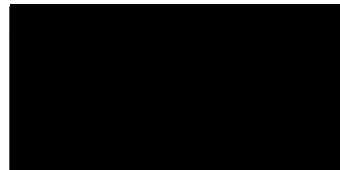
Dear Dr Fajer A Salloom,

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:

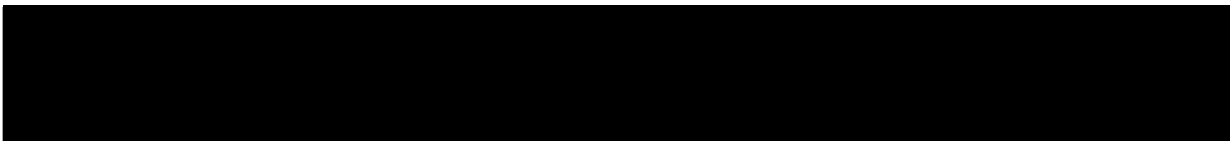


Official Stamp:



Date:

8/5/12



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](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: 2 May 2012

FMDV type O

Country: Bahrain

Period: 2012

No. of samples: 2

BATCH: WRLFMD/2012/00016



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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 02/05/2012
WRLFMD Ref No: BAR/4/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00016	Checked by: D.P. King
Sender Ref: 0565	
Location: Farm 1 Vet Quarantine, Bahrain	Topotype: ME-SA
Date collected: 05/03/2012	Genotype/strain: PanAsia-2 <sup>ANT-10</sup>
Date received by WRLFMD: 30/03/2012	Sequence filename: BAR12-04.SEQ
Date received for sequencing: 24/04/2012	Date sequence last updated: 02/05/2012
Species: Cattle	No. of Nt determined: 639
Material used: RS2	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3271
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 33 days
	Sequencing time: 8 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/BAR/5/2012	BAR12-05	639	639	0	100.00	0.00	ME-SA	PanAsia-2 <sup>ANT-10</sup>
2	O/KUW/2/2012	KUW12-02	639	636	0	99.53	0.47	ME-SA	PanAsia-2 <sup>ANT-10</sup>
3	O/KUW/3/2012	KUW12-03	639	636	0	99.53	0.47	ME-SA	PanAsia-2 <sup>ANT-10</sup>
4	O/KUW/1/2012	KUW12-01	639	629	0	98.44	1.56	ME-SA	PanAsia-2 <sup>ANT-10</sup>
5	O/KUW/10/2011	KUW11-10	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
6	O/KUW/11/2011	KUW11-11	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
7	O/KUW/4/2011	KUW11-04	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
8	O/KUW/5/2011	KUW11-05	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
9	O/KUW/6/2011	KUW11-06	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
10	O/KUW/8/2011	KUW11-08	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-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	O/IRN/88/2009	IRN09-88	639	619	0	96.87	3.13	ME-SA	PanAsia-2 <sup>ANT-10</sup>
2	O/IRN/8/2005	IRN05-08	639	602	0	94.21	5.79	ME-SA	PanAsia-2
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	599	0	93.74	6.26	ME-SA	PanAsia-2 <sup>TER-08</sup>
4	O/IRN/31/2009	IRN09-31	639	597	0	93.43	6.57	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/IRN/18/2010	IRN10-18	639	596	0	93.27	6.73	ME-SA	PanAsia-2 <sup>BAL-09</sup>
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	596	0	93.27	6.73	ME-SA	PanAsia-2 <sup>SAN-09</sup>
7	O/PAK/16/2010	PAK10-16	639	595	0	93.11	6.89	ME-SA	PanAsia-2 <sup>PUN-10</sup>
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	581	0	90.92	9.08	ME-SA	PanAsia
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	568	1	89.03	10.97	ME-SA	Im-2001
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	568	0	88.89	11.11	ME-SA	Ind-2001a

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 02/05/2012
WRLFMD Ref No: BAR/5/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00016	Checked by: D.P. King
Sender Ref: 0556	
Location: Farm 1 Vet Quarantine, Bahrain	Topotype: ME-SA
Date collected: 05/03/2012	Genotype/strain: PanAsia-2 <sup>ANT-10</sup>
Date received by WRLFMD: 30/03/2012	Sequence filename: BAR12-05.SEQ
Date received for sequencing: 24/04/2012	Date sequence last updated: 02/05/2012
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3271
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 33 days
	Sequencing time: 8 days
Comments:	

Most Closely Related Viruses									
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3	O/KUW/3/2012	KUW12-03	639	636	0	99.53	0.47	ME-SA	PanAsia-2 <sup>ANT-10</sup>
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6	O/KUW/11/2011	KUW11-11	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
7	O/KUW/4/2011	KUW11-04	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
8	O/KUW/5/2011	KUW11-05	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
9	O/KUW/6/2011	KUW11-06	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-10</sup>
10	O/KUW/8/2011	KUW11-08	639	628	0	98.28	1.72	ME-SA	PanAsia-2 <sup>ANT-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	O/IRN/88/2009	IRN09-88	639	619	0	96.87	3.13	ME-SA	PanAsia-2 <sup>ANT-10</sup>
2	O/IRN/8/2005	IRN05-08	639	602	0	94.21	5.79	ME-SA	PanAsia-2
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	599	0	93.74	6.26	ME-SA	PanAsia-2 <sup>TER-08</sup>
4	O/IRN/31/2009	IRN09-31	639	597	0	93.43	6.57	ME-SA	PanAsia-2 <sup>FAR-09</sup>
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7	O/PAK/16/2010	PAK10-16	639	595	0	93.11	6.89	ME-SA	PanAsia-2 <sup>PUN-10</sup>
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	581	0	90.92	9.08	ME-SA	PanAsia
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	568	1	89.03	10.97	ME-SA	Im-2001
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	568	0	88.89	11.11	ME-SA	Ind-2001a

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# Report on FMDV O in Bahrain in 2012

Batch: WRLFMD/2012/00016

◆ 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 : 642

No Of Bootstrap Reps = 1000

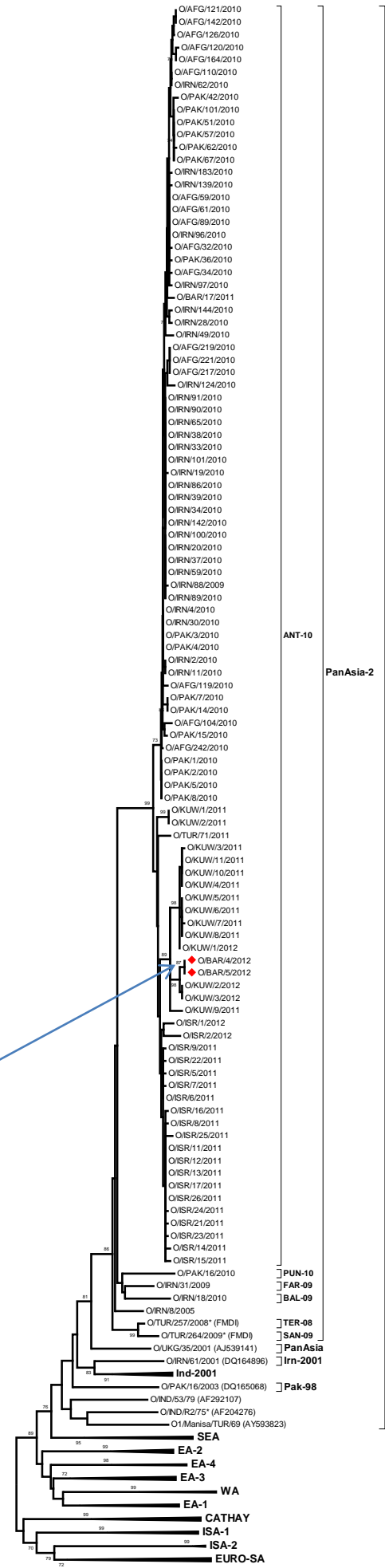
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 02 May 2012

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ANT-10  
PanAsia-2  
ME-SA