

FAO World Reference Laboratory for Foot-and-Mouth Disease

Genotyping Report

Report date for this batch: 04-Apr-2014

FMDV type: O

Country: HONG KONG, SAR OF PRC

Year: 2014

WRL BATCH: WRLFMD/2014/00015



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Genotyping Results

WRL Batch: WRLFMD/2014/00015

Batch: IAHB/2014/00154

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

Genotyping Report

Report Date for this Batch: 4 April 2014

FMDV type O

Country: Hong Kong SAR

Period: 2014

No. of samples: 1

BATCH: WRLFMD/2014/00015



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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O	Report date: 04/04/2014
WRLFMD Ref No: HKN/11/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00015	Checked by: K. Bachanek-Bankowska
Sender Ref: FMD 05/14, 14-03915	
Location: not given, Hong Kong SAR	Topotype: CATHAY
Date collected: 06/03/2014	Genotype/strain: unnamed
Date received by WRLFMD: 27/03/2014	Sequence filename: HKN14-11.SEQ
Date received for sequencing: 02/04/2014	Date sequence last updated: 03/04/2014
Species: Pig	No. of Nt determined: 639
Material used: RS1 28/03/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3820
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 8 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/HKN/4/2014	HKN14-04	639	637	0	99.69	0.31	CATHAY	unnamed
2	O/HKN/6/2014	HKN14-06	639	637	0	99.69	0.31	CATHAY	unnamed
3	O/HKN/5/2014	HKN14-05	639	636	0	99.53	0.47	CATHAY	unnamed
4	O/HKN/7/2014	HKN14-07	639	635	0	99.37	0.63	CATHAY	unnamed
5	O/HKN/8/2014	HKN14-08	639	635	0	99.37	0.63	CATHAY	unnamed
6	O/HKN/1/2013	HKN13-01	639	623	0	97.50	2.50	CATHAY	unnamed
7	O/HKN/3/2011	HKN11-03	639	621	0	97.18	2.82	CATHAY	unnamed
8	O/HKN/5/2011	HKN11-05	639	621	0	97.18	2.82	CATHAY	unnamed
9	O/HKN/6/2011	HKN11-06	639	621	0	97.18	2.82	CATHAY	unnamed
10	O/HKN/7/2011	HKN11-07	639	621	0	97.18	2.82	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	572	0	89.51	10.49	CATHAY	unnamed
2	O/PHI/7/96 (AJ294926)	PHI96-07	639	569	0	89.05	10.95	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	637	550	2	86.34	13.66	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	524	2	82.26	17.74	CATHAY	unnamed
5	O/UGA/17/98 (HM211075)	UGA98-17	639	513	0	80.28	19.72	EA-4	unnamed
6	O/IND/53/79 (AF292107)	IND79A53	639	511	0	79.97	20.03	ME-SA	unnamed
7	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	511	0	79.97	20.03	ME-SA	unnamed
8	O/MAL/1/98 (DQ165074)	MAL98-01	639	509	0	79.66	20.34	EA-2	unnamed
9	O/TAN/2/2004 (KF561679)	TAN04-02	639	508	0	79.50	20.50	EA-2	unnamed
10	O/ETH/58/2005 (FJ798141)	ETH05-58	639	507	0	79.34	20.66	EA-4	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV O in Hong Kong SAR in 2014

Batch: WRLFMD/2014/00015

◆ 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

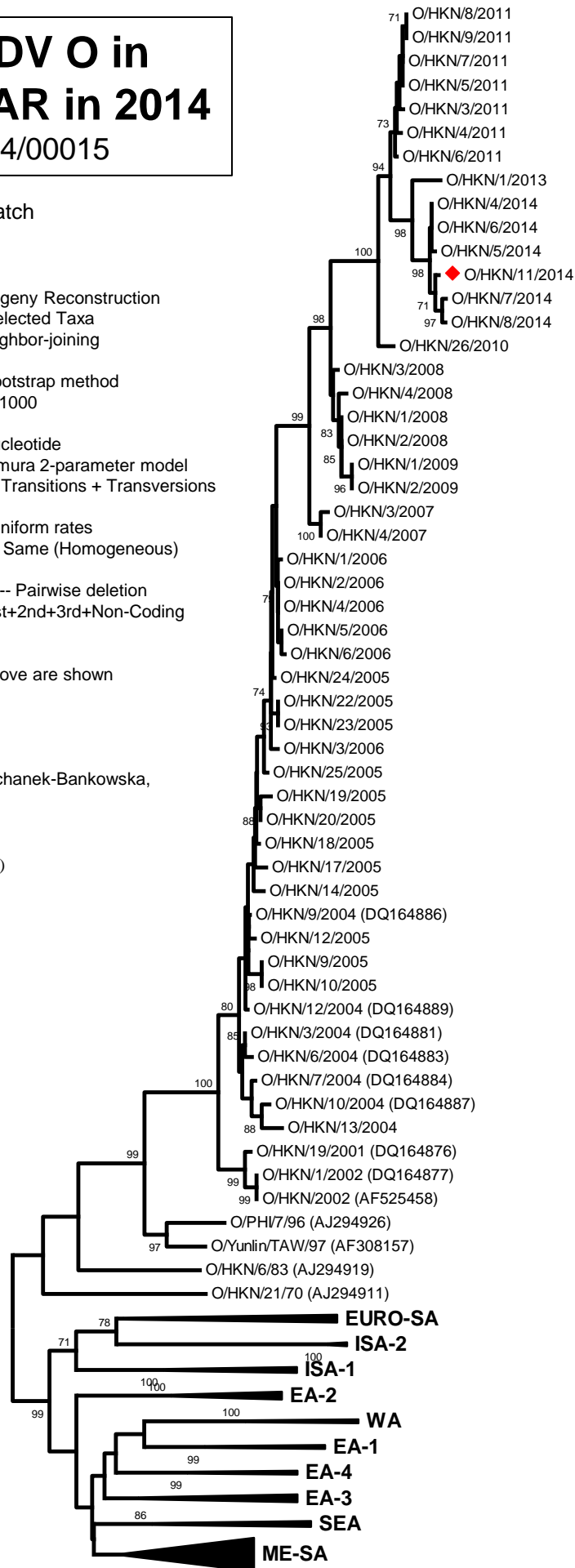
*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,

04 April 2014

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CATHAY

0.02