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

Genotyping Report

Report Date for this Batch: 7 August 2014

FMDV type O
Country: Thailand
Period: 2013
No. of samples: 2

BATCH: WRLFMD/2014/00022

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: TAI/10/2013
Batch No: WRLFMD/2014/00022
Sender Ref: 27/13 R3B2
Location: Ratchaburi Province, Thailand
Date collected: 01/10/2013
Date received by WRLFMD: 19/06/2014
Date received for sequencing: 23/07/2014
Species: Cattle
Material used: BTy1 17/07/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 07/08/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: SEA
Genotype/strain: Mya-98
Sequence filename: TAI13-10.SEQ
Date sequence last updated: 05/08/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3936
Min. no. of nt for comparison: 600
Total turn-around time: 49 days
Sequencing time: 15 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/TAI/11/2013	TAI13-11	639	635	0	99.37	0.63	SEA	Mya-98
2	O/TAI/2/2010	TAI10-02	639	623	0	97.50	2.50	SEA	Mya-98
3	O/TAI/27/2009	TAI09-27	639	623	0	97.50	2.50	SEA	Mya-98
4	O/TAI/5/2010	TAI10-05	639	623	0	97.50	2.50	SEA	Mya-98
5	O/TAI/3/2010	TAI10-03	639	622	0	97.34	2.66	SEA	Mya-98
6	O/VIT/5/2010 (JQ070323)	VIT10-05	639	622	0	97.34	2.66	SEA	Mya-98
7	O/TAI/4/2010	TAI10-04	639	621	0	97.18	2.82	SEA	Mya-98
8	O/TAI/6/2010	TAI10-06	639	621	0	97.18	2.82	SEA	Mya-98
9	O/TAI/9/2010	TAI10-09	639	621	0	97.18	2.82	SEA	Mya-98
10	O/VIT/18/2010	VIT10-18	639	621	0	97.18	2.82	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	587	0	91.86	8.14	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	570	0	89.20	10.80	SEA	unnamed
3	O/IRN/31/2009	IRN09-31	639	551	0	86.23	13.77	ME-SA	PanAsia-2$^{\text{FAR-09}}$
4	O/PAK/16/2010	PAK10-16	639	549	0	85.92	14.08	ME-SA	PanAsia-2$^{\text{PUN-10}}$
5	O/UKG/35/2001 (AJ539141)	UKG01-35	639	547	0	85.60	14.40	ME-SA	PanAsia
6	O/IRN/8/2005	IRN05-08	639	546	0	85.45	14.55	ME-SA	PanAsia-2
7	O/CAM/3/98 (AJ294910)	CAM98-03	639	544	0	85.13	14.87	SEA	Cam-94
8	O/IND/R2/75* (AF204276)	IND75--A	639	543	0	84.98	15.02	ME-SA	unnamed
9	O/IRN/18/2010	IRN10-18	639	542	0	84.82	15.18	ME-SA	PanAsia-2$^{\text{BAL-09}}$
10	O/IRN/88/2009	IRN09-88	639	542	0	84.82	15.18	ME-SA	PanAsia-2$^{\text{ANT-10}}$

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 07/08/2014
WRLFMD Ref No: TAI/11/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00022	Checked by: K. Bachanek-Bankowska
Sender Ref: 30/13 R1B1	
Location: Nakhon Pathom Province, Thailand	Topotype: SEA
Date collected: 09/10/2013	Genotype/strain: Mya-98
Date received by WRLFMD: 19/06/2014	Sequence filename: TAI13-11.SEQ
Date received for sequencing: 23/07/2014	Date sequence last updated: 05/08/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 18/07/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3936
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
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3	O/TAI/27/2009	TAI09-27	639	621	0	97.18	2.82	SEA	Mya-98
4	O/TAI/4/2010	TAI10-04	639	621	0	97.18	2.82	SEA	Mya-98
5	O/TAI/5/2010	TAI10-05	639	621	0	97.18	2.82	SEA	Mya-98
6	O/TAI/3/2010	TAI10-03	639	620	0	97.03	2.97	SEA	Mya-98
7	O/VIT/5/2010 (JQ070323)	VIT10-05	639	620	0	97.03	2.97	SEA	Mya-98
8	O/TAI/6/2010	TAI10-06	639	619	0	96.87	3.13	SEA	Mya-98
9	O/TAI/9/2010	TAI10-09	639	619	0	96.87	3.13	SEA	Mya-98
10	O/VIT/18/2010	VIT10-18	639	619	0	96.87	3.13	SEA	Mya-98

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5	O/UKG/35/2001 (AJ539141)	UKG01-35	639	547	0	85.60	14.40	ME-SA	PanAsia
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7	O/IRN/8/2005	IRN05-08	639	544	0	85.13	14.87	ME-SA	PanAsia-2
8	O/CAM/3/98 (AJ294910)	CAM98-03	639	541	0	84.66	15.34	SEA	Cam-94
9	O/IRN/88/2009	IRN09-88	639	541	0	84.66	15.34	ME-SA	PanAsia-2^{ANT-10}
10	O/IND/53/79 (AF292107)	IND79A53	639	540	0	84.51	15.49	ME-SA	unnamed

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in Thailand in 2013

Batch: WRLFMD/2014/00022

◆ indicates viruses in this batch

Software: MEGA 6.06

Only bootstrap values of 70% and above are shown
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

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
07 August 2014