

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

Genotyping Report

Report Date for this Batch: 17 December 2015

FMDV type A

Country: Cambodia

Period: 2015

No. of samples: 2

BATCH: WRLFMD/2015/00033



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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 WRLFMD Ref No: CAM/2/2015 Batch No: WRLFMD/2015/00033 Sender Ref: CAM6/15R3B4 Location: Phnom Srouch, Kampong Speu, Cambodia Date collected: 14/09/2015 Date received by WRLFMD: 26/11/2015 Date received for sequencing: 09/12/2015 Species: Cattle Material used: BTy1 03/12/2015 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 17/12/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ASIA Genotype/strain: Sea-97 Sequence filename: CAM15-02.SEQ Date sequence last updated: 10/12/2015 No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636 Total no. of comparisons: 2090 Min. no. of nt for comparison: 600 Total turn-around time: 21 days Sequencing time: 8 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/CAM/5/2015	CAM15-05	636	636	0	100.00	0.00	ASIA	Sea-97
2	A/CAM/2/2008 (HQ116294)	CAM08-02	636	616	0	96.86	3.14	ASIA	Sea-97
3	A/CAM 4/08* (TRRL)	CAM08-AA	636	613	0	96.38	3.62	ASIA	Sea-97
4	A/CAM/2/2006 (HQ116293)	CAM06-02	636	612	0	96.23	3.77	ASIA	Sea-97
5	A/LAO/1/07* (TRRL)	LAO06-AA	636	612	0	96.23	3.77	ASIA	Sea-97
6	A/LAO/15/07* (TRRL)	LAO06-AN	636	612	0	96.23	3.77	ASIA	Sea-97
7	A/LAO/16/07* (TRRL)	LAO06-AO	636	612	0	96.23	3.77	ASIA	Sea-97
8	A/LAO/2/07* (TRRL)	LAO06-AB	636	612	0	96.23	3.77	ASIA	Sea-97
9	A/LAO/4/07* (TRRL)	LAO06-AD	636	612	0	96.23	3.77	ASIA	Sea-97
10	A/LAO/6/2006 (EU667457)	LAO06-06	636	612	0	96.23	3.77	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	578	0	90.88	9.12	ASIA	Sea-97
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	561	0	88.21	11.79	ASIA	Thai-87
4	A/IRN/2/87 (EF208770)	IRN87-02	633	523	0	82.62	17.38	ASIA	Iran-87
5	A22/IRQ/64 (AY593763)	IRQ64--A	636	523	0	82.23	17.77	ASIA	A ₂₂
6	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	521	0	81.92	18.08	ASIA	A15
7	A/AFG/10/2010	AFG10-10	636	520	0	81.76	18.24	ASIA	Iran-05 ^{HER-10}
8	A/IRN/1/2011	IRN11-01	636	520	0	81.76	18.24	ASIA	Iran-05 ^{FAR-11}
9	A/IRN/1/96 (EF208771)	IRN96-01	635	519	1	81.73	18.27	ASIA	Iran-96
10	A/TUR/3/2010	TUR10-03	636	518	0	81.45	18.55	ASIA	Iran-05 ^{KSS-09}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Serotype: A WRLFMD Ref No: CAM/5/2015 Batch No: WRLFMD/2015/00033 Sender Ref: CAM15/15R3B2 Location: Phnom Srouch, Kampong Speu, Cambodia Date collected: 14/09/2015 Date received by WRLFMD: 26/11/2015 Date received for sequencing: 11/12/2015 Species: Cattle Material used: Original tissue culture fluid (R3B2), BTy1 05/12/2015 and BTy2 08/12/2015 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 17/12/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ASIA Genotype/strain: Sea-97 Sequence filename: CAM15-05.SEQ Date sequence last updated: 15/12/2015 No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636 Total no. of comparisons: 2090 Min. no. of nt for comparison: 600 Total turn-around time: 21 days Sequencing time: 6 days
Comments: This sample was identified by the Ref Lab in Pakchong as Asia 1; therefore the original TC fluid and BTy1 were also tested for the presence of types A and Asia 1, however, only type A was found. The VP1 sequences of the original TC fluid, BTy1 and BTy2 were all identical.	

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Report on FMDV A in Cambodia in 2015

Batch: WRLFMD/2015/00033

◆ indicates viruses in this batch

Software: MEGA 6.06

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

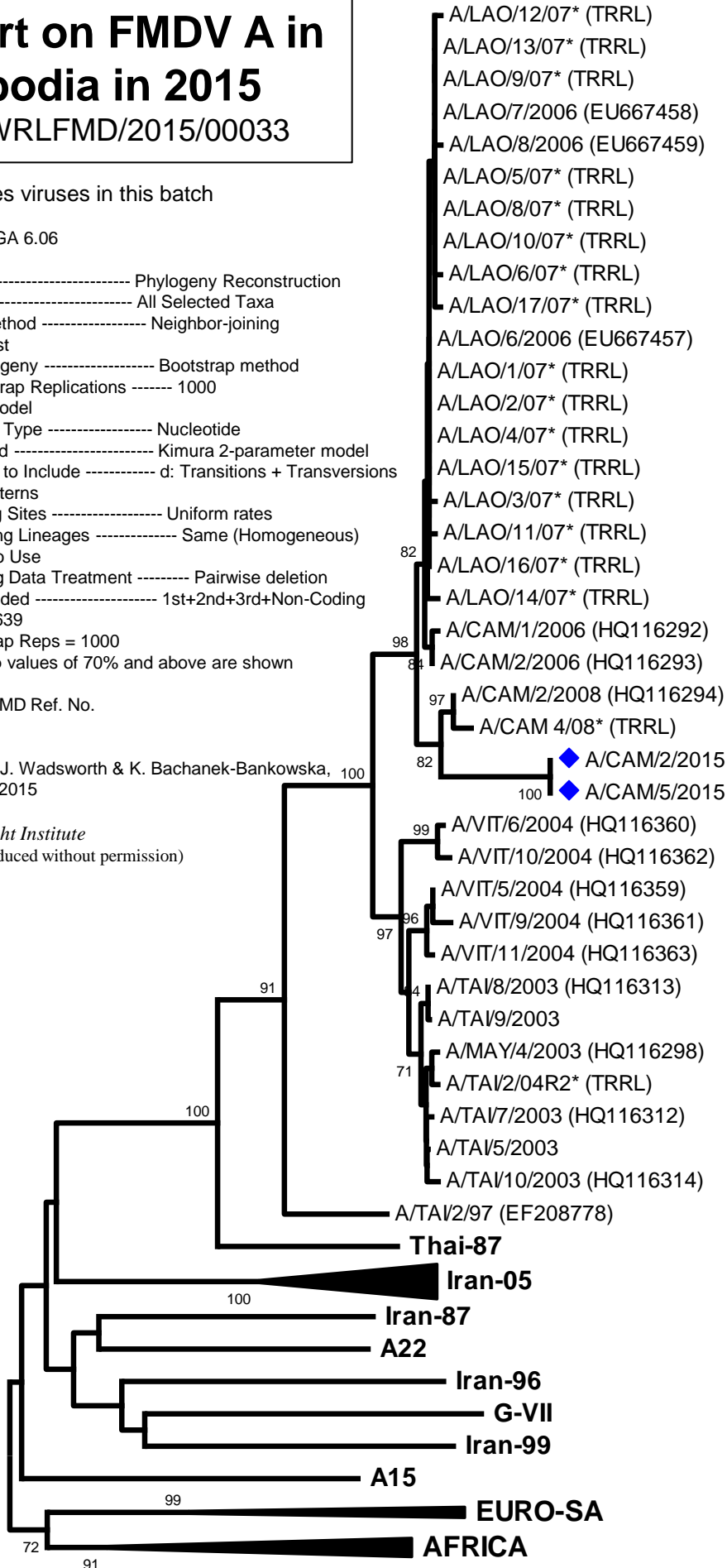
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska, 100
17 December 2015

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Sea-97

ASIA

0.02