



**INSTITUTE FOR ANIMAL HEALTH**

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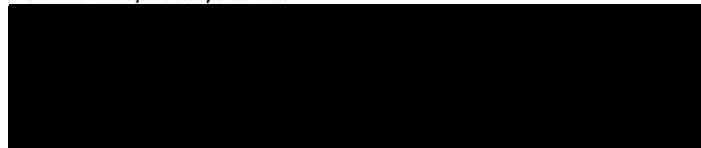
Intn Tel: 00 44 1483 232441

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## FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2011/00007

Sender Details:



Date Received: 9<sup>th</sup> February 2011

Country of Origin: Libya

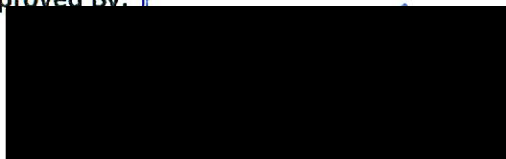
Date Reported: 24<sup>th</sup> February 2011

Dear Dr. Taher Ahmed Maatoug,

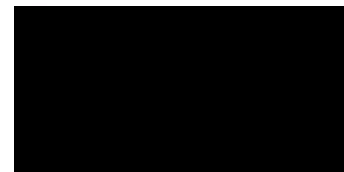
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

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

Results Approved By:



Official Stamp:



Date:

25/2/11



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.wilson@bbsrc.ac.uk](mailto:elizabeth.wilson@bbsrc.ac.uk))

# FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

## Genotyping Report

Report Date for this Batch: 24 February 2011

FMDV type O (only genome detected)

Country: Libya

Period: 2011

No. of samples: 1

BATCH: WRLFMD/2011/00007



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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/6/2011 Batch No: WRLFMD/2011/00007 Sender Ref: C3 Location: Bier Muamer, Zawiyah, Zawiyah, Libya Date collected: 31/01/2011 Date received by WRLFMD: 09/02/2011 Date received for sequencing: 18/02/2011 Species: Cattle Material used: OS Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 23/02/2011 Reported by: N.J. Knowles Checked by: V. Mioulet Topotype: ME-SA Genotype/strain: PanAsia-2 <sup>ANT-10</sup> Sequence filename: LIB11-06.SEQ Date sequence last updated: 23/02/2011 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2667 Min. no. of nt for comparison: 600 Total turn-around time: 14 days Sequencing time: 5 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/4/2010	LIB10-04	639	636	0	99.53	0.47	ME-SA	PanAsia-2 <sup>ANT-10</sup>
2	O/PAK/100/2010	PAK10100	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
3	O/PAK/53/2010	PAK10-53	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
4	O/PAK/54/2010	PAK10-54	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
5	O/PAK/60/2010	PAK10-60	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
6	O/PAK/61/2010	PAK10-61	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
7	O/PAK/68/2010	PAK10-68	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
8	O/PAK/71/2010	PAK10-71	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
9	O/PAK/75/2010	PAK10-75	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
10	O/PAK/76/2010	PAK10-76	639	633	0	99.06	0.94	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	630	0	98.59	1.41	ME-SA	PanAsia-2 <sup>ANT-10</sup>
2	O/IRN/8/2005	IRN05-08	639	598	0	93.58	6.42	ME-SA	PanAsia-2
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	598	0	93.58	6.42	ME-SA	PanAsia-2 <sup>TER-08</sup>
4	O/IRN/31/2009	IRN09-31	639	596	0	93.27	6.73	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/TUR/264/2009* (FMDI)	TUR09-AK	639	593	0	92.80	7.20	ME-SA	PanAsia-2 <sup>SAN-09</sup>
6	O/IRN/18/2010	IRN10-18	639	592	0	92.64	7.36	ME-SA	PanAsia-2 <sup>BAL-09</sup>
7	O/PAK/16/2010	PAK10-16	639	590	0	92.33	7.67	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/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	567	1	88.87	11.13	ME-SA	Irn-2001

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v3.11

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# Report on FMDV O in Libya in 2011

Batch: WRLFMD/2011/00007

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, 24 February 2011

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