

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

Genotyping Report

Report Date for this Batch: 5 July 2016

FMDV type O

Country: Lao PDR

Period: 2016

No. of samples: 1

BATCH: WRLFMD/2016/00014

Note: although FMDV genome was detected in samples LAO/1/2016 (LAO1/16R1) and LAO/3/2016 (LAO3/16R1) it was not possible to amplify the VP1 region for sequencing.



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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 WRLFMD Ref No: LAO/2/2016 Batch No: WRLFMD/2016/00014 Sender Ref: LAO2/16R1 Location: Natharm, Parkngueum, Vientiane capital, Laos Date collected: 23/03/2016 Date received by WRLFMD: 21/04/2016 Date received for sequencing: 10/05/2016 Species: Water Buffalo Material used: Orig susp Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R	Report date: 05/07/2016 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: SEA Genotype/strain: Mya-98 Sequence filename: LAO16-02.SEQ Date sequence last updated: 24/05/2016 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4210 Min. no. of nt for comparison: 600 Total turn-around time: 33 days Sequencing time: 14 days
Comments: No virus isolated on cell cultures. Two thirds of the VP1 sequence was only determined on the negative DNA strand.	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/TAI/28/2015	TAI15-28	639	637	0	99.69	0.31	SEA	Mya-98
2	O/TAI/4/2016	TAI16-04	639	635	0	99.37	0.63	SEA	Mya-98
3	O/TAI/2/2016	TAI16-02	639	631	0	98.75	1.25	SEA	Mya-98
4	O/VIT/21/2014	VIT14-21	639	629	0	98.44	1.56	SEA	Mya-98
5	O/VIT/26/2014	VIT14-26	639	629	0	98.44	1.56	SEA	Mya-98
6	O/VIT/27/2014	VIT14-27	639	629	0	98.44	1.56	SEA	Mya-98
7	O/MAY/2/2014	MAY14-02	639	627	0	98.12	1.88	SEA	Mya-98
8	O/TAI/10/2014	TAI14-10	639	627	0	98.12	1.88	SEA	Mya-98
9	O/VIT/18/2014	VIT14-18	639	627	0	98.12	1.88	SEA	Mya-98
10	O/TAI/9/2015	TAI15-09	639	626	0	97.97	2.03	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	588	0	92.02	7.98	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	568	0	88.89	11.11	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	551	0	86.23	13.77	ME-SA	unnamed
4	O/CAM/3/98 (AJ294910)	CAM98-03	639	547	0	85.60	14.40	SEA	Cam-94
5	O/UAE/4/2008 (KM921876)	UAE08-04	636	544	0	85.53	14.47	ME-SA	Ind-2001c
6	O/KUW/3/97 (DQ164904)	KUW97-03	639	546	0	85.45	14.55	ME-SA	Ind-2001a
7	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	546	0	85.45	14.55	ME-SA	unnamed
8	O/IRN/31/2009	IRN09-31	639	545	0	85.29	14.71	ME-SA	PanAsia-2 ^{FAR-09}
9	O/TUR/264/2009* (FMDI)	TUR09-AK	639	545	0	85.29	14.71	ME-SA	PanAsia-2 ^{SAN-09}
10	O/IRN/88/2009	IRN09-88	639	543	0	84.98	15.02	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.5

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Report on FMDV O in Laos in 2016

Batch: WRLFMD/2016/00014

◆ 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

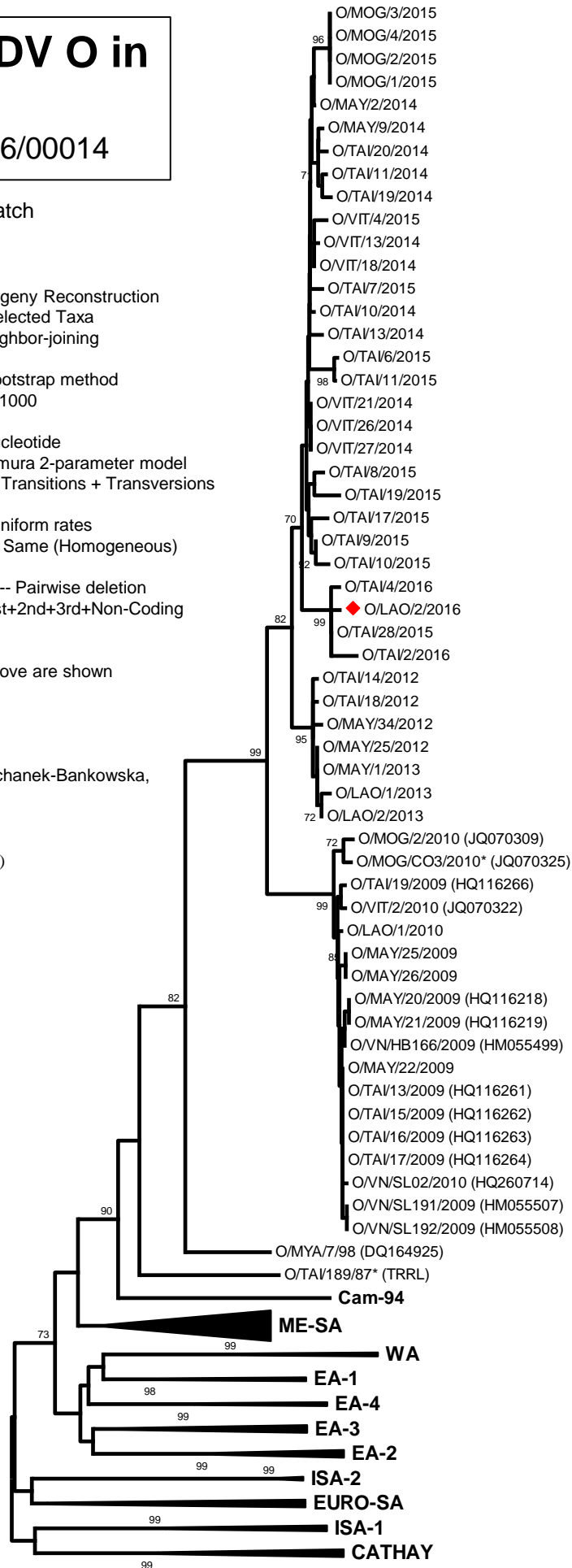
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
24 May 2016

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Mya-98

SEA

0.02

From: [reference laboratories reporting](#)
To: [donald king](#); [Nick Knowles](#)
Subject: FW: Laos - Genotyping Report (O) - July 2016
Date: 06 July 2016 08:38:28
Attachments: [image001.png](#)
[image002.png](#)

Request from Dr Rodtian.....

Sarah

From: Pranee Rodtian [mailto:pranee.rodtian@gmail.com]
Sent: 05 July 2016 18:12
To: reference laboratories reporting; Alongkorn Pantumart; sahawatcharau@dld.go.th; Amonrat Choornasard; somkiat sripisuth
Subject: Re: Laos - Genotyping Report (O) - July 2016

Dear Sarah,

Thanks for Laos genotyping, may you please compare to those two consecutive year of recently samples which has been submitted from TAI, Cam, Viet, Myanmar, Laos on phylogenetic tree. etc especially Tai 16, how it jump out from the group. I has asked my staff to repeat this sample again. to make sure that he has put on the right group.

Thailand - FMD Genotyping Report (O) - February 2016.pdf - Adobe Reader

Serotype: O	Report date: 24/02/2016
WRLFMD Ref No: TAI16/2015	Reported by: N.J. Knowles
Batch No: WRLFMD 2015 00032	Checked by: K. Ischaneek-Bankowska
Sender Ref: 52-215R3B2	
Location: Lumpayaklang, Muehle, Saraburi, Thailand	Topotype: ME-SA
Date collected: 20/05/2015	Genotype/strain: Pan/Asia
Date received by WRLFMD: 26/11/2015	Sequence filename: TAI15-16.SEQ
Date received for sequencing: 19/02/2016	Date sequence last updated: 24/02/2016
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 09/02/2016	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4220
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total run-around time: 90 days
	Sequencing time: 5 days

Comments:

Most Closely Related Viruses

Viruses	No. of	No. of	No. of	% ID	% DIF	Tree	Strain

WRLFMD Director: Dr. Bryan Charleston WRLFMD

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FMD Genotyping Report

Lab Reference WRL batch Number: WRLFMD/2015/00032

Sender Details: Dr. Pranee Rodtian, Dept. of Livestock Development, Regional Reference Laboratory for FMD in SEA, Pakchong, Thailand, PHONE - 66 44 279112, FAX - 66 44 314889, EMAIL - pranee.rodtian@gmail.com

2016-07-05 20:00 GMT+07:00 reference laboratories reporting
<reporting@pirbright.ac.uk>:

Dear Dr Rodtian,

Please find attached the Genotyping report (O) – Laos for the samples submitted to The Pirbright Institute. This is one of the samples that was originally reported as FMD-GD (FMD Genome Detected) which has been subsequently sequenced. The other two samples in this batch failed to generate sequence data.

Kind regards,

Sarah

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