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

Genotyping Report

Report Date for this Batch: 3 March 2014

FMDV type O
Country: Saudi Arabia
Period: 2014
No. of samples: 1

BATCH: WRLFMD/2014/00005

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: SAU/1/2014
Batch No: WRLFMD/2014/00005
Sender Ref: Almarai FMDV sample epithelium 12/2/14
Location: Haradh Rd, Al Kharj, Central Region, Saudi Arabia
Date collected: 01/02/2014
Date received by WRLFMD: 17/02/2014
Date received for sequencing: 24/02/2014
Species: Cattle
Material used: BTy1 19/02/2014
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: SAU14-01.SEQ
Date sequence last updated: 26/02/2014
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
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/SAU/6/2013	SAU13-06	639	636	0	99.53	0.47	ME-SA	Ind-2001d
2	O/SAU/7/2013	SAU13-07	639	636	0	99.53	0.47	ME-SA	Ind-2001d
3	O/SAU/8/2013	SAU13-08	639	636	0	99.53	0.47	ME-SA	Ind-2001d
4	O/SAU/3/2013	SAU13-03	639	634	0	99.22	0.78	ME-SA	Ind-2001d
5	O/SAU/4/2013	SAU13-04	639	634	0	99.22	0.78	ME-SA	Ind-2001d
6	O/IND127/2013* (PD-FMD)	IND13-AC	639	633	0	99.06	0.94	ME-SA	Ind-2001d
7	O/SAU/1/2013	SAU13-01	639	633	0	99.06	0.94	ME-SA	Ind-2001d
8	O/IND179/2013* (PD-FMD)	IND13-AD	639	632	0	98.90	1.10	ME-SA	Ind-2001d
9	O/IND52/2013* (PD-FMD)	IND13-AB	639	632	0	98.90	1.10	ME-SA	Ind-2001d
10	O/LIB/1/2013	LIB13-01	639	629	0	98.44	1.56	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	613	0	95.93	4.07	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	586	0	91.71	8.29	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	583	0	91.24	8.76	ME-SA	Ind-2001a
4	O/UAE/4/2008	UAE08-04	636	575	0	90.41	9.59	ME-SA	Ind-2001c
5	O/IRN/31/2009	IRN09-31	639	574	0	89.83	10.17	ME-SA	PanAsia-2$^{\text{FAR-09}}$
6	O/IRN/8/2005	IRN05-08	639	572	0	89.51	10.49	ME-SA	PanAsia-2
7	O/PAK/16/2010	PAK10-16	639	571	0	89.36	10.64	ME-SA	PanAsia-2$^{\text{PUN-10}}$
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	570	0	89.20	10.80	ME-SA	PanAsia
9	O/IRN/18/2010	IRN10-18	639	568	0	88.89	11.11	ME-SA	PanAsia-2$^{\text{BAL-09}}$
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 v4.1

Report on FMDV O in Saudi Arabia in 2014

Batch: WRLFMD/2014/00005

◆ 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