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

Genotyping Report

Report Date for this Batch: 3 March 2014

FMDV type O
Country: United Arab Emirates
Period: 2014
No. of samples: 2

BATCH: WRLFMD/2014/00007

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 01/03/2014
WRLFMD Ref No: UAE/1/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00007	Checked by: K. Bachanek-Bankowska
Sender Ref: D63/14 A	
Location: Al Warsan, Al Aiban, Abu Dhabi, United Arab Emirates	Topotype: ME-SA
Date collected: 08/01/2014	Genotype/strain: Ind-2001d
Date received by WRLFMD: 17/02/2014	Sequence filename: UAE14-01.SEQ
Date received for sequencing: 27/02/2014	Date sequence last updated: 01/03/2014
Species: Gazelle	No. of Nt determined: 639
Material used: BTy1 25/02/2002	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3799
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 12 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/UAE/2/2014	UAE14-02	639	639	0	100.00	0.00	ME-SA	Ind-2001d
2	O/IND205/2013* (PD-FMD)	IND13-AF	639	637	0	99.69	0.31	ME-SA	Ind-2001d
3	O/IND189/2013* (PD-FMD)	IND13-AE	639	636	0	99.53	0.47	ME-SA	Ind-2001d
4	O/IND219/2013* (PD-FMD)	IND13-AG	639	636	0	99.53	0.47	ME-SA	Ind-2001d
5	O/NEP/18/2013	NEP13-18	639	636	0	99.53	0.47	ME-SA	Ind-2001d
6	O/NEP/3/2013	NEP13-03	639	636	0	99.53	0.47	ME-SA	Ind-2001d
7	O/IND222/2013* (PD-FMD)	IND13-AH	639	635	0	99.37	0.63	ME-SA	Ind-2001d
8	O/NEP/11/2013	NEP13-11	639	635	0	99.37	0.63	ME-SA	Ind-2001d
9	O/NEP/12/2013	NEP13-12	639	635	0	99.37	0.63	ME-SA	Ind-2001d
10	O/NEP/2/2014	NEP14-02	639	635	0	99.37	0.63	ME-SA	Ind-2001d

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/BHU/3/2009	BHU09-03	639	614	0	96.09	3.91	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	591	0	92.49	7.51	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	590	0	92.33	7.67	ME-SA	Ind-2001a
4	O/UAE/4/2008	UAE08-04	636	576	0	90.57	9.43	ME-SA	Ind-2001c
5	O/UKG/35/2001 (AJ539141)	UKG01-35	639	576	0	90.14	9.86	ME-SA	PanAsia
6	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2$^{\text{FAR-09}}$
7	O/IRN/18/2010	IRN10-18	639	572	0	89.51	10.49	ME-SA	PanAsia-2$^{\text{BAL-09}}$
8	O/IRN/8/2005	IRN05-08	639	570	0	89.20	10.80	ME-SA	PanAsia-2
9	O/PAK/16/2003 (DQ165068)	PAK03-16	639	569	0	89.05	10.95	ME-SA	Pak-98
10	O/TUR/257/2008* (FMDI)	TUR08-AD	639	569	0	89.05	10.95	ME-SA	PanAsia-2$^{\text{TER-08}}$

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: UAE/2/2014
Batch No: WRLFMD/2014/00007
Sender Ref: D63/14 B
Location: Al Warsan, Al Aiban, Abu Dhabi, United Arab Emirates
Date collected: 08/01/2014
Date received by WRLFMD: 17/02/2014
Date received for sequencing: 27/02/2014
Species: Gazelle
Material used: BTy1 25/02/2002
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 01/03/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: ME-SA
Genotype/strain: Ind-2001d
Sequence filename: UAE14-02.SEQ
Date sequence last updated: 01/03/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3799
Min. no. of nt for comparison: 600
Total turn-around time: 12 days
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Assembled with Report Generator v4.1

Report on FMDV O in the United Arab Emirates in 2014

Batch: WRLFMD/2014/00007

◆ indicates viruses in this batch

Software: MEGA 6.06
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 & K. Bachanek-Bankowska,
03 March 2014