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

Genotyping Report

Report Date for this Batch: 4 December 2014

FMDV type O
Country: Republic of Korea
Period: 2014
No. of sequences: 1 (VP1)
Originator: Kwang-Nyeong Lee, Foot-and-Mouth Disease Division, Animal and Plant Quarantine Agency, Minstry of Agriculture, Food and Rural Affairs, Republic of Korea.

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: JC/CB/ROK/2014
Batch No: WRLMEG/2014/00038
Sender Ref: O/JC/CB/ROK
Location: Jincheon-Gun, Chungbuk, Republic of Korea
Date collected: 03/12/2014
Date received by WRLFMD: 04/12/2014
Date received for sequencing: n/a
Species: Pigs
Material used: not known
Region sequenced: VP1
RT-PCR primers: Not known

Report date: 04/12/2014
Reported by: N.J. Knowles
Checked by: D.P. King

Topotype: SEA
Genotype/strain: Mya-98
Sequence filename: SKR14-AB.SEQ
Date sequence last updated: 04/12/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 4096
Min. no. of nt for comparison: 600
Total turn-around time: 0 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/GZ-MT/CHA/2013 (KJ646655)	CHA13-AP	639	621	0	97.18	2.82	SEA	Mya-98
2	O/Primorskiy/RUS/2014 (ARRIAH)	RUS14-AD	639	619	0	96.87	3.13	SEA	Mya-98
3	O/SKR/01/2014* (APQA)	SKR14-AA	639	617	0	96.56	3.44	SEA	Mya-98
4	O/SKR/6/2014	SKR14-06	639	617	0	96.56	3.44	SEA	Mya-98
5	O/HKN/10/2010	HKN10-10	639	615	0	96.24	3.76	SEA	Mya-98
6	O/HKN/11/2010	HKN10-11	639	615	0	96.24	3.76	SEA	Mya-98
7	O/HKN/12/2010	HKN10-12	639	615	0	96.24	3.76	SEA	Mya-98
8	O/HKN/9/2010 (JQ070304)	HKN10-09	639	615	0	96.24	3.76	SEA	Mya-98
9	O/MY/CHA/2010 (HQ652079)	CHA10-AU	639	615	0	96.24	3.76	SEA	Mya-98
10	O/SKR/4/2010 (JQ070320)	SKR10-04	639	615	0	96.24	3.76	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	586	0	91.71	8.29	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	563	0	88.11	11.89	SEA	unnamed
3	O/PAK/16/2010	PAK10-16	639	535	0	83.72	16.28	ME-SA	PanAsia-2$^{\text{PUN-10}}$
4	O/IND/R2/75* (AF204276)	IND75--A	639	534	0	83.57	16.43	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	533	0	83.41	16.59	ME-SA	PanAsia-2
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	532	0	83.26	16.74	ME-SA	PanAsia-2$^{\text{TER-08}}$
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	531	0	83.10	16.90	ME-SA	PanAsia-2$^{\text{SAN-09}}$
8	O/UAE/4/2008 (KM921876)	UAE08-04	636	528	0	83.02	16.98	ME-SA	Ind-2001c
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	530	0	82.94	17.06	ME-SA	PanAsia
10	O/ETH/3/2004 (FJ798109)	ETH04-03	639	529	0	82.79	17.21	EA-3	unnamed

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in the Republic of Korea in 2014

Batch: WRLMEG/2014/00038

◆ 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,
04 December 2014