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

Genotyping Report

Report Date for this Batch: 17 January 2016

FMDV type O
Country: Republic of Korea (South Korea)
Period: 2016
No. of sequences: 1 (VP1)
Originator: [redacted]

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: Gimje/KOR/2016*
Batch No: WRLMEG/2016/00001
Sender Ref: Gimje/KOR/2016
Location: Gimje, Jeonbuk, South Korea, Republic of
Date collected: 11/01/2016
Date received by WRLFMD: 13/01/2016
Date received for sequencing:
Species: Pig
Material used:
Region sequenced: VP1
RT-PCR primers:

Report date: 17/01/2016
Reported by: N.J. Knowles
Checked by: D.P. King

Topotype: SEA
Genotype/strain: Mya-98
Sequence filename: SKR16-AA.SEQ
Date sequence last updated: 17/01/2016
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 4192
Min. no. of nt for comparison: 600
Total turn-around time: 4 days
Sequencing time: Not known 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/JC/CB/ROK (APQA)	SKR14-AB	639	633	0	99.06	0.94	SEA	Mya-98
2	O/SKR/14/2014	SKR14-14	639	633	0	99.06	0.94	SEA	Mya-98
3	O/SKR/16/2014	SKR14-16	639	633	0	99.06	0.94	SEA	Mya-98
4	O/SKR/18/2014	SKR14-18	639	633	0	99.06	0.94	SEA	Mya-98
5	O/SKR/12/2014	SKR14-12	639	632	0	98.90	1.10	SEA	Mya-98
6	O/GZ-MT/CHA/2013 (KJ646655)	CHA13-AP	639	615	0	96.24	3.76	SEA	Mya-98
7	O/Primorskiy/RUS/2014 (ARRIAH)	RUS14-AD	639	615	0	96.24	3.76	SEA	Mya-98
8	O/SKR/01/2014* (APQA)	SKR14-AA	639	612	0	95.77	4.23	SEA	Mya-98
9	O/SKR/6/2014	SKR14-06	639	612	0	95.77	4.23	SEA	Mya-98
10	O/HKN/10/2010	HKN10-10	639	609	0	95.31	4.69	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	583	0	91.24	8.76	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	564	0	88.26	11.74	SEA	unnamed
3	O/PAK/16/2010	PAK10-16	639	536	0	83.88	16.12	ME-SA	PanAsia-2$^{\text{PUN-10}}$
4	O/IND/R2/75* (AF204276)	IND75--A	639	535	0	83.72	16.28	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	532	0	83.26	16.74	ME-SA	PanAsia-2
6	O/UAE/4/2008 (KM921876)	UAE08-04	636	529	0	83.18	16.82	ME-SA	Ind-2001c
7	O/TUR/257/2008* (FMDI)	TUR08-AD	639	531	0	83.10	16.90	ME-SA	PanAsia-2$^{\text{TER-08}}$
8	O/ETH/3/2004 (FJ798109)	ETH04-03	639	530	0	82.94	17.06	EA-3	unnamed
9	O/IRN/31/2009	IRN09-31	639	530	0	82.94	17.06	ME-SA	PanAsia-2$^{\text{FAR-09}}$
10	O/TUR/264/2009* (FMDI)	TUR09-AK	639	530	0	82.94	17.06	ME-SA	PanAsia-2$^{\text{SAN-09}}$

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in South Korea in 2016

Batch: WRLMEG/2016/00001

◆ 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,
17 January 2016