WRLFMD

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FMD Sequencing Report

Lab Reference WRL Batch Number:	WRLFMD/2011/00007
Sender Details:	[redacted]
Date Received:	9th February 2011
Country of Origin:	Libya
Date Reported:	24th 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: [redacted]

Official Stamp: [redacted]

Date: 25/2/11

[redacted]

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)

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

FAO World Reference Laboratory for FMD Genotyping Report

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$^{\text{ANT-10}}$
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$^{\text{ANT-10}}$
2	O/PAK/100/2010	PAK10100	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
3	O/PAK/53/2010	PAK10-53	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
4	O/PAK/54/2010	PAK10-54	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
5	O/PAK/60/2010	PAK10-60	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
6	O/PAK/61/2010	PAK10-61	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
7	O/PAK/68/2010	PAK10-68	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
8	O/PAK/71/2010	PAK10-71	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
9	O/PAK/75/2010	PAK10-75	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
10	O/PAK/76/2010	PAK10-76	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$

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	630	0	98.59	1.41	ME-SA	PanAsia-2$^{\text{ANT-10}}$
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$^{\text{TER-08}}$
4	O/IRN/31/2009	IRN09-31	639	596	0	93.27	6.73	ME-SA	PanAsia-2$^{\text{FAR-09}}$
5	O/TUR/264/2009* (FMDI)	TUR09-AK	639	593	0	92.80	7.20	ME-SA	PanAsia-2$^{\text{SAN-09}}$
6	O/IRN/18/2010	IRN10-18	639	592	0	92.64	7.36	ME-SA	PanAsia-2$^{\text{BAL-09}}$
7	O/PAK/16/2010	PAK10-16	639	590	0	92.33	7.67	ME-SA	PanAsia-2$^{\text{PUN-10}}$
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

Report on FMDV O in Libya in 2011

Batch: WRLFMD/2011/00007

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, 24 February 2011