

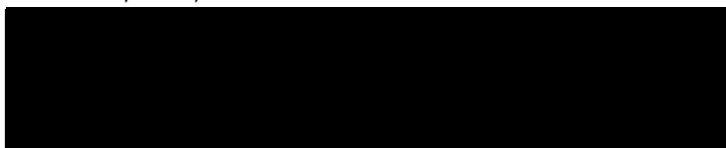


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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00010

Sender Details:



Date Received: 27th February 2012

Country of Origin: Libya

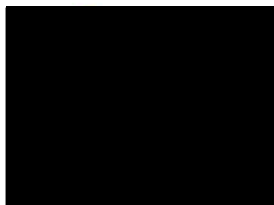
Date Reported: 8th March 2012

Dear Dr Milad Farhat

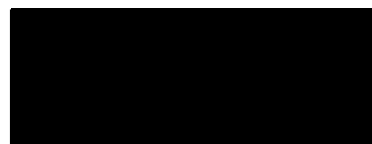
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

<http://www.wrlfmd.org/>

Results Approved By:

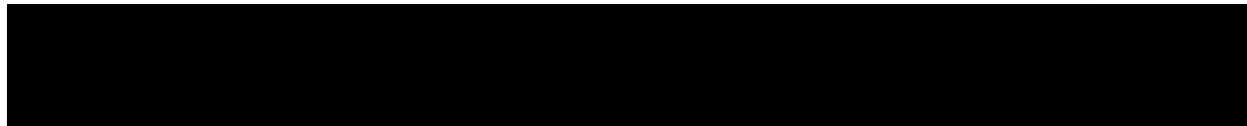


Official Stamp:



Date:

9/3/12 ✓



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. 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: 8 March 2012

FMDV type O

Country: Libya

Period: 2012

No. of samples: 1

BATCH: WRLFMD/2012/00010



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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: 08/03/2012
WRLFMD Ref No: LIB/48/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00010	Checked by: D.P. King
Sender Ref: Q1	
Location: Al Qba, Derrnah, East Province, Libya	Topotype: ME-SA
Date collected: 18/02/2012	Genotype/strain: PanAsia-2 ^{ANT-10}
Date received by WRLFMD: 27/02/2012	Sequence filename: LIB12-48.SEQ
Date received for sequencing: 06/03/2012	Date sequence last updated: 08/03/2012
Species: Cattle	No. of Nt determined: 639
Material used: BTy2	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3233
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 10 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	O/LIB/5/2012	LIB12-05	639	638	0	99.84	0.16	ME-SA	PanAsia-2 ^{ANT-10}
2	O/LIB/25/2011	LIB11-25	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{ANT-10}
3	O/LIB/26/2011	LIB11-26	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{ANT-10}
4	O/LIB/3/2012	LIB12-03	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{ANT-10}
5	O/LIB/33/2011	LIB11-33	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{ANT-10}
6	O/LIB/31/2011	LIB11-31	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{ANT-10}
7	O/LIB/7/2012	LIB12-07	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{ANT-10}
8	O/LIB/1/2012	LIB12-01	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{ANT-10}
9	O/LIB/2/2012	LIB12-02	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{ANT-10}
10	O/LIB/29/2011	LIB11-29	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{ANT-10}
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	O/IRN/88/2009	IRN09-88	639	624	0	97.65	2.35	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	596	0	93.27	6.73	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	595	0	93.11	6.89	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	591	0	92.49	7.51	ME-SA	PanAsia-2 ^{TER-08}
5	O/IRN/18/2010	IRN10-18	639	589	0	92.18	7.82	ME-SA	PanAsia-2 ^{BAL-09}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	587	0	91.86	8.14	ME-SA	PanAsia-2 ^{SAN-09}
7	O/PAK/16/2010	PAK10-16	639	586	0	91.71	8.29	ME-SA	PanAsia-2 ^{PUN-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	583	0	91.24	8.76	ME-SA	PanAsia
9	O/OMN/7/2001 (DQ164941)	OMN01-07	639	570	0	89.20	10.80	ME-SA	Ind-2001b
10	O/IRN/61/2001 (DQ164896)	IRN01-61	638	569	1	89.18	10.82	ME-SA	Irn-2001

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV O in Libya in 2012

Batch: WRLFMD/2012/00009

◆ 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 : 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, 08 March 2012

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