

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

Genotyping Report

Report Date for this Batch: 29 May 2015

FMDV type A

Country: Taiwan POC

Period: 2015

No. of sequences: 1 (VP1)

Originator: XXXXXXXXXX



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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: 29/05/2015
WRLFMD Ref No: KM/TAW/2015*	Reported by: N.J. Knowles
Batch No: WRLMEG/2015/00005	Checked by: D.P. King
Sender Ref: A KM TAW 2015	
Location: Kinmen Island, Taiwan	Topotype: ASIA
Date collected: 01/05/2015	Genotype/strain: Sea-97
Date received by WRLFMD: 29/05/2015	Sequence filename: TAW15-AA.SEQ
Date received for sequencing: n/a	Date sequence last updated: 29/05/2015
Species: Not Known	No. of Nt determined: 636
Material used: Not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 636
RT-PCR primers: 3093F/NK61	Total no. of comparisons: 2018
	Min. no. of nt for comparison: 600
	Total turn-around time: 0 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/Amur/2/RUS/2013 (ARRIAH)	RUS13-AH	636	629	0	98.9	1.1	ASIA	Sea-97
2	A/Amur/4/RUS/2013 (ARRIAH)	RUS13-AJ	636	629	0	98.9	1.1	ASIA	Sea-97
3	A/GDMM-CHA-2013-S (KF450794)	CHA13-AA	636	629	0	98.9	1.1	ASIA	Sea-97
4	A/GZ-HX/CHA/2013 (KJ646647)	CHA13-AG	636	629	0	98.9	1.1	ASIA	Sea-97
5	A/GZ-JC/CHA/2013 (KJ646650)	CHA13-AJ	636	629	0	98.9	1.1	ASIA	Sea-97
6	A/GZ-ZB/CHA/2013 (KJ646649)	CHA13-AI	636	629	0	98.9	1.1	ASIA	Sea-97
7	A/Zabaikalsky/RUS/2013 (ARRIAH)	RUS13-AA	636	629	0	98.9	1.1	ASIA	Sea-97
8	A/Amur/3/RUS/2013 (ARRIAH)	RUS13-AI	636	628	0	98.74	1.26	ASIA	Sea-97
9	A/GZ-BY/CHA/2013 (KJ646645)	CHA13-AE	636	628	0	98.74	1.26	ASIA	Sea-97
10	A/GZ-GY/CHA/2013 (KJ646651)	CHA13-AK	636	628	0	98.74	1.26	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	591	0	92.92	7.08	ASIA	Sea-97
2	A/TAI/2/97 (EF208778)	TAI97-02	636	573	0	90.09	9.91	ASIA	Sea-97
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	558	0	87.74	12.26	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	520	0	82.15	17.85	ASIA	Iran-87
6	A/IRN/1/2011	IRN11-01	636	517	0	81.29	18.71	ASIA	Iran-05 ^{FAR-11}
7	A/IRN/78/2009	IRN09-78	636	517	0	81.29	18.71	ASIA	Iran-05 ^{FAR-09}
8	A/TUR/1/2008 (FJ755133)	TUR08-01	636	516	0	81.13	18.87	ASIA	Iran-05 ^{ARD-07}
9	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	516	0	81.13	18.87	ASIA	A15
10	A/BAR/6/2008 (FJ755010)	BAR08-06	636	515	0	80.97	19.03	ASIA	Iran-05 ^{BAR-08}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV A in Taiwan in 2015

Batch: WRLMEG/2015/00005

◆ 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

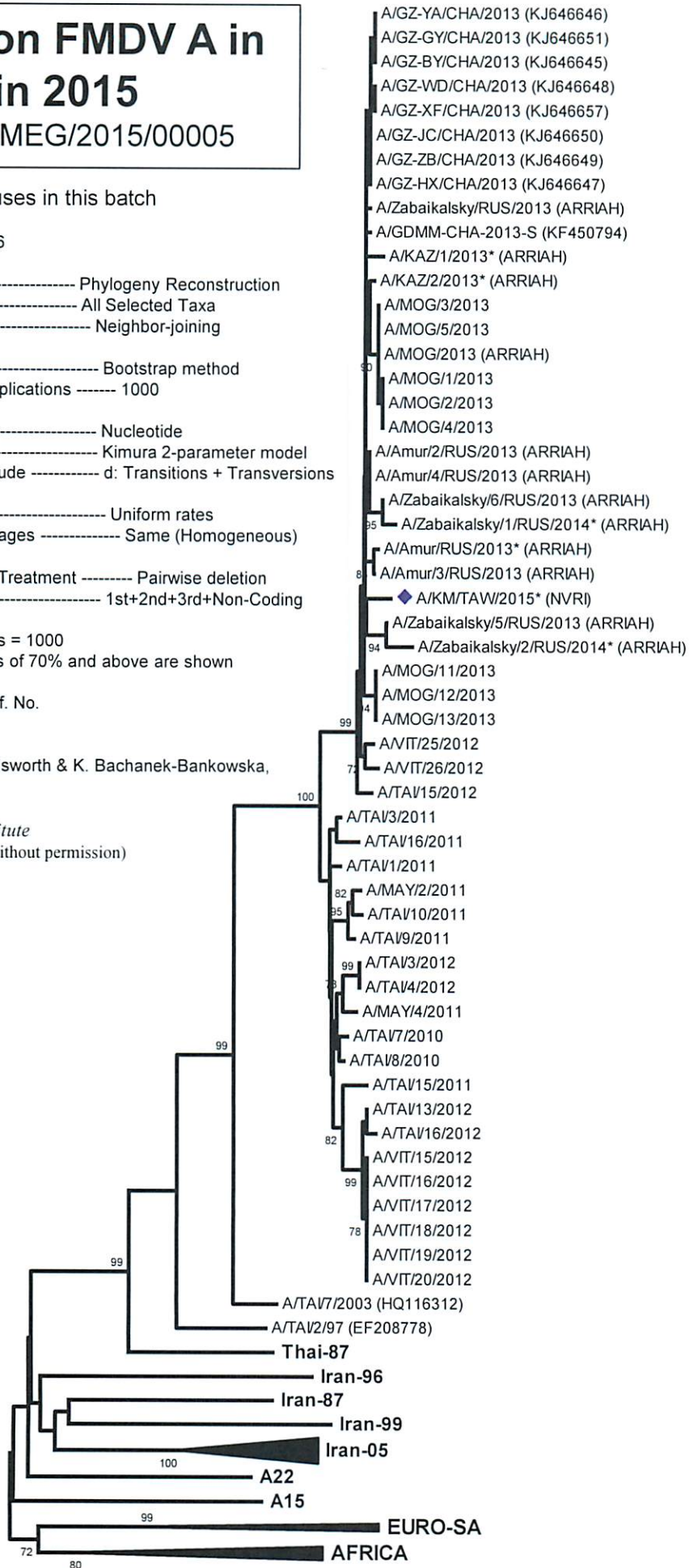
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
29 May 2015

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Sea-97

ASIA

0.02