

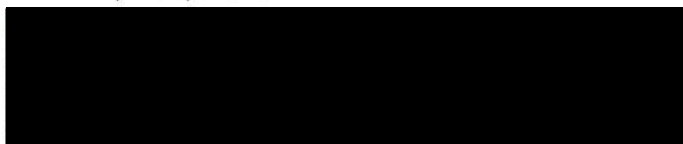


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## FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2011/00048

Sender Details:



Date Received: 9th December 2011

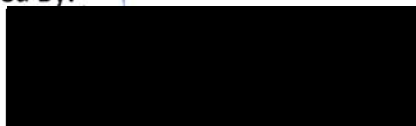
Country of Origin: Malaysia

Date Reported: 5th January 2012

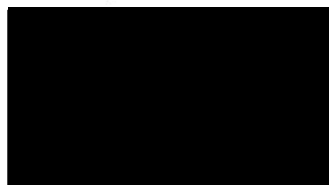
Dear Dr Norlida Bt Othman

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:

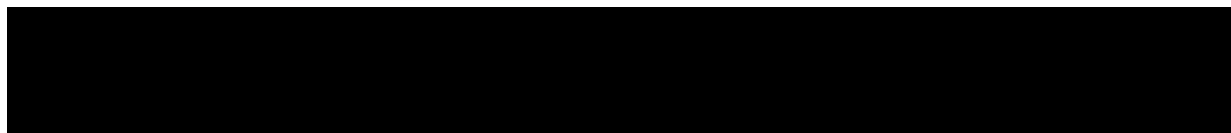


Official Stamp:



Date:

5 11 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](mailto: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: 4 January 2012

FMDV type O

Country: Malaysia

Period: 2011

No. of samples: 1

BATCH: WRLFMD/2011/00048



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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: MAY/13/2011 Batch No: WRLFMD/2011/00048 Sender Ref: 3641/11 Location: Felda Chemplak, Lqabis, Segamat, Johor, Malaysia Date collected: 07/07/2011 Date received by WRLFMD: 09/12/2011 Date received for sequencing: 22/12/2011 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 04/01/2012 Reported by: N.J. Knowles Checked by: D.P. King Topotype: SEA Genotype/strain: Mya-98 Sequence filename: MAY11-13.SEQ Date sequence last updated: 04/01/2012 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3196 Min. no. of nt for comparison: 600 Total turn-around time: 26 days Sequencing time: 13 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-GD/MAY/23/2009	MAY09-23	639	628	0	98.28	1.72	SEA	Mya-98
2	O-GD/MAY/24/2009	MAY09-24	639	627	0	98.12	1.88	SEA	Mya-98
3	O-GD/MAY/27/2009	MAY09-27	639	627	0	98.12	1.88	SEA	Mya-98
4	O/TAI/13/2009 (HQ116261)	TAI09-13	639	625	0	97.81	2.19	SEA	Mya-98
5	O/TAI/15/2009 (HQ116262)	TAI09-15	639	625	0	97.81	2.19	SEA	Mya-98
6	O/TAI/16/2009 (HQ116263)	TAI09-16	639	625	0	97.81	2.19	SEA	Mya-98
7	O/TAI/17/2009 (HQ116264)	TAI09-17	639	625	0	97.81	2.19	SEA	Mya-98
8	O-GD/MAY/22/2009	MAY09-22	639	625	0	97.81	2.19	SEA	Mya-98
9	O/VN/HB166/2009 (HM055499)	VIT09-AF	639	624	0	97.65	2.35	SEA	Mya-98
10	O/VN/SL02/2010 (HQ260714)	VIT10-AH	639	624	0	97.65	2.35	SEA	Mya-98
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
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	581	0	90.92	9.08	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	562	0	87.95	12.05	SEA	unnamed
3	O/PAK/16/2003 (DQ165068)	PAK03-16	639	544	0	85.13	14.87	ME-SA	Pak-98
4	O/IND/R2/75* (AF204276)	IND75--A	639	542	0	84.82	15.18	ME-SA	unnamed
5	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	541	0	84.66	15.34	ME-SA	unnamed
6	O/OMN/7/2001 (DQ164941)	OMN01-07	639	537	0	84.04	15.96	ME-SA	Ind-2001b
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	537	0	84.04	15.96	ME-SA	PanAsia-2 <sup>SAN-09</sup>
8	O/CAM/3/98 (AJ294910)	CAM98-03	639	536	0	83.88	16.12	SEA	Cam-94
9	O/IND/53/79 (AF292107)	IND79A53	639	536	0	83.88	16.12	ME-SA	unnamed
10	O/TUR/257/2008* (FMDI)	TUR08-AD	639	536	0	83.88	16.12	ME-SA	PanAsia-2 <sup>TER-08</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# Report on FMDV O in Malaysia in 2011

Batch: WRLFMD/2011/00048

◆ indicates viruses in this batch

Software: MEGA 5.0

Analysis

----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

----- 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

----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

----- 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, 04 January 2012

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