

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

Genotyping Report

Report Date for this Batch: 25 March 2013

FMDV type O

Country: United Arab Emirates

Period: 2013

No. of samples: 2

BATCH: WRLFMD/2013/00004



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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: UAE/1/2013 Batch No: WRLFMD/2013/00004 Sender Ref: D199/13 Location: Abu Dhabi, United Arab Emirates Date collected: 29/01/2013 Date received by WRLFMD: 07/03/2013 Date received for sequencing: 19/03/2013 Species: Scimitar-horned Oryx (<i>Oryx dammah</i>) Material used: BTy1 12/03/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 22/03/2013 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ME-SA Genotype/strain: PanAsia-2 ^{ANT-10} Sequence filename: UAE13-01.SEQ Date sequence last updated: 22/03/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3476 Min. no. of nt for comparison: 600 Total turn-around time: 15 days Sequencing time: 3 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/UAE/2/2013	UAE13-02	639	639	0	100.00	0.00	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/13/2012	IRN12-13	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
3	O/IRN/11/2013	IRN13-11	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
4	O/IRN/9/2013	IRN13-09	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
5	O/IRN/8/2013	IRN13-08	639	626	0	97.97	2.03	ME-SA	PanAsia-2 ^{ANT-10}
6	O/IRN/36/2012	IRN12-36	639	623	0	97.50	2.50	ME-SA	PanAsia-2 ^{ANT-10}
7	O/IRN/35/2010	IRN10-35	639	614	0	96.09	3.91	ME-SA	PanAsia-2 ^{ANT-10}
8	O/AFG/242/2010	AFG10242	630	605	9	96.03	3.97	ME-SA	PanAsia-2 ^{ANT-10}
9	O/IRN/55/2010	IRN10-55	639	613	0	95.93	4.07	ME-SA	PanAsia-2 ^{ANT-10}
10	O/PAK/1/2010	PAK10-01	639	613	0	95.93	4.07	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	610	0	95.46	4.54	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	589	0	92.18	7.82	ME-SA	PanAsia-2 ^{FAR-09}
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	589	0	92.18	7.82	ME-SA	PanAsia-2 ^{TER-08}
4	O/TUR/264/2009* (FMDI)	TUR09-AK	639	587	0	91.86	8.14	ME-SA	PanAsia-2 ^{SAN-09}
5	O/IRN/18/2010	IRN10-18	639	586	0	91.71	8.29	ME-SA	PanAsia-2 ^{BAL-09}
6	O/IRN/8/2005	IRN05-08	639	584	0	91.39	8.61	ME-SA	PanAsia-2
7	O/PAK/16/2010	PAK10-16	639	580	0	90.77	9.23	ME-SA	PanAsia-2 ^{PUN-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	574	0	89.83	10.17	ME-SA	PanAsia
9	O/PAK/16/2003 (DQ165068)	PAK03-16	639	559	0	87.48	12.52	ME-SA	Pak-98
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	558	0	87.32	12.68	ME-SA	Ind-2001a

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O	Report date: 22/03/2013
WRLFMD Ref No: UAE/2/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00004	Checked by: D.P. King
Sender Ref: D199/13	
Location: Abu Dhabi, United Arab Emirates	Topotype: ME-SA
Date collected: 29/01/2013	Genotype/strain: PanAsia-2 ^{ANT-10}
Date received by WRLFMD: 07/03/2013	Sequence filename: UAE13-02.SEQ
Date received for sequencing: 19/03/2013	Date sequence last updated: 22/03/2013
Species: Scimitar-horned Oryx (<i>Oryx dammah</i>)	No. of Nt determined: 639
Material used: BTy1 12/03/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3476
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 15 days
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Report on FMDV O in the United Arab Emirates in 2013

Batch: WRLFMD/2013/00004

◆ indicates viruses in this batch

Software: MEGA 5.1

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, K. Bachanek-Bankowska & J. Wadsworth,
25 March 2013

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