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

Genotyping Report

Report Date for this Batch: 10 June 2014

FMDV type O
Country: People's Republic of China
Period: 2013
No. of sequences: 1 (VP1)
Originator: Sequences deposited on GenBank by the College of Animal Science, Guizhou University, Xueshi Road, Guiyang, Guizhou 550025, P.R. China.

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 09/06/2014
WRLFMD Ref No: GZ-MT/CHA/2013	Reported by: N.J. Knowles
Batch No: WRLMEG/2014/00012	Checked by: K. Bachanek-Bankowska
Sender Ref: GZ-MT	
Location: GuiZhou Province, China	Topotype: SEA
Date collected: 15/03/2013	Genotype/strain: Mya-98
Date received by WRLFMD: 07/06/2014	Sequence filename: CHA13-AP.SEQ
Date received for sequencing: n/a	Date sequence last updated: 09/06/2014
Species: Swine	No. of Nt determined: 639
Material used: Not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: Not known	Total no. of comparisons: 3846
	Min. no. of nt for comparison: 600
	Total turn-around 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/MY/CHA/2010 (HQ652079)	CHA10-AU	639	623	0	97.5	2.5	SEA	Mya-98
2	O/VIT/NCVD-9/2010 (NVRQS)	VIT10-AB	639	623	0	97.5	2.5	SEA	Mya-98
3	O/VN/LC169/2009 (HM055510)	VIT09-AQ	639	623	0	97.5	2.5	SEA	Mya-98
4	O/VN/YB09/2010 (HQ260719)	VIT10-AM	639	623	0	97.5	2.5	SEA	Mya-98
5	O/VIT/NCVD-8/2010 (NVRQS)	VIT10-AA	639	622	0	97.34	2.66	SEA	Mya-98
6	O/VN/YB10/2010 (HQ260720)	VIT10-AN	639	622	0	97.34	2.66	SEA	Mya-98
7	O/GZ/CHA/2010 (JN998086)	CHA10-AY	639	621	0	97.18	2.82	SEA	Mya-98
8	O/VN/YB08/2010 (HQ260718)	VIT10-AL	639	621	0	97.18	2.82	SEA	Mya-98
9	O/33-P/CHA/2010 (JQ973889)	CHA10-BA	639	620	0	97.03	2.97	SEA	Mya-98
10	O/GSLX/CHA/2010 (JQ900581)	CHA10-AZ	639	620	0	97.03	2.97	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	594	0	92.96	7.04	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	571	0	89.36	10.64	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	540	0	84.51	15.49	ME-SA	unnamed
4	O/CAM/3/98 (AJ294910)	CAM98-03	639	539	0	84.35	15.65	SEA	Cam-94
5	O/PAK/16/2010	PAK10-16	639	539	0	84.35	15.65	ME-SA	PanAsia-2^{PUN-10}
6	O/ETH/3/2004 (FJ798109)	ETH04-03	639	536	0	83.88	16.12	EA-3	unnamed
7	O/IRN/8/2005	IRN05-08	639	536	0	83.88	16.12	ME-SA	PanAsia-2
8	O/TUR/264/2009* (FMDI)	TUR09-AK	639	534	0	83.57	16.43	ME-SA	PanAsia-2^{SAN-09}
9	O/IRN/18/2010	IRN10-18	639	533	0	83.41	16.59	ME-SA	PanAsia-2^{BAL-09}
10	O/IRN/88/2009	IRN09-88	639	533	0	83.41	16.59	ME-SA	PanAsia-2^{ANT-10}

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in P.R. China in 2013

Batch: WRLMEG/2014/00012

◆ 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,
10 June 2014