

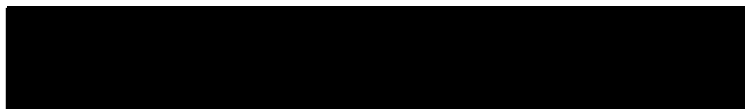


INSTITUTE FOR ANIMAL HEALTH
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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00021

Sender Details:



Date Received: 22nd May 2012

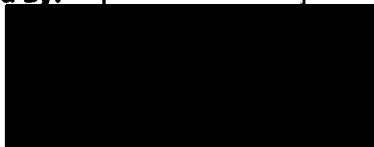
Country of Origin: LIBYA

Date Reported: 11th July 2012

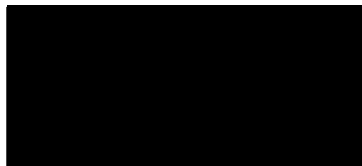
Dear Milad A Farhat,

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:

12/7/12



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: 10 July 2012

FMDV type O

Country: Libya

Period: 2012

No. of samples: 2

BATCH: WRLFMD/2012/00021



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: O	Report date: 10/07/2012
WRLFMD Ref No: LIB/54/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00021	Checked by: D.P. King
Sender Ref: Al HAWARI 1 B	
Location: Al Hawari, Benghazi, Libya	Topotype: EA-3
Date collected: 19/04/2012	Genotype/strain: unnamed
Date received by WRLFMD: 22/05/2012	Sequence filename: LIB12-54.SEQ
Date received for sequencing: 11/06/2012	Date sequence last updated: 10/07/2012
Species: Sheep/goat	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: 3289
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 49 days
	Sequencing time: 29 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/ETH/59/2011	ETH11-59	639	637	0	99.69	0.31	EA-3	unnamed
2	O/ETH/26/2011	ETH11-26	639	636	0	99.53	0.47	EA-3	unnamed
3	O/ETH/28/2011	ETH11-28	639	636	0	99.53	0.47	EA-3	unnamed
4	O/SUD/5/2008 (GU566061)	SUD08-05	639	607	0	94.99	5.01	EA-3	unnamed
5	O/SUD/6/2008 (GU566062)	SUD08-06	639	606	0	94.84	5.16	EA-3	unnamed
6	O/SUD/3/2008 (GU566059)	SUD08-03	639	599	0	93.74	6.26	EA-3	unnamed
7	O/SUD/4/2008 (GU566060)	SUD08-04	639	599	0	93.74	6.26	EA-3	unnamed
8	O/SUD/1/99 (DQ165076)	SUD99-01	639	593	0	92.80	7.20	EA-3	unnamed
9	O/SUD/3/99 (GU566043)	SUD99-03	639	593	0	92.80	7.20	EA-3	unnamed
10	O/SUD/4/99 (GU566044)	SUD99-04	639	593	0	92.80	7.20	EA-3	unnamed
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/SUD/2/86 (DQ165075)	SUD86-02	639	587	0	91.86	8.14	EA-3	unnamed
2	O/ETH/1/2007 (FJ798137)	ETH07-01	639	556	0	87.01	12.99	EA-3	unnamed
3	O/ETH/3/2004 (FJ798109)	ETH04-03	639	550	0	86.07	13.93	EA-3	unnamed
4	O/IND/53/79 (AF292107)	IND79A53	639	550	0	86.07	13.93	ME-SA	unnamed
5	O/MAL/1/98 (DQ165074)	MAL98-01	639	549	0	85.92	14.08	EA-2	unnamed
6	O/TAN/2/2004	TAN04-02	639	549	0	85.92	14.08	EA-2	unnamed
7	O/BHU/3/2009	BHU09-03	639	547	0	85.60	14.40	ME-SA	Ind-2001d
8	O/UGA/3/2002 (DQ165077)	UGA02-03	639	547	0	85.60	14.40	EA-2	unnamed
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	546	1	85.58	14.42	ME-SA	Irn-2001
10	O/K83/79* (AJ303511)	KEN79B83	638	546	1	85.58	14.42	EA-1	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: O WRLFMD Ref No: LIB/74/2012 Batch No: WRLFMD/2012/00021 Sender Ref: Tripoli 23 APRIL 2012 Z1 (Tissue) Location: Enjala, Tripoli, Libya Date collected: 23/04/2012 Date received by WRLFMD: 22/05/2012 Date received for sequencing: 11/06/2012 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 10/07/2012 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ME-SA Genotype/strain: PanAsia-2 ^{ANT-10} Sequence filename: LIB12-74.SEQ Date sequence last updated: 10/07/2012 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3289 Min. no. of nt for comparison: 600 Total turn-around time: 49 days Sequencing time: 29 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/1/2012	LIB12-01	639	633	0	99.06	0.94	ME-SA	PanAsia-2 ^{ANT-10}
2	O/LIB/2/2012	LIB12-02	639	633	0	99.06	0.94	ME-SA	PanAsia-2 ^{ANT-10}
3	O/LIB/3/2012	LIB12-03	639	633	0	99.06	0.94	ME-SA	PanAsia-2 ^{ANT-10}
4	O/LIB/5/2012	LIB12-05	639	632	0	98.90	1.10	ME-SA	PanAsia-2 ^{ANT-10}
5	O/LIB/25/2011	LIB11-25	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
6	O/LIB/26/2011	LIB11-26	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
7	O/LIB/33/2011	LIB11-33	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
8	O/LIB/48/2012	LIB12-48	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
9	O/LIB/31/2011	LIB11-31	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
10	O/LIB/7/2012	LIB12-07	639	630	0	98.59	1.41	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	620	0	97.03	2.97	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	590	0	92.33	7.67	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	589	0	92.18	7.82	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	587	0	91.86	8.14	ME-SA	PanAsia-2 ^{TER-08}
5	O/IRN/18/2010	IRN10-18	639	584	0	91.39	8.61	ME-SA	PanAsia-2 ^{BAL-09}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	584	0	91.39	8.61	ME-SA	PanAsia-2 ^{SAN-09}
7	O/PAK/16/2010	PAK10-16	639	582	0	91.08	8.92	ME-SA	PanAsia-2 ^{PUN-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	575	0	89.98	10.02	ME-SA	PanAsia
9	O/UAE/4/2008	UAE08-04	636	560	0	88.05	11.95	ME-SA	Ind-2001c
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	562	0	87.95	12.05	ME-SA	Ind-2001b

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/2012/00021

◆ indicates viruses in this batch

Software: MEGA 5.0

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, 10 July 2012

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