

FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

Report Date for this Batch: 7 February 2016

FMDV type O

Country: Hong Kong SAR

Period: 2015

No. of samples: 1

BATCH: WRLFMD/2016/00002



The contents of this report are copyright and should not be reproduced without permission

© The Pirbright Institute

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: HKN/12/2015 Batch No: WRLFMD/2016/00002 Sender Ref: 15-17625 Location: Shueng Shui, Hong Kong Date collected: 02/12/2015 Date received by WRLFMD: 13/01/2016 Date received for sequencing: 02/02/2016 Species: Pig Material used: RS1 21/01/2016 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 07/02/2016 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: CATHAY Genotype/strain: unnamed Sequence filename: HKN15-12.SEQ Date sequence last updated: 07/02/2016 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4201 Min. no. of nt for comparison: 600 Total turn-around time: 25 days Sequencing time: 5 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/1/2015	HKN15-01	639	629	0	98.44	1.56	CATHAY	unnamed
2	O/HKN/8/2015	HKN15-08	639	629	0	98.44	1.56	CATHAY	unnamed
3	O/HKN/10/2015	HKN15-10	639	628	0	98.28	1.72	CATHAY	unnamed
4	O/HKN/15/2014	HKN14-15	639	627	0	98.12	1.88	CATHAY	unnamed
5	O/HKN/2/2015	HKN15-02	639	627	0	98.12	1.88	CATHAY	unnamed
6	O/HKN/11/2014	HKN14-11	639	626	0	97.97	2.03	CATHAY	unnamed
7	O/HKN/9/2015	HKN15-09	639	626	0	97.97	2.03	CATHAY	unnamed
8	O/HKN/5/2015	HKN15-05	639	625	0	97.81	2.19	CATHAY	unnamed
9	O/HKN/6/2015	HKN15-06	639	625	0	97.81	2.19	CATHAY	unnamed
10	O/HKN/7/2015	HKN15-07	639	625	0	97.81	2.19	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	566	0	88.58	11.42	CATHAY	unnamed
2	O/PHI/7/96 (AJ294926;KM243058)	PHI96-07	639	563	0	88.11	11.89	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	637	544	2	85.40	14.60	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	520	2	81.63	18.37	CATHAY	unnamed
5	O/UGA/17/98 (HM211075)	UGA98-17	639	514	0	80.44	19.56	EA-4	unnamed
6	O/IND/53/79 (AF292107)	IND79A53	639	512	0	80.13	19.87	ME-SA	unnamed
7	O/TAN/2/2004 (KF561679)	TAN04-02	639	508	0	79.50	20.50	EA-2	unnamed
8	O/MAL/1/98 (DQ165074)	MAL98-01	639	507	0	79.34	20.66	EA-2	unnamed
9	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	507	0	79.34	20.66	ME-SA	unnamed
10	O/ETH/58/2005 (FJ798141)	ETH05-58	639	505	0	79.03	20.97	EA-4	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

© *The Pirbright Institute* (not to be reproduced without permission)

Report on FMDV O in Hong Kong SAR in 2015

Batch: WRLFMD/2016/00002

◆ indicates viruses in this batch

Software: MEGA 6.06

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

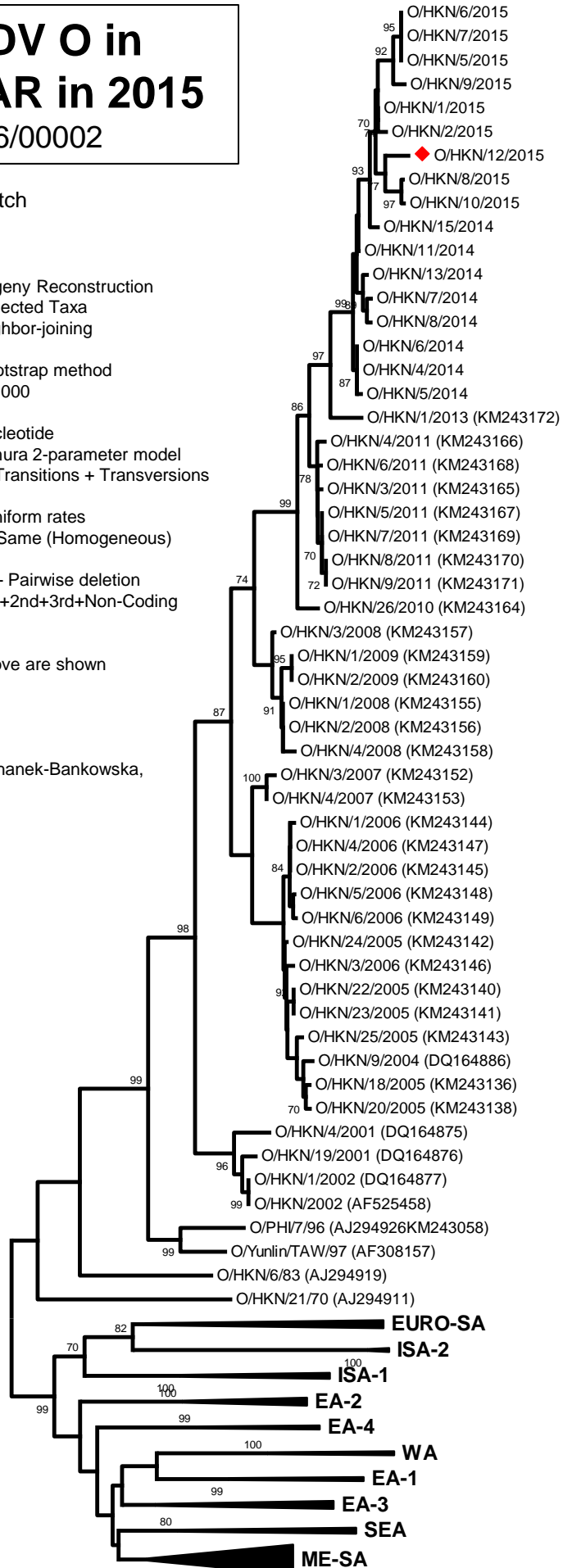
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
7 February 2016

© *The Pirbright Institute*

(not to be reproduced without permission)



0.02