

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

Genotyping Report

Report Date for this Batch: 9 September 2015

FMDV type O

Country: Vietnam

Period: 2015

No. of samples: 1

BATCH: WRLFMD/2015/00018



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: O	Report date: 09/09/2015
WRLFMD Ref No: VIT/4/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00018	Checked by: K. Bachanek-Bankowska
Sender Ref: VIT 14/15 B1R3	
Location: Long An, Vietnam	Topotype: SEA
Date collected: 27/04/2015	Genotype/strain: Mya-98
Date received by WRLFMD: 12/08/2015	Sequence filename: VIT15-04.SEQ
Date received for sequencing: 28/08/2015	Date sequence last updated: 07/09/2015
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 15/08/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4156
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 28 days
	Sequencing time: 12 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/VIT/18/2014	VIT14-18	639	636	0	99.53	0.47	SEA	Mya-98
2	O/VIT/13/2014	VIT14-13	639	635	0	99.37	0.63	SEA	Mya-98
3	O/MAY/2/2014	MAY14-02	639	634	0	99.22	0.78	SEA	Mya-98
4	O/TAI/10/2014	TAI14-10	639	634	0	99.22	0.78	SEA	Mya-98
5	O/VIT/21/2014	VIT14-21	639	634	0	99.22	0.78	SEA	Mya-98
6	O/VIT/26/2014	VIT14-26	639	634	0	99.22	0.78	SEA	Mya-98
7	O/VIT/27/2014	VIT14-27	639	634	0	99.22	0.78	SEA	Mya-98
8	O/MAY/9/2014	MAY14-09	639	632	0	98.90	1.10	SEA	Mya-98
9	O/MOG/1/2015	MOG15-01	639	632	0	98.90	1.10	SEA	Mya-98
10	O/MOG/2/2015	MOG15-02	639	632	0	98.90	1.10	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	567	0	88.73	11.27	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	556	0	87.01	12.99	ME-SA	unnamed
4	O/CAM/3/98 (AJ294910)	CAM98-03	639	552	0	86.38	13.62	SEA	Cam-94
5	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	548	0	85.76	14.24	ME-SA	unnamed
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	547	0	85.60	14.40	ME-SA	PanAsia-2 ^{SAN-09}
7	O/UAE/4/2008 (KM921876)	UAE08-04	636	544	0	85.53	14.47	ME-SA	Ind-2001c
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	546	0	85.45	14.55	ME-SA	PanAsia
9	O/IRN/31/2009	IRN09-31	639	545	0	85.29	14.71	ME-SA	PanAsia-2 ^{FAR-09}
10	O/IRN/88/2009	IRN09-88	639	544	0	85.13	14.87	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV O in Vietnam in 2015

Batch: WRLFMD/2015/00018

◆ 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

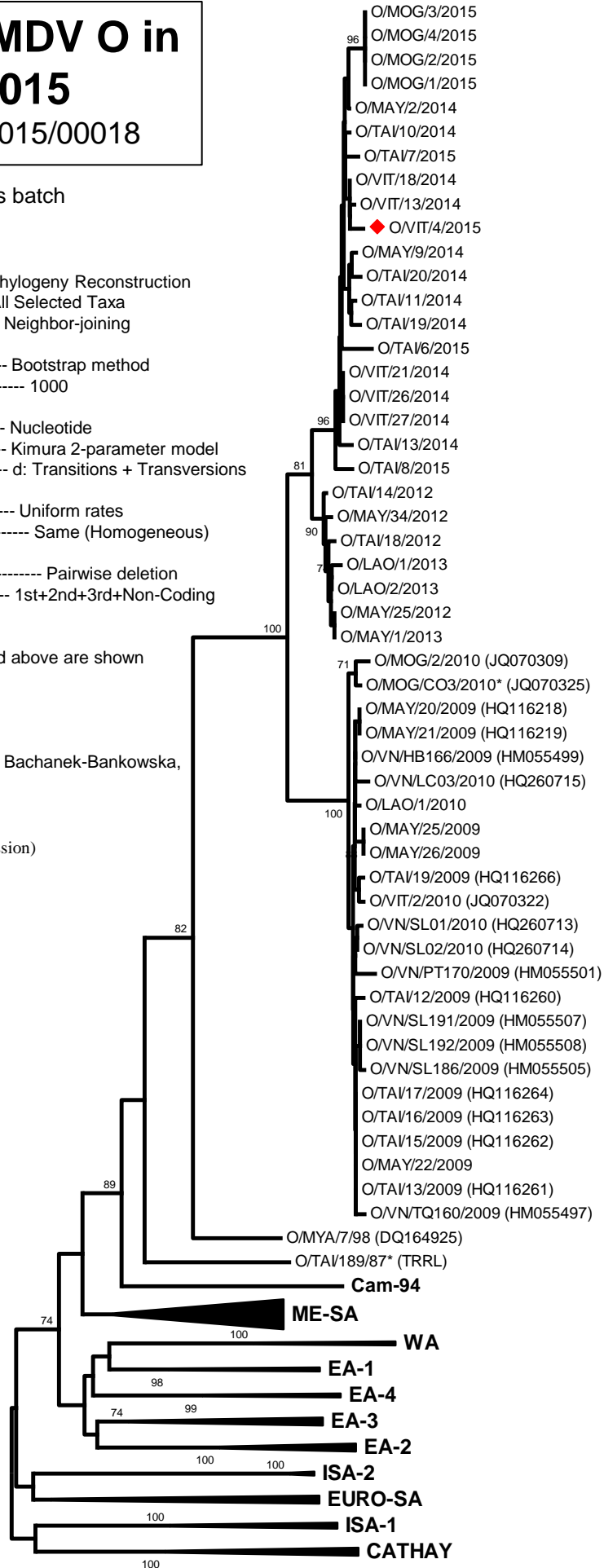
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
9 September 2015

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Mya-98

SEA