

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

Genotyping Report

Report Date for this Batch: 30 March 2015

FMDV type O

Country: Republic of Korea

Period: 2014

No. of samples: 4

BATCH: WRLFMD/2014/00040



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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: 30/03/2015
WRLFMD Ref No: SKR/12/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00040	Checked by: K. Bachanek-Bankowska
Sender Ref: PIG LY-67	
Location: not given, Republic of Korea	Topotype: SEA
Date collected: 03/12/2014	Genotype/strain: Mya-98
Date received by WRLFMD: 22/12/2014	Sequence filename: SKR14-12.SEQ
Date received for sequencing: 19/03/2015	Date sequence last updated: 24/03/2015
Species: Pig	No. of Nt determined: 639
Material used: RS2 04/03/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4097
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 98 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/JC/CB/ROK (APQA)	SKR14-AB	639	638	0	99.84	0.16	SEA	Mya-98
2	O/SKR/14/2014	SKR14-14	639	638	0	99.84	0.16	SEA	Mya-98
3	O/SKR/16/2014	SKR14-16	639	638	0	99.84	0.16	SEA	Mya-98
4	O/SKR/18/2014	SKR14-18	639	638	0	99.84	0.16	SEA	Mya-98
5	O/GZ-MT/CHA/2013 (KJ646655)	CHA13-AP	639	620	0	97.03	2.97	SEA	Mya-98
6	O/Primorskiy/RUS/2014 (ARRIAH)	RUS14-AD	639	618	0	96.71	3.29	SEA	Mya-98
7	O/SKR/01/2014* (APQA)	SKR14-AA	639	616	0	96.40	3.60	SEA	Mya-98
8	O/SKR/6/2014	SKR14-06	639	616	0	96.40	3.60	SEA	Mya-98
9	O/HKN/10/2010	HKN10-10	639	614	0	96.09	3.91	SEA	Mya-98
10	O/HKN/11/2010	HKN10-11	639	614	0	96.09	3.91	SEA	Mya-98
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/MYA/7/98 (DQ164925)	MYA98-07	639	585	0	91.55	8.45	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	562	0	87.95	12.05	SEA	unnamed
3	O/PAK/16/2010	PAK10-16	639	534	0	83.57	16.43	ME-SA	PanAsia-2 ^{PUN-10}
4	O/IND/R2/75* (AF204276)	IND75--A	639	533	0	83.41	16.59	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	532	0	83.26	16.74	ME-SA	PanAsia-2
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	531	0	83.10	16.90	ME-SA	PanAsia-2 ^{TER-08}
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	530	0	82.94	17.06	ME-SA	PanAsia-2 ^{SAN-09}
8	O/UAE/4/2008 (KM921876)	UAE08-04	636	527	0	82.86	17.14	ME-SA	Ind-2001c
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	529	0	82.79	17.21	ME-SA	PanAsia
10	O/ETH/3/2004 (FJ798109)	ETH04-03	639	528	0	82.63	17.37	EA-3	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O	Report date: 30/03/2015
WRLFMD Ref No: SKR/14/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00040	Checked by: K. Bachanek-Bankowska
Sender Ref: PIG LY-72	
Location: not given, Republic of Korea	Topotype: SEA
Date collected: 03/12/2014	Genotype/strain: Mya-98
Date received by WRLFMD: 22/12/2014	Sequence filename: SKR14-14.SEQ
Date received for sequencing: 19/03/2015	Date sequence last updated: 24/03/2015
Species: Pig	No. of Nt determined: 639
Material used: RS1 26/02/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4097
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 98 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/JC/CB/ROK (APQA)	SKR14-AB	639	639	0	100.00	0.00	SEA	Mya-98
2	O/SKR/16/2014	SKR14-16	639	639	0	100.00	0.00	SEA	Mya-98
3	O/SKR/18/2014	SKR14-18	639	639	0	100.00	0.00	SEA	Mya-98
4	O/SKR/12/2014	SKR14-12	639	638	0	99.84	0.16	SEA	Mya-98
5	O/GZ-MT/CHA/2013 (KJ646655)	CHA13-AP	639	621	0	97.18	2.82	SEA	Mya-98
6	O/Primorskiy/RUS/2014 (ARRIAH)	RUS14-AD	639	619	0	96.87	3.13	SEA	Mya-98
7	O/SKR/01/2014* (APQA)	SKR14-AA	639	617	0	96.56	3.44	SEA	Mya-98
8	O/SKR/6/2014	SKR14-06	639	617	0	96.56	3.44	SEA	Mya-98
9	O/HKN/10/2010	HKN10-10	639	615	0	96.24	3.76	SEA	Mya-98
10	O/HKN/11/2010	HKN10-11	639	615	0	96.24	3.76	SEA	Mya-98
Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
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1	O/MYA/7/98 (DQ164925)	MYA98-07	639	586	0	91.71	8.29	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	563	0	88.11	11.89	SEA	unnamed
3	O/PAK/16/2010	PAK10-16	639	535	0	83.72	16.28	ME-SA	PanAsia-2 ^{PUN-10}
4	O/IND/R2/75* (AF204276)	IND75--A	639	534	0	83.57	16.43	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	533	0	83.41	16.59	ME-SA	PanAsia-2
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	532	0	83.26	16.74	ME-SA	PanAsia-2 ^{TER-08}
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	531	0	83.10	16.90	ME-SA	PanAsia-2 ^{SAN-09}
8	O/UAE/4/2008 (KM921876)	UAE08-04	636	528	0	83.02	16.98	ME-SA	Ind-2001c
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	530	0	82.94	17.06	ME-SA	PanAsia
10	O/ETH/3/2004 (FJ798109)	ETH04-03	639	529	0	82.79	17.21	EA-3	unnamed

nt, nucleotides

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Serotype: O	Report date: 30/03/2015
WRLFMD Ref No: SKR/16/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00040	Checked by: K. Bachanek-Bankowska
Sender Ref: PIG LY-123	
Location: not given, Republic of Korea	Topotype: SEA
Date collected: 03/12/2014	Genotype/strain: Mya-98
Date received by WRLFMD: 22/12/2014	Sequence filename: SKR14-16.SEQ
Date received for sequencing: 19/03/2015	Date sequence last updated: 24/03/2015
Species: Pig	No. of Nt determined: 639
Material used: RS1 26/02/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4097
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 98 days
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Comments:	

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Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/JC/CB/ROK (APQA)	SKR14-AB	639	639	0	100.00	0.00	SEA	Mya-98
2	O/SKR/14/2014	SKR14-14	639	639	0	100.00	0.00	SEA	Mya-98
3	O/SKR/18/2014	SKR14-18	639	639	0	100.00	0.00	SEA	Mya-98
4	O/SKR/12/2014	SKR14-12	639	638	0	99.84	0.16	SEA	Mya-98
5	O/GZ-MT/CHA/2013 (KJ646655)	CHA13-AP	639	621	0	97.18	2.82	SEA	Mya-98
6	O/Primorskiy/RUS/2014 (ARRIAH)	RUS14-AD	639	619	0	96.87	3.13	SEA	Mya-98
7	O/SKR/01/2014* (APQA)	SKR14-AA	639	617	0	96.56	3.44	SEA	Mya-98
8	O/SKR/6/2014	SKR14-06	639	617	0	96.56	3.44	SEA	Mya-98
9	O/HKN/10/2010	HKN10-10	639	615	0	96.24	3.76	SEA	Mya-98
10	O/HKN/11/2010	HKN10-11	639	615	0	96.24	3.76	SEA	Mya-98
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8	O/UAE/4/2008 (KM921876)	UAE08-04	636	528	0	83.02	16.98	ME-SA	Ind-2001c
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	530	0	82.94	17.06	ME-SA	PanAsia
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Batch No: WRLFMD/2014/00040	Checked by: K. Bachanek-Bankowska
Sender Ref: PIG LY-138	
Location: not given, Republic of Korea	Topotype: SEA
Date collected: 03/12/2014	Genotype/strain: Mya-98
Date received by WRLFMD: 22/12/2014	Sequence filename: SKR14-18.SEQ
Date received for sequencing: 19/03/2015	Date sequence last updated: 24/03/2015
Species: Pig	No. of Nt determined: 639
Material used: RS1 26/02/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4097
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3	O/SKR/16/2014	SKR14-16	639	639	0	100.00	0.00	SEA	Mya-98
4	O/SKR/12/2014	SKR14-12	639	638	0	99.84	0.16	SEA	Mya-98
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3	O/PAK/16/2010	PAK10-16	639	535	0	83.72	16.28	ME-SA	PanAsia-2 ^{PUN-10}
4	O/IND/R2/75* (AF204276)	IND75--A	639	534	0	83.57	16.43	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	533	0	83.41	16.59	ME-SA	PanAsia-2
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	532	0	83.26	16.74	ME-SA	PanAsia-2 ^{TER-08}
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	531	0	83.10	16.90	ME-SA	PanAsia-2 ^{SAN-09}
8	O/UAE/4/2008 (KM921876)	UAE08-04	636	528	0	83.02	16.98	ME-SA	Ind-2001c
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10	O/ETH/3/2004 (FJ798109)	ETH04-03	639	529	0	82.79	17.21	EA-3	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV O in South Korea in 2014

Batch: WRLFMD/2014/00040

◆ 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

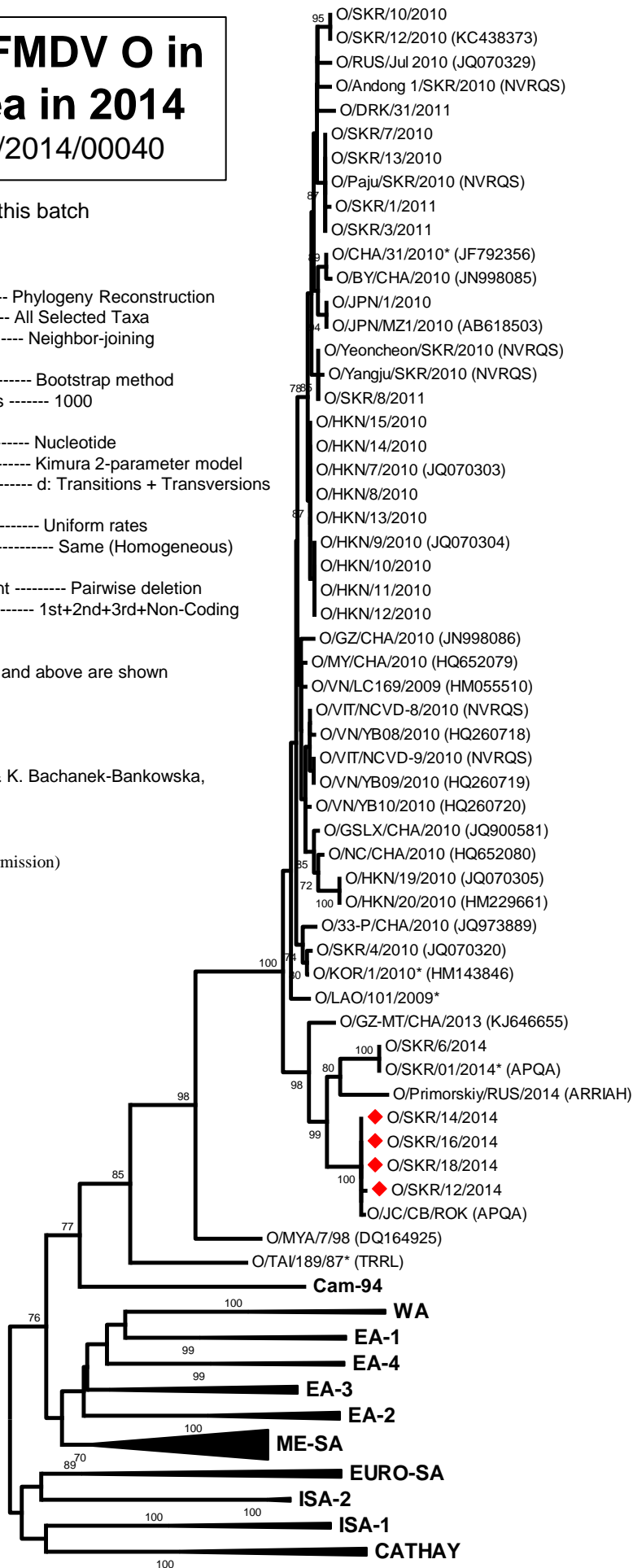
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
30 March 2015

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Mya-98

SEA

0.02