

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

Genotyping Report

Report Date for this Batch: 10 September 2013

FMDV type A

Country: Vietnam

Period: 2012

No. of samples: 2

BATCH: WRLFMD/2013/00017



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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: 10/09/2013
WRLFMD Ref No: VIT/25/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00017	Checked by: D.P. King
Sender Ref: DS-NVB-2	
Location: Nghe An province, Vietnam	Topotype: ASIA
Date collected: 10/11/2012	Genotype/strain: Sea-97
Date received by WRLFMD: 16/08/2013	Sequence filename: VIT12-25.SEQ
Date received for sequencing: 04/09/2013	Date sequence last updated: 09/09/2013
Species: Cattle	No. of Nt determined: 636
Material used: BTy1 21/08/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 636
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1675
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 25 days
	Sequencing time: 6 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	631	0	99.21	0.79	ASIA	Sea-97
2	A/GDMM-CHA-2013-S (LVRI)	CHA13-AA	636	631	0	99.21	0.79	ASIA	Sea-97
3	A/VIT/26/2012	VIT12-26	636	631	0	99.21	0.79	ASIA	Sea-97
4	A/Zabaikalsky/RUS/2013 (ARRIAH)	RUS13-AA	636	631	0	99.21	0.79	ASIA	Sea-97
5	A/Amur/3/RUS/2013 (ARRIAH)	RUS13-AI	636	630	0	99.06	0.94	ASIA	Sea-97
6	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	630	0	99.06	0.94	ASIA	Sea-97
7	A/Amur/RUS/2013* (ARRIAH)	RUS13-AG	636	629	0	98.90	1.10	ASIA	Sea-97
8	A/MOG/2013 (ARRIAH)	MOG13-AA	636	629	0	98.90	1.10	ASIA	Sea-97
9	A/MOG/3/2013	MOG13-03	636	629	0	98.90	1.10	ASIA	Sea-97
10	A/MOG/5/2013	MOG13-05	636	629	0	98.90	1.10	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	597	0	93.87	6.13	ASIA	Sea-97
2	A/TAI/2/97 (EF208778)	TAI97-02	636	575	0	90.41	9.59	ASIA	Sea-97
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	557	0	87.58	12.42	ASIA	Thai-87
4	A22/IRQ/64 (AY593763)	IRQ64--A	636	521	0	81.92	18.08	ASIA	A ₂₂
5	A/IRN/2/87 (EF208770)	IRN87-02	633	518	0	81.83	18.17	ASIA	Iran-87
6	A/IRN/78/2009	IRN09-78	636	515	0	80.97	19.03	ASIA	Iran-05 ^{FAR-09}
7	A/TUR/1/2008	TUR08-01	636	515	0	80.97	19.03	ASIA	Iran-05 ^{ARD-07}
8	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	636	515	0	80.97	19.03	ASIA	A15
9	A/TUR/33/2008	TUR08-33	636	514	0	80.82	19.18	ASIA	Iran-05 ^{EZM-07}
10	A/IRN/1/96 (EF208771)	IRN96-01	635	512	1	80.63	19.37	ASIA	Iran-96

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: A	Report date: 10/09/2013
WRLFMD Ref No: VIT/26/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00017	Checked by: D.P. King
Sender Ref: DS-NTC-2	
Location: Nghe An province, Vietnam	Topotype: ASIA
Date collected: 10/11/2012	Genotype/strain: Sea-97
Date received by WRLFMD: 16/08/2013	Sequence filename: VIT12-26.SEQ
Date received for sequencing: 04/09/2013	Date sequence last updated: 09/09/2013
Species: Cattle	No. of Nt determined: 636
Material used: BTy2 22/08/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 636
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1675
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
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5	A/Amur/3/RUS/2013 (ARRIAH)	RUS13-AI	636	629	0	98.90	1.10	ASIA	Sea-97
6	A/KAZ/2/2013* (ARRIAH)	KAZ13-AB	636	629	0	98.90	1.10	ASIA	Sea-97
7	A/Amur/RUS/2013* (ARRIAH)	RUS13-AG	636	628	0	98.74	1.26	ASIA	Sea-97
8	A/MOG/2013 (ARRIAH)	MOG13-AA	636	628	0	98.74	1.26	ASIA	Sea-97
9	A/MOG/3/2013	MOG13-03	636	628	0	98.74	1.26	ASIA	Sea-97
10	A/MOG/5/2013	MOG13-05	636	628	0	98.74	1.26	ASIA	Sea-97
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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	520	0	81.76	18.24	ASIA	A ₂₂
5	A/IRN/2/87 (EF208770)	IRN87-02	633	517	0	81.67	18.33	ASIA	Iran-87
6	A/IRN/78/2009	IRN09-78	636	513	0	80.66	19.34	ASIA	Iran-05 ^{FAR-09}
7	A/TUR/1/2008	TUR08-01	636	513	0	80.66	19.34	ASIA	Iran-05 ^{ARD-07}
8	A/IRN/1/96 (EF208771)	IRN96-01	635	512	1	80.63	19.37	ASIA	Iran-96
9	A/BAR/6/2008	BAR08-06	636	512	0	80.50	19.50	ASIA	Iran-05 ^{BAR-08}
10	A/IRN/1/2005 (EF208769)	IRN05-01	636	512	0	80.50	19.50	ASIA	Iran-05

nt, nucleotides

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Report on FMDV A in Vietnam in 2012

Batch: WRLFMD/2013/00017

◆ indicates viruses in this batch

Software: MEGA 5.2

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, K. Bachanek-Bankowska & J. Wadsworth,
10 September 2013

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Sea-97

ASIA

0.02