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

Genotyping Report

Report Date for this Batch: 8 August 2014

FMDV type O
Country: Republic of Korea
Period: 2014
No. of samples: 1

BATCH: WRLFMD/2014/00027

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: SKR/6/2014
Batch No: WRLFMD/2014/00027
Sender Ref: 2014-0001-06
Location: Bian-Myeon,Uiseong-Gun,Gyeongbuk,
Republic of Korea.
Date collected: 23/07/2014
Date received by WRLFMD: 31/07/2014
Date received for sequencing: 06/08/2014
Species: Pig 6-3
Material used: RS1 02/08/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 08/08/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: SEA
Genotype/strain: Mya-98
Sequence filename: SKR14-06.SEQ
Date sequence last updated: 08/08/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3937
Min. no. of nt for comparison: 600
Total turn-around time: 8 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/SKR/01/2014* (APQA)	SKR14-AA	639	639	0	100	0	SEA	Mya-98
2	O/Primorskiy/RUS/2014 (ARRIAH)	RUS14-AD	639	619	0	96.87	3.13	SEA	Mya-98
3	O/GZ-MT/CHA/2013 (KJ646655)	CHA13-AP	639	617	0	96.56	3.44	SEA	Mya-98
4	O/HKN/13/2010	HKN10-13	639	612	0	95.77	4.23	SEA	Mya-98
5	O/HKN/14/2010	HKN10-14	639	612	0	95.77	4.23	SEA	Mya-98
6	O/HKN/15/2010	HKN10-15	639	612	0	95.77	4.23	SEA	Mya-98
7	O/HKN/7/2010 (JQ070303)	HKN10-07	639	612	0	95.77	4.23	SEA	Mya-98
8	O/HKN/8/2010	HKN10-08	639	612	0	95.77	4.23	SEA	Mya-98
9	O/HKN/10/2010	HKN10-10	639	611	0	95.62	4.38	SEA	Mya-98
10	O/HKN/11/2010	HKN10-11	639	611	0	95.62	4.38	SEA	Mya-98

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/MYA/7/98 (DQ164925)	MYA98-07	639	584	0	91.39	8.61	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	564	0	88.26	11.74	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	541	0	84.66	15.34	ME-SA	unnamed
4	O/IRN/8/2005	IRN05-08	639	534	0	83.57	16.43	ME-SA	PanAsia-2
5	O/ETH/3/2004 (FJ798109)	ETH04-03	639	531	0	83.10	16.90	EA-3	unnamed
6	O/PAK/16/2010	PAK10-16	639	531	0	83.10	16.90	ME-SA	PanAsia-2^{PUN-10}
7	O/CAM/3/98 (AJ294910)	CAM98-03	639	530	0	82.94	17.06	SEA	Cam-94
8	O/TUR/257/2008* (FMDI)	TUR08-AD	639	529	0	82.79	17.21	ME-SA	PanAsia-2^{TER-08}
9	O/TUR/264/2009* (FMDI)	TUR09-AK	639	529	0	82.79	17.21	ME-SA	PanAsia-2^{SAN-09}
10	O/IRN/31/2009	IRN09-31	639	528	0	82.63	17.37	ME-SA	PanAsia-2^{FAR-09}

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in South Korea in 2014

Batch: WRLFMD/2014/00027

◆ 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,
08 August 2014