WRLFMD

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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00035
Sender Details: [redacted]

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: [redacted]

Official Stamp: [redacted]

Date: 30/11/10

[redacted]

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

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: A
WRLFMD Ref No: VIT/1/2010
Batch No: WRLFMD/2010/00035
Sender Ref: 10-NCVD01 (NCVDA)
Location: Cao Bang, Vietnam
Date collected: 01/01/2010
Date received by WRLFMD: 05/11/2010
Date received for sequencing: 12/11/2010
Species: Cattle
Material used: BHK BTy1
Region sequenced: VP1
RT-PCR primers: A-1C562F/EUR-2B52R
A-1C612F/EUR-2B52R

Report date: 22/11/2010
Reported by: N.J. Knowles
Checked by: D.P. King

Topotype: ASIA
Genotype/strain: unnamed
Sequence filename: VIT10-01.SEQ
Date sequence last updated: 22/11/2010
No. of Nt determined: 636
No. of ambiguities: 0
Gene length: 636
Total no. of comparisons: 1174
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	A_{22}
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	$\text{Iran-05}^{\text{BAR-08}}$
8	A/TUR/33/2008	TUR08-33	636	515	0	80.97	19.03	ASIA	$\text{Iran-05}^{\text{EZM-07}}$
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	$\text{Iran-05}^{\text{AFG-07}}$

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v3.11

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\fmdv\a\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