

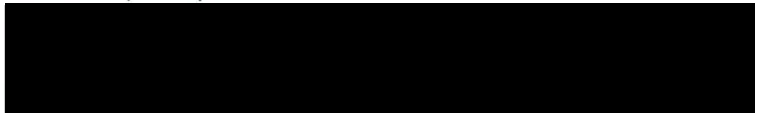


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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00035

Sender Details:



Date Received: 5th November 2010
Country of Origin: Vietnam
Date Reported: 29th November 2010

Dear Dr. Nguyen Xuan Binh,

Re.: Serotype A

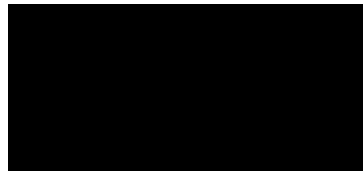
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

Please note this sample was collected more than six months ago.

Results Approved By:



Official Stamp:



Date:

30 / 11 / 10



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)

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

Genotyping Report

Report Date for this Batch: 22 November 2010

FMDV type A

Country: Vietnam

Period: 2010

No. of isolates: 1

BATCH: WRLFMD/2010/00035



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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: 22/11/2010
WRLFMD Ref No: VIT/1/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00035	Checked by: D.P. King
Sender Ref: 10-NCVD01 (NCVDA)	
Location: Cao Bang, Vietnam	Topotype: ASIA
Date collected: 01/01/2010	Genotype/strain: unnamed
Date received by WRLFMD: 05/11/2010	Sequence filename: VIT10-01.SEQ
Date received for sequencing: 12/11/2010	Date sequence last updated: 22/11/2010
Species: Cattle	No. of Nt determined: 636
Material used: BHK BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 636
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1174
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 17 days
	Sequencing time: 10 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/9/2009	TAI09-09	636	631	0	99.21	0.79	ASIA	Unnamed
2	A/TAI/8/2009	TAI09-08	636	630	0	99.06	0.94	ASIA	Unnamed
3	A/TAI/7/2009	TAI09-07	636	629	0	98.90	1.10	ASIA	Unnamed
4	A/TAI/10/2008	TAI08-10	636	627	0	98.58	1.42	ASIA	Unnamed
5	A/TAI/4/2008	TAI08-04	636	627	0	98.58	1.42	ASIA	Unnamed
6	A/TAI/9/2008	TAI08-09	636	627	0	98.58	1.42	ASIA	Unnamed
7	A/TAI/11/2008	TAI08-11	636	626	0	98.43	1.57	ASIA	Unnamed
8	A/TAI/14/2008	TAI08-14	636	626	0	98.43	1.57	ASIA	Unnamed
9	A/VIT/3/2008	VIT08-03	636	626	0	98.43	1.57	ASIA	Unnamed
10	A/VIT/8/2008	VIT08-08	636	626	0	98.43	1.57	ASIA	Unnamed
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	TAI03-07	636	597	0	93.87	6.13	ASIA	Unnamed
2	A/TAI/2/97 (EF208778)	TAI97-02	636	574	0	90.25	9.75	ASIA	Thai-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	A22
6	A/IRN/1/2005 (EF208769)	IRN05-01	636	517	0	81.29	18.71	ASIA	Iran-05
7	A/BAR/6/2008	BAR08-06	636	516	0	81.13	18.87	ASIA	Iran-05 ^{BAR-08}
8	A/TUR/33/2008	TUR08-33	636	515	0	80.97	19.03	ASIA	Iran-05 ^{EZM-07}
9	A/IRN/1/96 (EF208771)	IRN96-01	635	514	1	80.94	19.06	ASIA	Iran-96
10	A/AFG/6/2007	AFG07-06	636	514	0	80.82	19.18	ASIA	Iran-05 ^{AFG-07}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.11

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Report on FMDV A in Vietnam in 2010

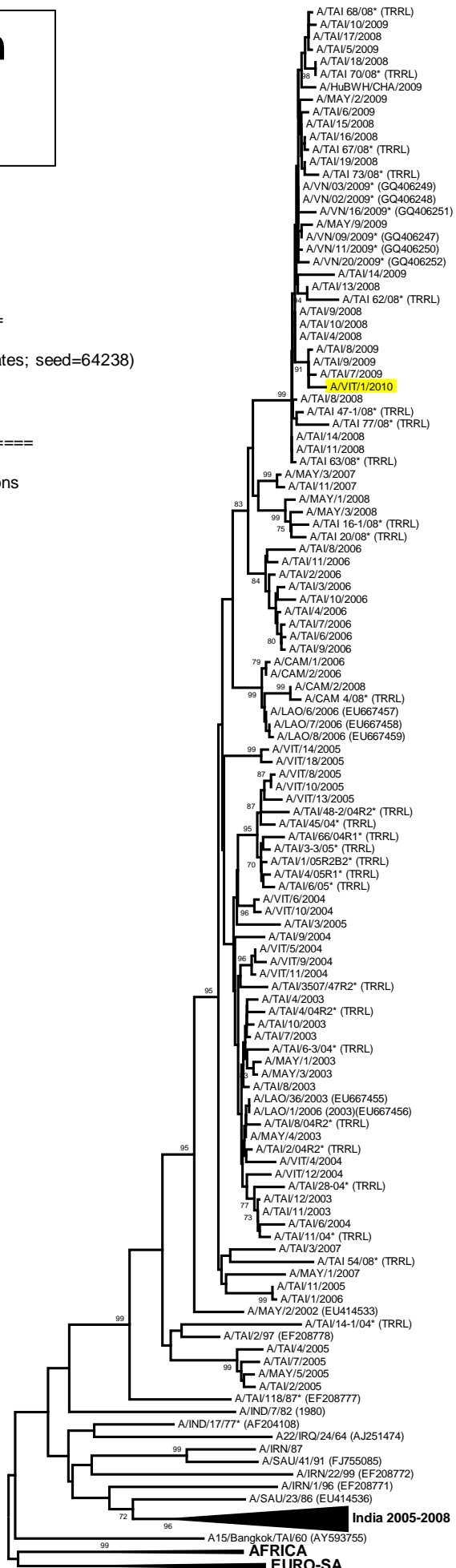
Batch: WRLFMD/2010/00035

Software: MEGA 4.0
 No. of Taxa : 141
 Data File : n:\evd\meg\db\fmv\la\VIT2010a.meg
 Data Title : A Vietnam 2010
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)
 Include Sites : =====
 ->Gaps/Missing Data : Pairwise Deletion
 ->Codon Positions : 1st+2nd+3rd+Noncoding
 Substitution Model : =====
 ->Model : Nucleotide: Kimura 2-parameter
 ->Substitutions to Include : d: Transitions + Transversions
 ->Pattern among Lineages : Same (Homogeneous)
 ->Rates among sites : Uniform rates
 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, 22 November 2010

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ASIA

0.02