

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

Genotyping Report

Report Date for this Batch: 16 November 2015

FMDV type O

Country: Hong Kong SAR

Period: 2015

No. of samples: 3

BATCH: WRLFMD/2015/00026



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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 WRLFMD Ref No: HKN/5/2015 Batch No: WRLFMD/2015/00026 Sender Ref: 15-13921(1) Location: Lung Wo Village No. 2, Clear Water Bay, Sai Kung, New Territories, Hong Kong Date collected: 18/09/2015 Date received by WRLFMD: 07/10/2015 Date received for sequencing: 10/11/2015 Species: Porcine Material used: RS1 15/10/2015 & RS2 31/10/2015 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 15/11/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: CATHAY Genotype/strain: unnamed Sequence filename: HKN15-05.SEQ Date sequence last updated: 15/11/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4171 Min. no. of nt for comparison: 600 Total turn-around time: 39 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/6/2015	HKN15-06	639	639	0	100.00	0.00	CATHAY	unnamed
2	O/HKN/7/2015	HKN15-07	639	639	0	100.00	0.00	CATHAY	unnamed
3	O/HKN/1/2015	HKN15-01	639	633	0	99.06	0.94	CATHAY	unnamed
4	O/HKN/2/2015	HKN15-02	639	631	0	98.75	1.25	CATHAY	unnamed
5	O/HKN/15/2014	HKN14-15	639	629	0	98.44	1.56	CATHAY	unnamed
6	O/HKN/11/2014	HKN14-11	639	628	0	98.28	1.72	CATHAY	unnamed
7	O/HKN/4/2014	HKN14-04	639	626	0	97.97	2.03	CATHAY	unnamed
8	O/HKN/6/2014	HKN14-06	639	626	0	97.97	2.03	CATHAY	unnamed
9	O/HKN/13/2014	HKN14-13	639	625	0	97.81	2.19	CATHAY	unnamed
10	O/HKN/5/2014	HKN14-05	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	569	0	89.05	10.95	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	543	2	85.24	14.76	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	521	2	81.79	18.21	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	639	512	0	80.13	19.87	ME-SA	unnamed
6	O/TAN/2/2004 (KF561679)	TAN04-02	639	511	0	79.97	20.03	EA-2	unnamed
7	O/MAL/1/98 (DQ165074)	MAL98-01	639	510	0	79.81	20.19	EA-2	unnamed
8	O/UGA/17/98 (HM211075)	UGA98-17	639	510	0	79.81	20.19	EA-4	unnamed
9	O/UGA/3/2002 (DQ165077)	UGA02-03	639	510	0	79.81	20.19	EA-2	unnamed
10	O1/Manisa/TUR/69 (AY593823)	TUR69-G	639	510	0	79.81	20.19	ME-SA	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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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 WRLFMD Ref No: HKN/6/2015 Batch No: WRLFMD/2015/00026 Sender Ref: 15-13921(2) Location: Lung Wo Village No. 2, Clear Water Bay, Sai Kung, New Territories, Hong Kong Date collected: 18/09/2015 Date received by WRLFMD: 07/10/2015 Date received for sequencing: 10/11/2015 Species: Porcine Material used: RS1 15/10/2015 & RS2 31/10/2015 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 15/11/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: CATHAY Genotype/strain: unnamed Sequence filename: HKN15-06.SEQ Date sequence last updated: 15/11/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4171 Min. no. of nt for comparison: 600 Total turn-around time: 39 days Sequencing time: 5 days
Comments:	

Most Closely Related Viruses									
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1	O/HKN/5/2015	HKN15-05	639	639	0	100.00	0.00	CATHAY	unnamed
2	O/HKN/7/2015	HKN15-07	639	639	0	100.00	0.00	CATHAY	unnamed
3	O/HKN/1/2015	HKN15-01	639	633	0	99.06	0.94	CATHAY	unnamed
4	O/HKN/2/2015	HKN15-02	639	631	0	98.75	1.25	CATHAY	unnamed
5	O/HKN/15/2014	HKN14-15	639	629	0	98.44	1.56	CATHAY	unnamed
6	O/HKN/11/2014	HKN14-11	639	628	0	98.28	1.72	CATHAY	unnamed
7	O/HKN/4/2014	HKN14-04	639	626	0	97.97	2.03	CATHAY	unnamed
8	O/HKN/6/2014	HKN14-06	639	626	0	97.97	2.03	CATHAY	unnamed
9	O/HKN/13/2014	HKN14-13	639	625	0	97.81	2.19	CATHAY	unnamed
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3	O/HKN/6/83 (AJ294919)	HKN83-06	637	543	2	85.24	14.76	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	521	2	81.79	18.21	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	639	512	0	80.13	19.87	ME-SA	unnamed
6	O/TAN/2/2004 (KF561679)	TAN04-02	639	511	0	79.97	20.03	EA-2	unnamed
7	O/MAL/1/98 (DQ165074)	MAL98-01	639	510	0	79.81	20.19	EA-2	unnamed
8	O/UGA/17/98 (HM211075)	UGA98-17	639	510	0	79.81	20.19	EA-4	unnamed
9	O/UGA/3/2002 (DQ165077)	UGA02-03	639	510	0	79.81	20.19	EA-2	unnamed
10	O1/Manisa/TUR/69 (AY593823)	TUR69-G	639	510	0	79.81	20.19	ME-SA	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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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 WRLFMD Ref No: HKN/7/2015 Batch No: WRLFMD/2015/00026 Sender Ref: 15-13921(3) Location: Lung Wo Village No. 2, Clear Water Bay, Sai Kung, New Territories, Hong Kong Date collected: 18/09/2015 Date received by WRLFMD: 07/10/2015 Date received for sequencing: 10/11/2015 Species: Porcine Material used: RSI 15/10/2015 Region sequenced: VPI RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 15/11/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: CATHAY Genotype/strain: unnamed Sequence filename: HKN15-07.SEQ Date sequence last updated: 15/11/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4171 Min. no. of nt for comparison: 600 Total turn-around time: 39 days Sequencing time: 5 days
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8	O/HKN/6/2014	HKN14-06	639	626	0	97.97	2.03	CATHAY	unnamed
9	O/HKN/13/2014	HKN14-13	639	625	0	97.81	2.19	CATHAY	unnamed
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nt, nucleotides

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Report on FMDV O in Hong Kong SAR in 2015

Batch: WRLFMD/2015/00026

◆ indicates viruses in this batch

Software: MEGA 6.06

Analysis

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

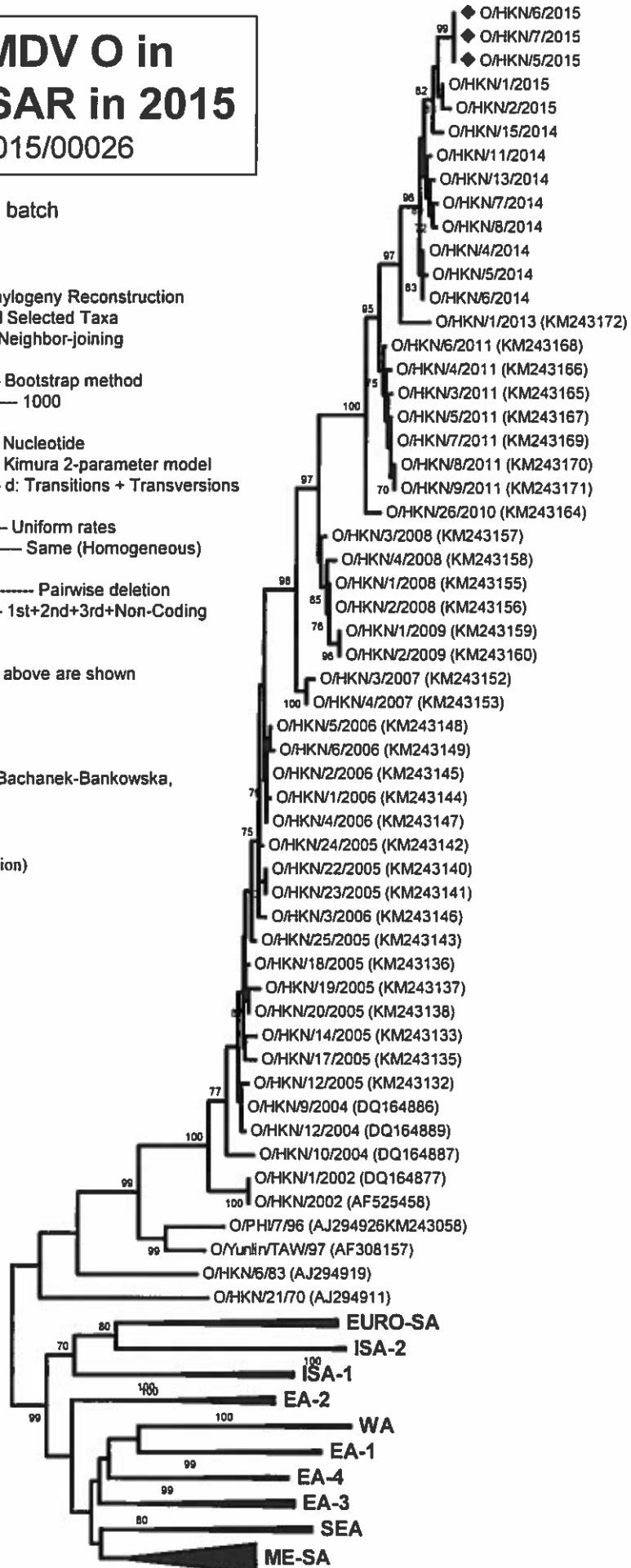
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
 16 November 2015

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CATHAY

0.02