

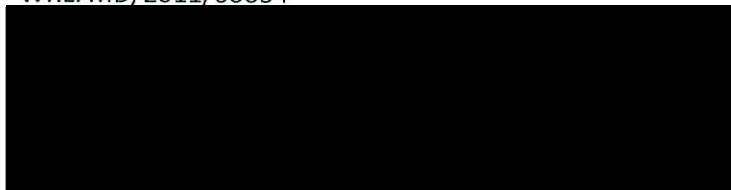


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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2011/00034

Sender Details:

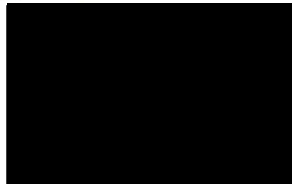


Date Received: 28th July 2011
Country of Origin: Vietnam
Date Reported: 30th August 2011

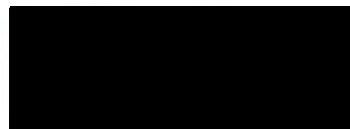
Dear Wilai Linchongsubongkoch,

Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

Results Approved By:



Official Stamp:



Date:

30/08/11

A UKAS accredited testing laboratory No. 4025.

To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: elizabeth.wilson@bbsrc.ac.uk). IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

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

Genotyping Report

Report Date for this Batch: 26 August 2011

FMDV type A

Country: Vietnam

Period: 2010

No. of samples: 1

BATCH: WRLFMD/2011/00034



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FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: A	Report date: 26/08/2011
WRLFMD Ref No: VIT/17/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2011/00034	Checked by: D.P. King
Sender Ref: VIT 1/10 R3 B2	
Location: Cao Bang, Vietnam	Topotype: ASIA
Date collected: 01/01/2010	Genotype/strain: Sea-97
Date received by WRLFMD: 28/07/2011	Sequence filename: VIT10-17.SEQ
Date received for sequencing: 05/08/2011	Date sequence last updated: 18/08/2011
Species: Cattle	No. of Nt determined: 636
Material used: LK3 BHK2 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 636
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1325
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 29 days
	Sequencing time: 21 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/VIT/1/2010	VIT10-01	636	636	0	100.00	0.00	ASIA	Sea-97
2	A/VIT 1/10* (TRRL)	VIT10-AA	636	636	0	100.00	0.00	ASIA	Sea-97
3	A/TAI/9/2009 (HQ116352)	TAI09-09	636	631	0	99.21	0.79	ASIA	Sea-97
4	A/TAI/8/2009 (HQ116351)	TAI09-08	636	630	0	99.06	0.94	ASIA	Sea-97
5	A/TAI/7/2009 (HQ116350)	TAI09-07	636	629	0	98.90	1.10	ASIA	Sea-97
6	A/TAI/10/2008 (HQ116339)	TAI08-10	636	627	0	98.58	1.42	ASIA	Sea-97
7	A/TAI/4/2008 (HQ116336)	TAI08-04	636	627	0	98.58	1.42	ASIA	Sea-97
8	A/TAI/9/2008 (HQ116338)	TAI08-09	636	627	0	98.58	1.42	ASIA	Sea-97
9	A/TAI/11/2008 (HQ116340)	TAI08-11	636	626	0	98.43	1.57	ASIA	Sea-97
10	A/TAI/14/2008 (HQ116342)	TAI08-14	636	626	0	98.43	1.57	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	574	0	90.25	9.75	ASIA	Sea-97
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	559	0	87.89	12.11	ASIA	Thai-87
4	A/IRN/2/87 (EF208770)	IRN87-02	633	519	0	81.99	18.01	ASIA	Iran-87
5	A22/IRQ/64 (AY593763)	IRQ64--A	636	521	0	81.92	18.08	ASIA	A ₂₂
6	A/IRN/78/2009	IRN09-78	636	519	0	81.60	18.40	ASIA	Iran-05 ^{FAR-09}
7	A/IRN/1/2005 (EF208769)	IRN05-01	636	517	0	81.29	18.71	ASIA	Iran-05
8	A/BAR/6/2008	BAR08-06	636	516	0	81.13	18.87	ASIA	Iran-05 ^{BAR-08}
9	A/TUR/33/2008	TUR08-33	636	515	0	80.97	19.03	ASIA	Iran-05 ^{EZM-07}
10	A/IRN/1/96 (EF208771)	IRN96-01	635	514	1	80.94	19.06	ASIA	Iran-96

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV A in Vietnam in 2010

Batch: WRLFMD/2011/00034

◆ indicates viruses in this batch

Software: MEGA 5.0

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

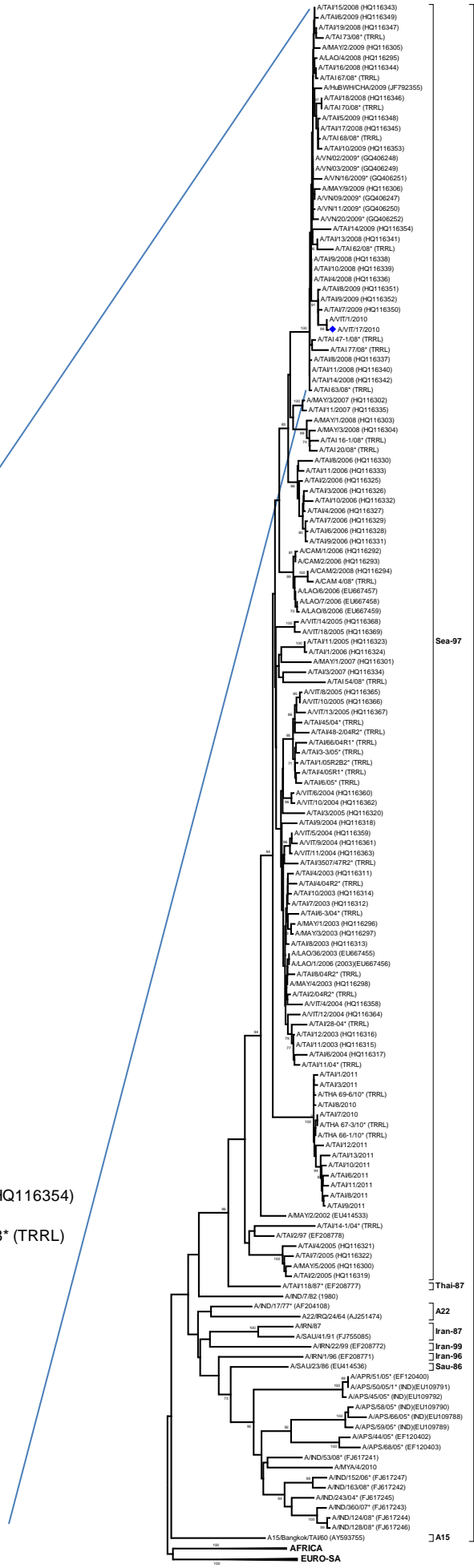
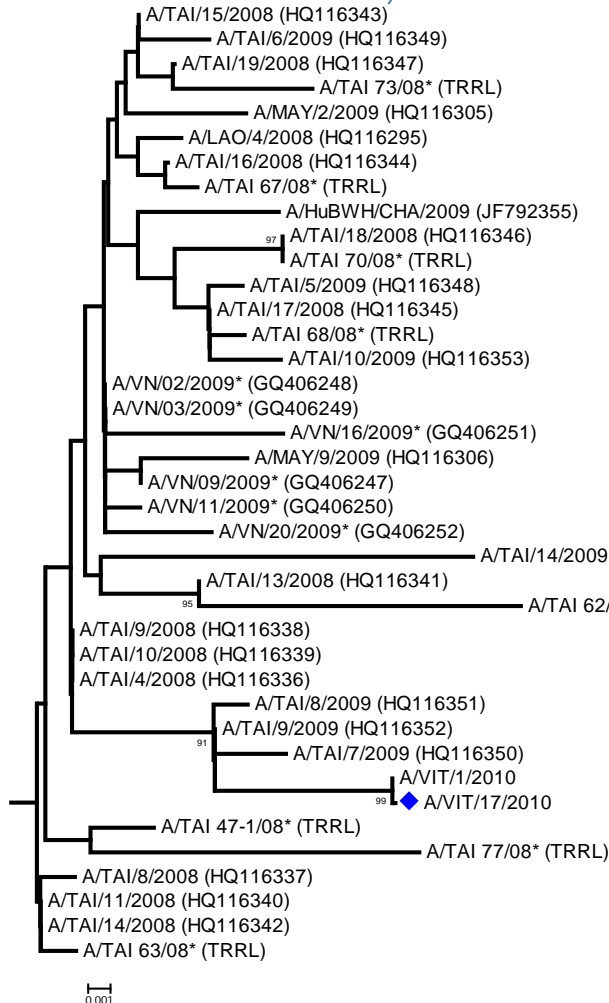
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 26 August 2011

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Sea-97

ASIA

Thai-87

A22

Iran-87

Iran-99

Iran-96

Sau-86

A15

AFRICA
EURO-SA