FAO World Reference Laboratory for Foot-and-Mouth Disease

Genotyping Report

Report date for this batch: 25-Mar-2014

FMDV type: O

Country: HONG KONG, SAR OF PRC

Year: 2014

WRL BATCH: WRLFMD/2014/00008

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

Genotyping Report

Report Date for this Batch: 25 March 2014

FMDV type O
Country: Hong Kong SAR
Period: 2014
No. of samples: 3

BATCH: WRLFMD/2014/00008

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: HKN/4/2014
Batch No: WRLFMD/2014/00008
Sender Ref: 14-02340 (1)
Location: Ki Lun Shan, Hong Kong
Date collected: 07/02/2014
Date received by WRLFMD: 26/02/2014
Date received for sequencing: 07/03/2014
Species: Porcine
Material used: RS1 05/03/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 18/03/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: CATHAY
Genotype/strain: unnamed
Sequence filename: HKN14-04.SEQ
Date sequence last updated: 15/03/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3804
Min. no. of nt for comparison: 600
Total turn-around time: 20 days
Sequencing time: 11 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/6/2014	HKN14-06	639	639	0	100.00	0.00	CATHAY	unnamed
2	O/HKN/5/2014	HKN14-05	639	638	0	99.84	0.16	CATHAY	unnamed
3	O/HKN/7/2014	HKN14-07	639	633	0	99.06	0.94	CATHAY	unnamed
4	O/HKN/8/2014	HKN14-08	639	633	0	99.06	0.94	CATHAY	unnamed
5	O/HKN/1/2013	HKN13-01	639	625	0	97.81	2.19	CATHAY	unnamed
6	O/HKN/3/2011	HKN11-03	639	623	0	97.50	2.50	CATHAY	unnamed
7	O/HKN/5/2011	HKN11-05	639	623	0	97.50	2.50	CATHAY	unnamed
8	O/HKN/6/2011	HKN11-06	639	623	0	97.50	2.50	CATHAY	unnamed
9	O/HKN/7/2011	HKN11-07	639	623	0	97.50	2.50	CATHAY	unnamed
10	O/HKN/4/2011	HKN11-04	639	622	0	97.34	2.66	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	548	2	86.03	13.97	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	526	2	82.57	17.43	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	639	513	0	80.28	19.72	ME-SA	unnamed
6	O/UGA/17/98 (HM211075)	UGA98-17	639	513	0	80.28	19.72	EA-4	unnamed
7	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	511	0	79.97	20.03	ME-SA	unnamed
8	O/TAN/2/2004 (KF561679)	TAN04-02	639	510	0	79.81	20.19	EA-2	unnamed
9	O/MAL/1/98 (DQ165074)	MAL98-01	639	509	0	79.66	20.34	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

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: HKN/5/2014
Batch No: WRLFMD/2014/00008
Sender Ref: 14-02340 (2)
Location: Ki Lun Shan, Hong Kong
Date collected: 07/02/2014
Date received by WRLFMD: 26/02/2014
Date received for sequencing: 07/03/2014
Species: Porcine
Material used: RS1 04/03/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 18/03/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: CATHAY
Genotype/strain: unnamed
Sequence filename: HKN14-05.SEQ
Date sequence last updated: 15/03/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3804
Min. no. of nt for comparison: 600
Total turn-around time: 20 days
Sequencing time: 11 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	638	0	99.84	0.16	CATHAY	unnamed
2	O/HKN/6/2014	HKN14-06	639	638	0	99.84	0.16	CATHAY	unnamed
3	O/HKN/7/2014	HKN14-07	639	632	0	98.90	1.10	CATHAY	unnamed
4	O/HKN/8/2014	HKN14-08	639	632	0	98.90	1.10	CATHAY	unnamed
5	O/HKN/1/2013	HKN13-01	639	624	0	97.65	2.35	CATHAY	unnamed
6	O/HKN/3/2011	HKN11-03	639	622	0	97.34	2.66	CATHAY	unnamed
7	O/HKN/5/2011	HKN11-05	639	622	0	97.34	2.66	CATHAY	unnamed
8	O/HKN/6/2011	HKN11-06	639	622	0	97.34	2.66	CATHAY	unnamed
9	O/HKN/7/2011	HKN11-07	639	622	0	97.34	2.66	CATHAY	unnamed
10	O/HKN/4/2011	HKN11-04	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	571	0	89.36	10.64	CATHAY	unnamed
2	O/PHI/7/96 (AJ294926)	PHI96-07	639	568	0	88.89	11.11	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	637	547	2	85.87	14.13	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	525	2	82.42	17.58	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/TAN/2/2004 (KF561679)	TAN04-02	639	509	0	79.66	20.34	EA-2	unnamed
9	O/MAL/1/98 (DQ165074)	MAL98-01	639	508	0	79.50	20.50	EA-2	unnamed
10	O/ETH/58/2005 (FJ798141)	ETH05-58	639	506	0	79.19	20.81	EA-4	unnamed

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: HKN/6/2014
Batch No: WRLFMD/2014/00008
Sender Ref: 14-02340 (3)
Location: Ki Lun Shan, Hong Kong
Date collected: 07/02/2014
Date received by WRLFMD: 26/02/2014
Date received for sequencing: 13/03/2014
Species: Porcine
Material used: RS1 05/03/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 18/03/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: CATHAY
Genotype/strain: unnamed
Sequence filename: HKN14-06.SEQ
Date sequence last updated: 15/03/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3804
Min. no. of nt for comparison: 600
Total turn-around time: 20 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/4/2014	HKN14-04	639	639	0	100.00	0.00	CATHAY	unnamed
2	O/HKN/5/2014	HKN14-05	639	638	0	99.84	0.16	CATHAY	unnamed
3	O/HKN/7/2014	HKN14-07	639	633	0	99.06	0.94	CATHAY	unnamed
4	O/HKN/8/2014	HKN14-08	639	633	0	99.06	0.94	CATHAY	unnamed
5	O/HKN/1/2013	HKN13-01	639	625	0	97.81	2.19	CATHAY	unnamed
6	O/HKN/3/2011	HKN11-03	639	623	0	97.50	2.50	CATHAY	unnamed
7	O/HKN/5/2011	HKN11-05	639	623	0	97.50	2.50	CATHAY	unnamed
8	O/HKN/6/2011	HKN11-06	639	623	0	97.50	2.50	CATHAY	unnamed
9	O/HKN/7/2011	HKN11-07	639	623	0	97.50	2.50	CATHAY	unnamed
10	O/HKN/4/2011	HKN11-04	639	622	0	97.34	2.66	CATHAY	unnamed

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3	O/HKN/6/83 (AJ294919)	HKN83-06	637	548	2	86.03	13.97	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	637	526	2	82.57	17.43	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	639	513	0	80.28	19.72	ME-SA	unnamed
6	O/UGA/17/98 (HM211075)	UGA98-17	639	513	0	80.28	19.72	EA-4	unnamed
7	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	511	0	79.97	20.03	ME-SA	unnamed
8	O/TAN/2/2004 (KF561679)	TAN04-02	639	510	0	79.81	20.19	EA-2	unnamed
9	O/MAL/1/98 (DQ165074)	MAL98-01	639	509	0	79.66	20.34	EA-2	unnamed
10	O/ETH/58/2005 (FJ798141)	ETH05-58	639	507	0	79.34	20.66	EA-4	unnamed

nt, nucleotides
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Assembled with Report Generator v4.1

Report on FMDV O in Hong Kong SAR in 2014

Batch: WRLFMD/2014/00008

◆ 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,
25 March 2014