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

Genotyping Report

Report Date for this Batch: 21 December 2014

FMDV type O
Country: Hong Kong SAR
Period: 2014
No. of samples: 1

BATCH: WRLFMD/2014/00039

FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

Serotype: O
WRLFMD Ref No: HKN/15/2014
Batch No: WRLFMD/2014/00039
Sender Ref: 14-18295, FMD 10/14
Location: Sheung Shui, New Territories, Hong Kong SAR
Date collected: 25/11/2014
Date received by WRLFMD: 11/12/2014
Date received for sequencing: 17/12/2014
Species: Pig
Material used: RS1 13/12/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 21/12/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: CATHAY
Genotype/strain: unnamed
Sequence filename: HKN14-15.SEQ
Date sequence last updated: 19/12/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 4105
Min. no. of nt for comparison: 600
Total turn-around time: 10 days
Sequencing time: 4 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/HKN/11/2014	HKN14-11	639	634	0	99.22	0.78	CATHAY	unnamed
2	O/HKN/4/2014	HKN14-04	639	632	0	98.90	1.10	CATHAY	unnamed
3	O/HKN/6/2014	HKN14-06	639	632	0	98.90	1.10	CATHAY	unnamed
4	O/HKN/13/2014	HKN14-13	639	631	0	98.75	1.25	CATHAY	unnamed
5	O/HKN/5/2014	HKN14-05	639	631	0	98.75	1.25	CATHAY	unnamed
6	O/HKN/7/2014	HKN14-07	639	630	0	98.59	1.41	CATHAY	unnamed
7	O/HKN/8/2014	HKN14-08	639	630	0	98.59	1.41	CATHAY	unnamed
8	O/HKN/1/2013 (KM243172)	HKN13-01	639	618	0	96.71	3.29	CATHAY	unnamed
9	O/HKN/3/2011 (KM243165)	HKN11-03	639	618	0	96.71	3.29	CATHAY	unnamed
10	O/HKN/5/2011 (KM243167)	HKN11-05	639	618	0	96.71	3.29	CATHAY	unnamed

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/Yunlin/TAW/97 (AF308157)	TAW97--B	639	569	0	89.05	10.95	CATHAY	unnamed
2	O/PHI/7/96 (AJ294926;KM243058)	PHI96-07	639	566	0	88.58	11.42	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	637	547	2	85.87	14.13	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	521	2	81.79	18.21	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	639	512	0	80.13	19.87	ME-SA	unnamed
6	O/TAN/2/2004 (KF561679)	TAN04-02	639	512	0	80.13	19.87	EA-2	unnamed
7	O/UGA/17/98 (HM211075)	UGA98-17	639	510	0	79.81	20.19	EA-4	unnamed
8	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	510	0	79.81	20.19	ME-SA	unnamed
9	O/MAL/1/98 (DQ165074)	MAL98-01	639	509	0	79.66	20.34	EA-2	unnamed
10	O/UGA/3/2002 (DQ165077)	UGA02-03	639	509	0	79.66	20.34	EA-2	unnamed

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in Hong Kong SAR in 2014

Batch: WRLFMD/2014/00039

◆ 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,
21 December 2014