

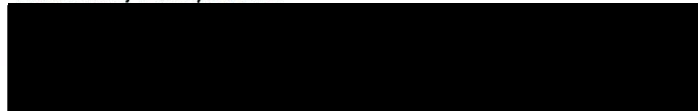


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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00010

Sender Details:

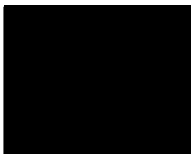


Date Received: 16th March 2010
Country of Origin: Hong Kong SAR
Date Reported: 20th April 2010

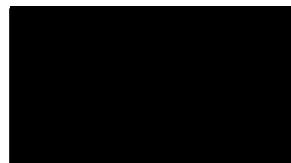
Dear Dr. Geraldine Luk,

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: 22/04/2010

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: 20 April 2010

FMDV type O

Country: Hong Kong SAR

Period: 2010

No. of isolates: 1

BATCH: WRLFMD/2010/00010



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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: 20/04/2010
WRLFMD Ref No: HKN/20/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00010	Checked by: D.P. King
Sender Ref: FMD 07/10 D-10-838	
Location: Not given, Hong Kong	Topotype: SEA
Date collected: 03/03/2010	Genotype/strain: Mya-98
Date received by WRLFMD: 16/03/2010	Sequence filename: HKN10-20.SEQ
Date received for sequencing: 22/03/2010	Date sequence last updated: 20/04/2010
Species: Pig	No. of Nt determined: 639
Material used: BTy2	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C272F/EUR-2B52R	Total no. of comparisons: 2358
	Min. no. of nt for comparison: 300
	Total turn-around time: 35 days
	Sequencing time: 29 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/HKN/19/2010	HKN10-19	639	639	0	100	0	SEA	Mya-98
2	O/HKN/1/2010	HKN10-01	639	632	0	98.9	1.1	SEA	Mya-98
3	O/HKN/18/2010	HKN10-18	639	632	0	98.9	1.1	SEA	Mya-98
4	O/HKN/4/2010	HKN10-04	639	632	0	98.9	1.1	SEA	Mya-98
5	O/HKN/6/2010	HKN10-06	639	631	0	98.75	1.25	SEA	Mya-98
6	O/HKN/13/2010	HKN10-13	639	626	0	97.97	2.03	SEA	Mya-98
7	O/HKN/14/2010	HKN10-14	639	626	0	97.97	2.03	SEA	Mya-98
8	O/HKN/15/2010	HKN10-15	639	626	0	97.97	2.03	SEA	Mya-98
9	O/HKN/7/2010	HKN10-07	639	626	0	97.97	2.03	SEA	Mya-98
10	O/HKN/8/2010	HKN10-08	639	626	0	97.97	2.03	SEA	Mya-98
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/MYA/7/98 (DQ164925)	MYA98-07	639	594	0	92.96	7.04	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	569	0	89.05	10.95	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	543	0	84.98	15.02	ME-SA	unnamed
4	O/ETH/3/2004 (FJ798109)	ETH04-03	639	541	0	84.66	15.34	EA-3	unnamed
5	O/IRN/8/2005	IRN05-08	639	540	0	84.51	15.49	ME-SA	PanAsia-2
6	O/UKG/35/2001 (AJ539141)	UKG01-35	639	539	0	84.35	15.65	ME-SA	PanAsia
7	O/CAM/3/98 (AJ294910)	CAM98-03	639	538	0	84.19	15.81	SEA	Cam-94
8	O/ETH/1/2007 (FJ798137)	ETH07-01	639	537	0	84.04	15.96	EA-3	unnamed
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	534	0	83.57	16.43	ME-SA	Ind-2001a
10	O/IRN/61/2001 (DQ164896)	IRN01-61	638	533	1	83.54	16.46	ME-SA	Iran-2001

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.1

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Report on FMDV O in Hong Kong SAR in 2010

Batch: WRLFMD/2010/00010

Software: MEGA 4.0
 No. of Taxa : 239
 Data File : n:\evd\meg\db\fmdv\o\HKN2010b.meg
 Data Title : O Hong Kong 2010
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (500 replicates; seed=24054)
 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 = 500
 Only bootstrap values of 70% and above are shown

* , not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & F. Hamid, 20 April 2010

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