

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

Genotyping Report

Report Date for this Batch: 14 September 2015

FMDV type A

Country: Laos

Period: 2015

No. of samples: 1

BATCH: WRLFMD/2015/00017



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: A	Report date: 14/09/2015
WRLFMD Ref No: LAO/1/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00017	Checked by: K. Bachanek-Bankowska
Sender Ref: LAO 5/15 R3B3	
Location: Xansai, Attapea, Laos	Topotype: ASIA
Date collected: 09/03/2015	Genotype/strain: Sea-97
Date received by WRLFMD: 12/08/2015	Sequence filename: LAO15-01.SEQ
Date received for sequencing: 28/08/2015	Date sequence last updated: 07/09/2015
Species: Cattle	No. of Nt determined: 636
Material used: BTy1 14/08/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 636
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 2059
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 33 days
	Sequencing time: 17 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/TAI/17/2014	TAI14-17	636	635	0	99.84	0.16	ASIA	Sea-97
2	A/TAI/21/2014	TAI14-21	636	634	0	99.69	0.31	ASIA	Sea-97
3	A/TAI/3/2015	TAI15-03	636	634	0	99.69	0.31	ASIA	Sea-97
4	A/Amur/2/RUS/2013 (ARRIAH)	RUS13-AH	636	633	0	99.53	0.47	ASIA	Sea-97
5	A/Amur/4/RUS/2013 (ARRIAH)	RUS13-AJ	636	633	0	99.53	0.47	ASIA	Sea-97
6	A/GDMM-CHA-2013-S (KF450794)	CHA13-AA	636	633	0	99.53	0.47	ASIA	Sea-97
7	A/GZ-HX/CHA/2013 (KJ646647)	CHA13-AG	636	633	0	99.53	0.47	ASIA	Sea-97
8	A/GZ-JC/CHA/2013 (KJ646650)	CHA13-AJ	636	633	0	99.53	0.47	ASIA	Sea-97
9	A/GZ-ZB/CHA/2013 (KJ646649)	CHA13-AI	636	633	0	99.53	0.47	ASIA	Sea-97
10	A/TAI/4/2015	TAI15-04	636	633	0	99.53	0.47	ASIA	Sea-97
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	A/TAI/7/2003 (HQ116312)	TAI03-07	636	596	0	93.71	6.29	ASIA	Sea-97
2	A/TAI/2/97 (EF208778)	TAI97-02	636	574	0	90.25	9.75	ASIA	Sea-97
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	556	0	87.42	12.58	ASIA	Thai-87
4	A22/IRQ/64 (AY593763)	IRQ64--A	636	524	0	82.39	17.61	ASIA	A ₂₂
5	A/IRN/2/87 (EF208770)	IRN87-02	633	519	0	81.99	18.01	ASIA	Iran-87
6	A/GHA/16/73 (KF561698)	GHA73-16	633	514	0	81.20	18.80	AFRICA	G-VI
7	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	516	0	81.13	18.87	ASIA	A15
8	A/IRN/1/2011	IRN11-01	636	515	0	80.97	19.03	ASIA	Iran-05 ^{FAR-11}
9	A/IRN/78/2009	IRN09-78	636	515	0	80.97	19.03	ASIA	Iran-05 ^{FAR-09}
10	A/TUR/1/2008 (FJ755133)	TUR08-01	636	514	0	80.82	19.18	ASIA	Iran-05 ^{ARD-07}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV A in Laos in 2015

Batch: WRLFMD/2015/00017

◆ 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 : 639

No Of Bootstrap Reps = 1000

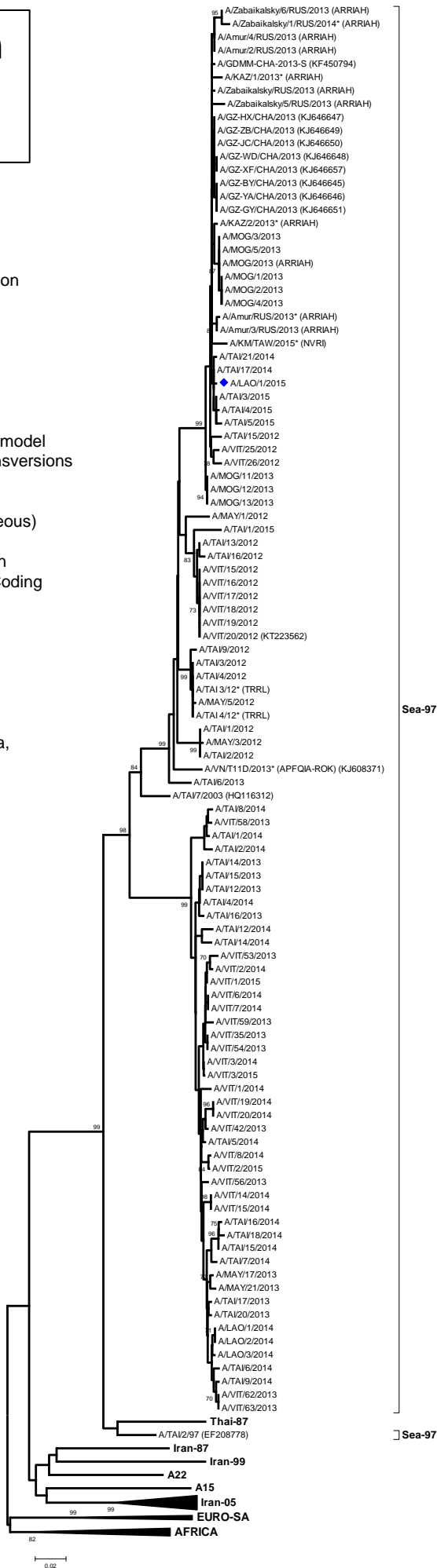
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

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

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Sea-97

ASIA

Sea-97

0.02