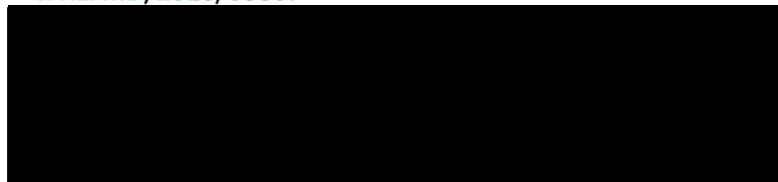




INSTITUTE FOR ANIMAL HEALTH
Director: Professor Martin W. Shirley, PhD
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00007
Sender Details:



Date Received: 5th February 2010
Country of Origin: Vietnam
Date Reported: 4th March 2010

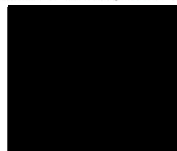
Re: Serotype O

Dear Dr. Linchongsubongkoch,

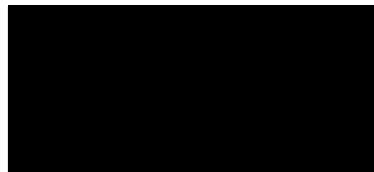
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

Please note that all of these samples were collected over 12 months ago.

Results Approved By:

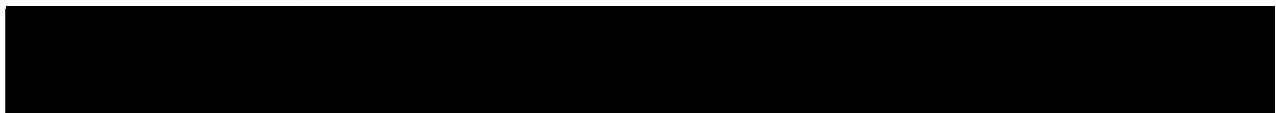


Official Stamp:



Date:

4/3/2010



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

Date: 3 March 2010

FMDV type O

Country: Vietnam

Period: 2008

No. of isolates: 1

BATCH: WRLFMD/2010/00007



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FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 02/03/2010
WRLFMD Ref No: VIT/1/2008	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00007	Checked by: D.P. King
Sender Ref: VIT 2/08 B1	
Location: Ho Chi Minh Province, Vietnam	Topotype: CATHAY
Date collected: 01/01/2008	Genotype/strain: Unnamed
Date received by WRLFMD: 05/02/2010	Sequence filename: VIT08-01.SEQ
Date received for sequencing: 24/02/2010	Date sequence last updated: 02/03/2010
Species: Pig	No. of Nt determined: 639
Material used: BHK1 RS1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2264
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 300
	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	O/VIT/1/2006	VIT06-01	639	639	0	100.00	0.00	CATHAY	unnamed
2	O/VIT/2/2006	VIT06-02	639	639	0	100.00	0.00	CATHAY	unnamed
3	O/VIT/3/2006	VIT06-03	639	637	0	99.69	0.31	CATHAY	unnamed
4	O/MAY/8/2005	MAY05-08	639	627	0	98.12	1.88	CATHAY	unnamed
5	O/VIT/2/05* (TRRL)	VIT05-AB	639	618	0	96.71	3.29	CATHAY	unnamed
6	O/VIT/9/2005	VIT05-09	639	612	0	95.77	4.23	CATHAY	unnamed
7	O/VIT/1/2005	VIT05-01	639	607	0	94.99	5.01	CATHAY	unnamed
8	O/VIT/7/05* (TRRL)	VIT05-AG	639	603	0	94.37	5.63	CATHAY	unnamed
9	O/VIT/1/05* (TRRL)	VIT05-AA	639	600	0	93.90	6.10	CATHAY	unnamed
10	OW/CHA/93 (CONFIDENTIAL)	CHA93--E	402	367	0	91.29	8.71	CATHAY	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	O/Yunlin/TAW/97 (AF308157)	TAW97--B	639	570	0	89.20	10.80	CATHAY	unnamed
2	O/PHI/7/96 (AJ294926)	PHI96-07	639	567	0	88.73	11.27	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	637	547	2	85.87	14.13	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	518	2	81.32	18.68	CATHAY	unnamed
5	O/UKG/35/2001 (AJ539141)	UKG01-35	639	514	0	80.44	19.56	ME-SA	PanAsia
6	O/IRN/8/2005	IRN05-08	639	511	0	79.97	20.03	ME-SA	PanAsia-2
7	O/SUD/2/86 (DQ165075)	SUD86-02	639	511	0	79.97	20.03	EA-3	unnamed
8	O/ETH/1/2007 (FJ798137)	ETH07-01	639	510	0	79.81	20.19	EA-3	unnamed
9	O/ISA/1/62 (AJ303500)	ISA62-01	639	510	0	79.81	20.19	ISA-1	unnamed
10	O/IND/53/79 (AF292107)	IND79A53	639	508	0	79.50	20.50	ME-SA	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.0

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Report on FMDV O in Vietnam in 2008

Batch: WRLFMD/2010/00007

Software: MEGA 4.0
 No. of Taxa : 222
 Data File : n:\evd\meg\db\fmdv\o\SEA2010a.meg
 Data Title : Southeast Asia 2008-2009
 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 : 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 & F. Hamid, 03 March 2010

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