

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

## Genotyping Report

Report Date for this Batch: 21 January 2016

FMDV type O

Country: Hong Kong SAR

Period: 2015

No. of samples: 3

BATCH: WRLFMD/2015/00036



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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	Report date: 21/01/2016
WRLFMD Ref No: HKN/8/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00036	Checked by: K. Bachanek-Bankowska
Sender Ref: FMD 17/15 15-16290 (2)	
Location: not known, Hong Kong	Topotype: CATHAY
Date collected: 07/11/2015	Genotype/strain: unnamed
Date received by WRLFMD: 02/12/2015	Sequence filename: HKN15-08.SEQ
Date received for sequencing: 11/12/2015	Date sequence last updated: 15/12/2015
Species: Porcine	No. of Nt determined: 639
Material used: RS1 04/12/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4195
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 50 days
	Sequencing time: 41 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/10/2015	HKN15-10	639	638	0	99.84	0.16	CATHAY	unnamed
2	O/HKN/1/2015	HKN15-01	639	631	0	98.75	1.25	CATHAY	unnamed
3	O/HKN/15/2014	HKN14-15	639	629	0	98.44	1.56	CATHAY	unnamed
4	O/HKN/2/2015	HKN15-02	639	629	0	98.44	1.56	CATHAY	unnamed
5	O/HKN/11/2014	HKN14-11	639	628	0	98.28	1.72	CATHAY	unnamed
6	O/HKN/4/2014	HKN14-04	639	626	0	97.97	2.03	CATHAY	unnamed
7	O/HKN/6/2014	HKN14-06	639	626	0	97.97	2.03	CATHAY	unnamed
8	O/HKN/9/2015	HKN15-09	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](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	566	0	88.58	11.42	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	637	545	2	85.56	14.44	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	517	2	81.16	18.84	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	639	511	0	79.97	20.03	ME-SA	unnamed
6	O/UGA/17/98 (HM211075)	UGA98-17	639	511	0	79.97	20.03	EA-4	unnamed
7	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	509	0	79.66	20.34	ME-SA	unnamed
8	O/TAN/2/2004 (KF561679)	TAN04-02	639	508	0	79.50	20.50	EA-2	unnamed
9	O/MAL/1/98 (DQ165074)	MAL98-01	639	507	0	79.34	20.66	EA-2	unnamed
10	O/UGA/3/2002 (DQ165077)	UGA02-03	639	507	0	79.34	20.66	EA-2	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

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# FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O	Report date: 21/01/2016
WRLFMD Ref No: HKN/9/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00036	Checked by: K. Bachanek-Bankowska
Sender Ref: FMD 17/15 16-16290 (3)	
Location: not known, Hong Kong	Topotype: CATHAY
Date collected: 07/11/2015	Genotype/strain: unnamed
Date received by WRLFMD: 02/12/2015	Sequence filename: HKN15-09.SEQ
Date received for sequencing: 11/12/2015	Date sequence last updated: 15/12/2015
Species: Porcine	No. of Nt determined: 639
Material used: RS1 04/12/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4195
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 50 days
	Sequencing time: 41 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/5/2015	HKN15-05	639	634	0	99.22	0.78	CATHAY	unnamed
2	O/HKN/6/2015	HKN15-06	639	634	0	99.22	0.78	CATHAY	unnamed
3	O/HKN/7/2015	HKN15-07	639	634	0	99.22	0.78	CATHAY	unnamed
4	O/HKN/1/2015	HKN15-01	639	632	0	98.90	1.10	CATHAY	unnamed
5	O/HKN/2/2015	HKN15-02	639	630	0	98.59	1.41	CATHAY	unnamed
6	O/HKN/15/2014	HKN14-15	639	628	0	98.28	1.72	CATHAY	unnamed
7	O/HKN/11/2014	HKN14-11	639	627	0	98.12	1.88	CATHAY	unnamed
8	O/HKN/8/2015	HKN15-08	639	626	0	97.97	2.03	CATHAY	unnamed
9	O/HKN/10/2015	HKN15-10	639	625	0	97.81	2.19	CATHAY	unnamed
10	O/HKN/4/2014	HKN14-04	639	625	0	97.81	2.19	CATHAY	unnamed

## Most Closely Related Reference Viruses

(see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](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	567	0	88.73	11.27	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	545	2	85.56	14.44	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	519	2	81.48	18.52	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	639	511	0	79.97	20.03	ME-SA	unnamed
6	O/MAL/1/98 (DQ165074)	MAL98-01	639	510	0	79.81	20.19	EA-2	unnamed
7	O/UGA/17/98 (HM211075)	UGA98-17	639	510	0	79.81	20.19	EA-4	unnamed
8	O/UGA/3/2002 (DQ165077)	UGA02-03	639	510	0	79.81	20.19	EA-2	unnamed
9	O/TAN/2/2004 (KF561679)	TAN04-02	639	509	0	79.66	20.34	EA-2	unnamed
10	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	509	0	79.66	20.34	ME-SA	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

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Serotype: O WRLFMD Ref No: HKN/10/2015 Batch No: WRLFMD/2015/00036 Sender Ref: FMD 17/15 16-16290 (4) Location: not known, Hong Kong Date collected: 07/11/2015 Date received by WRLFMD: 02/12/2015 Date received for sequencing: 11/12/2015 Species: Porcine Material used: RS1 04/12/2015 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 21/01/2016 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska  Topotype: CATHAY Genotype/strain: unnamed Sequence filename: HKN15-10.SEQ Date sequence last updated: 15/12/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4195 Min. no. of nt for comparison: 600 Total turn-around time: 50 days Sequencing time: 41 days
Comments:	

<b>Most Closely Related Viruses</b>									
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1	O/HKN/8/2015	HKN15-08	639	638	0	99.84	0.16	CATHAY	unnamed
2	O/HKN/1/2015	HKN15-01	639	630	0	98.59	1.41	CATHAY	unnamed
3	O/HKN/15/2014	HKN14-15	639	628	0	98.28	1.72	CATHAY	unnamed
4	O/HKN/2/2015	HKN15-02	639	628	0	98.28	1.72	CATHAY	unnamed
5	O/HKN/11/2014	HKN14-11	639	627	0	98.12	1.88	CATHAY	unnamed
6	O/HKN/4/2014	HKN14-04	639	625	0	97.81	2.19	CATHAY	unnamed
7	O/HKN/6/2014	HKN14-06	639	625	0	97.81	2.19	CATHAY	unnamed
8	O/HKN/9/2015	HKN15-09	639	625	0	97.81	2.19	CATHAY	unnamed
9	O/HKN/13/2014	HKN14-13	639	624	0	97.65	2.35	CATHAY	unnamed
10	O/HKN/5/2014	HKN14-05	639	624	0	97.65	2.35	CATHAY	unnamed
<b>Most Closely Related Reference Viruses</b>									
(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/Yunlin/TAW/97 (AF308157)	TAW97--B	639	570	0	89.20	10.80	CATHAY	unnamed
2	O/PHI/7/96 (AJ294926;KM243058)	PHI96-07	639	567	0	88.73	11.27	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	637	546	2	85.71	14.29	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	518	2	81.32	18.68	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	639	512	0	80.13	19.87	ME-SA	unnamed
6	O/UGA/17/98 (HM211075)	UGA98-17	639	512	0	80.13	19.87	EA-4	unnamed
7	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	510	0	79.81	20.19	ME-SA	unnamed
8	O/MAL/1/98 (DQ165074)	MAL98-01	639	508	0	79.50	20.50	EA-2	unnamed
9	O/ISA/1/62 (AJ303500)	ISA62-01	639	507	0	79.34	20.66	ISA-1	unnamed
10	O/TAN/2/2004 (KF561679)	TAN04-02	639	507	0	79.34	20.66	EA-2	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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# Report on FMDV O in Hong Kong SAR in 2015

Batch: WRLFMD/2015/00036

◆ indicates viruses in this batch

Software: MEGA 6.06

Analysis

----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

----- 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

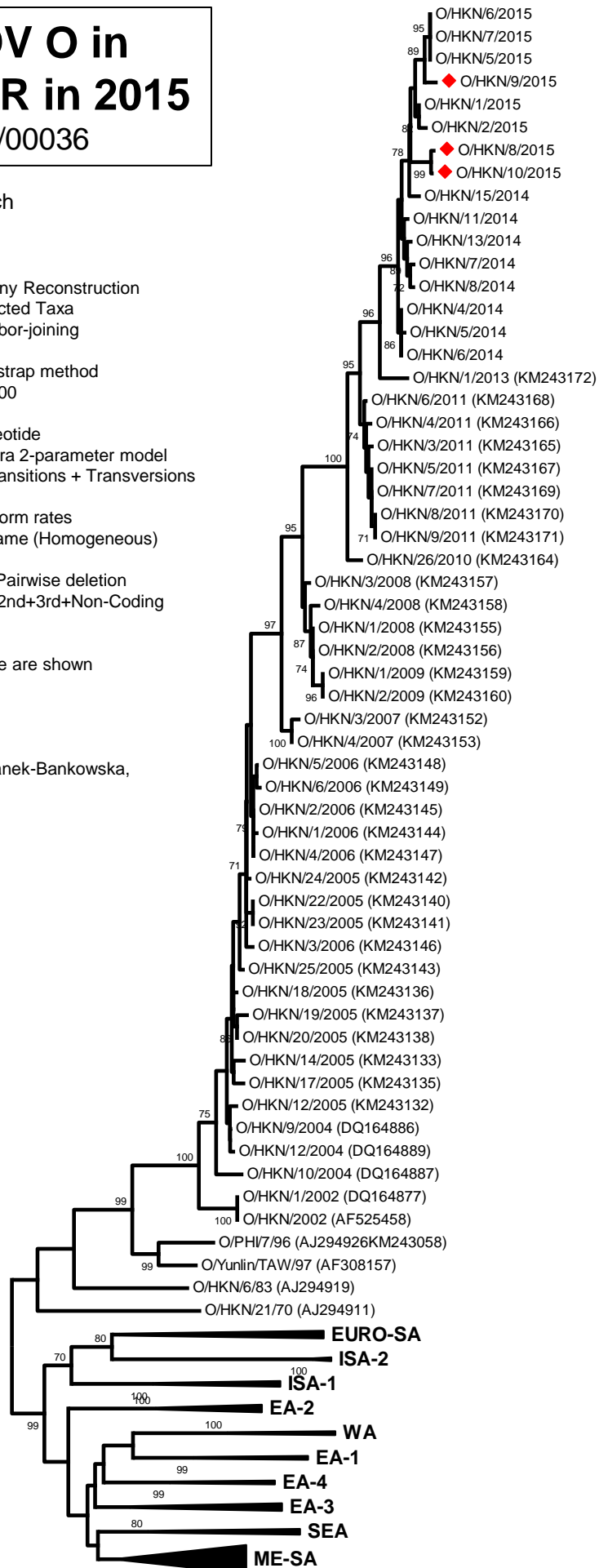
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,  
21 January 2016

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CATHAY

0.02