



INSTITUTE FOR ANIMAL HEALTH

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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00020

Sender Details:



Date Received: 16th May 2012

Country of Origin: Taiwan, Province of China

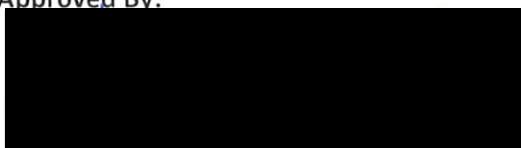
Date Reported: 24th May 2012

Dear Dr YL Lin

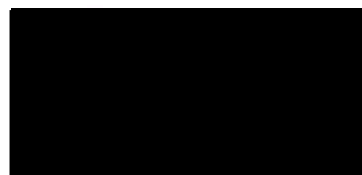
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

<http://www.wrlfmd.org/>

Results Approved By:

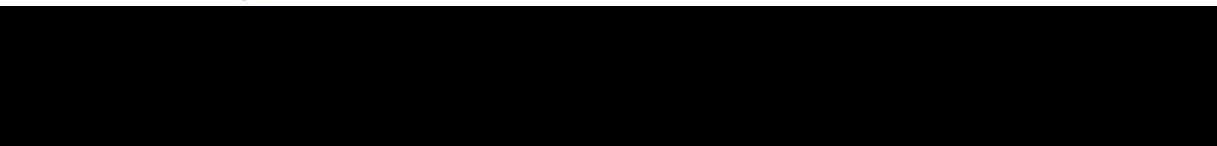


Official Stamp:



Date:

24/5/12



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: gareth.shimmon@iah.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: 23 May 2012

FMDV type O

Country: Taiwan POC

Period: 2012

No. of samples: 1

BATCH: WRLFMD/2012/00020



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: O WRLFMD Ref No: TAW/1/2012 Batch No: WRLFMD/2012/00020 Sender Ref: O1KM-1/2012 Location: Jim Ning Township, Kinmen County, Fukien, Taiwan POC. Date collected: 30/01/2012 Date received by WRLFMD: 16/05/2012 Date received for sequencing: 21/05/2012 Species: Pig Material used: EBK RS1 Region sequenced: VPI RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 23/05/2012 Reported by: N.J. Knowles Checked by: D.P. King Topotype: SEA Genotype/strain: Mya-98 Sequence filename: TAW12-01.SEQ Date sequence last updated: 23/05/2012 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3272 Min. no. of nt for comparison: 600 Total turn-around time: 7 days Sequencing time: 2 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/NC/CHA/2010 (HQ652080)	CHA10-AV	639	621	0	97.18	2.82	SEA	Mya-98
2	O/HKN/1/2010 (JQ070301)	HKN10-01	639	620	0	97.03	2.97	SEA	Mya-98
3	O/HKN/18/2010	HKN10-18	639	620	0	97.03	2.97	SEA	Mya-98
4	O/HKN/4/2010	HKN10-04	639	620	0	97.03	2.97	SEA	Mya-98
5	O/HKN/19/2010 (JQ070305)	HKN10-19	639	619	0	96.87	3.13	SEA	Mya-98
6	O/HKN/20/2010 (HM229661)	HKN10-20	639	619	0	96.87	3.13	SEA	Mya-98
7	O/HKN/6/2010 (JQ070302)	HKN10-06	639	619	0	96.87	3.13	SEA	Mya-98
8	O/VIT/NCVD-8/2010 (NVRQS)	VIT10-AA	639	618	0	96.71	3.29	SEA	Mya-98
9	O/VN/YB10/2010 (HQ260720)	VIT10-AN	639	618	0	96.71	3.29	SEA	Mya-98
10	O/MY/CHA/2010 (HQ652079)	CHA10-AU	639	617	0	96.56	3.44	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	584	0	91.39	8.61	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	559	0	87.48	12.52	SEA	unnamed
3	O/ETH/3/2004 (FJ798109)	ETH04-03	639	538	0	84.19	15.81	EA-3	unnamed
4	O/IND/R2/75* (AF204276)	IND75--A	639	538	0	84.19	15.81	ME-SA	unnamed
5	O/PAK/16/2010	PAK10-16	639	536	0	83.88	16.12	ME-SA	PanAsia-2 ^{PUN-10}
6	O/CAM/3/98 (AJ294910)	CAM98-03	639	534	0	83.57	16.43	SEA	Cam-94
7	O/IRN/8/2005	IRN05-08	639	531	0	83.10	16.90	ME-SA	PanAsia-2
8	O/ETH/1/2007 (FJ798137)	ETH07-01	639	529	0	82.79	17.21	EA-3	unnamed
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	529	0	82.79	17.21	ME-SA	Ind-2001a
10	O/IND/53/79 (AF292107)	IND79A53	639	528	0	82.63	17.37	ME-SA	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV O in Taiwan POC in 2012

Batch: WRLFMD/2012/00012

◆ indicates viruses in this batch

Software: MEGA 5.0

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

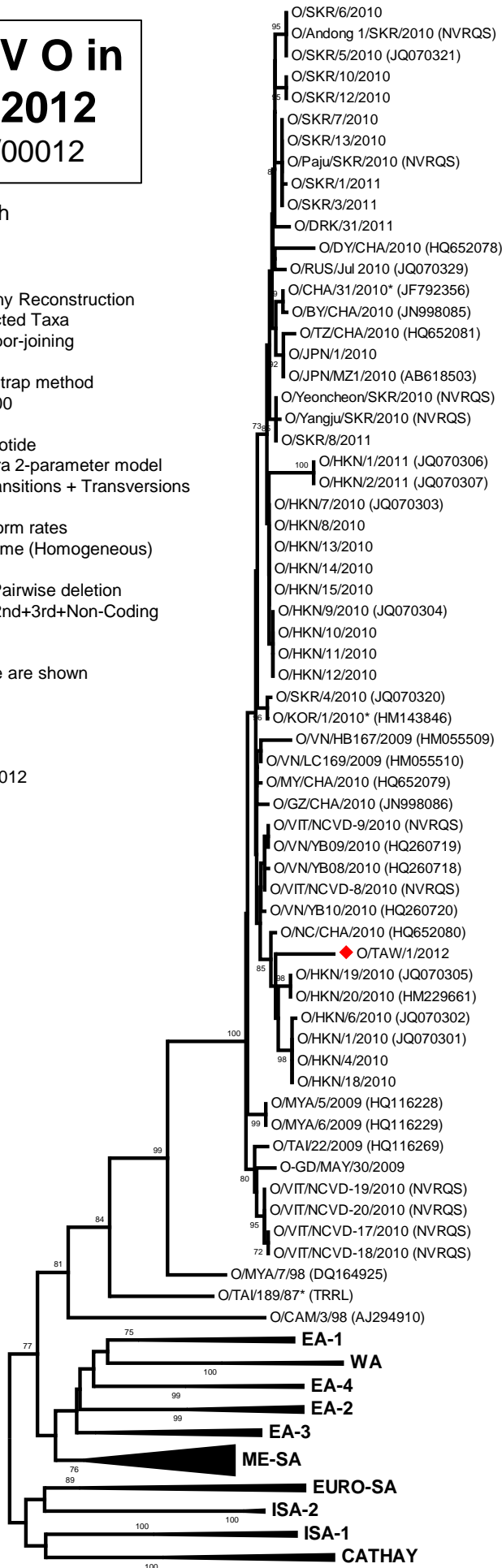
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 23 May 2012

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Mya-98

SEA

Cam-94

0.02