

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

Genotyping Report

Report Date for this Batch: 24 February 2016

FMDV type O

Country: Republic of Korea

Period: 2016

No. of samples: 2

BATCH: WRLFMD/2016/00006



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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O WRLFMD Ref No: SKR/6/2016 Batch No: WRLFMD/2016/00006 Sender Ref: 2016-0001-01, GJ-01 Location: Youngsu 6 Gil, Gimje, Jeonbuk, Republic of Korea Date collected: 12/01/2016 Date received by WRLFMD: 01/02/2016 Date received for sequencing: 19/02/2016 Species: Pig Material used: RS1 09/02/2016; RS2 13/02/2016 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 24/02/2016 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: SEA Genotype/strain: Mya-98 Sequence filename: SKR16-06.SEQ Date sequence last updated: 24/02/2016 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4225 Min. no. of nt for comparison: 600 Total turn-around time: 23 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/Gimje/KOR/2016* (QIA)	SKR16-AA	639	639	0	100.00	0.00	SEA	Mya-98
2	O/SKR/1/2016	SKR16-01	639	639	0	100.00	0.00	SEA	Mya-98
3	O/SKR/2/2016	SKR16-02	639	639	0	100.00	0.00	SEA	Mya-98
4	O/SKR/3/2016	SKR16-03	639	639	0	100.00	0.00	SEA	Mya-98
5	O/SKR/4/2016	SKR16-04	639	639	0	100.00	0.00	SEA	Mya-98
6	O/SKR/5/2016	SKR16-05	639	639	0	100.00	0.00	SEA	Mya-98
7	O/SKR/7/2016	SKR16-07	639	639	0	100.00	0.00	SEA	Mya-98
8	O/JC/CB/ROK (APQA)	SKR14-AB	639	633	0	99.06	0.94	SEA	Mya-98
9	O/SKR/14/2014	SKR14-14	639	633	0	99.06	0.94	SEA	Mya-98
10	O/SKR/16/2014	SKR14-16	639	633	0	99.06	0.94	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	583	0	91.24	8.76	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	564	0	88.26	11.74	SEA	unnamed
3	O/PAK/16/2010	PAK10-16	639	536	0	83.88	16.12	ME-SA	PanAsia-2 ^{PUN-10}
4	O/IND/R2/75* (AF204276)	IND75--A	639	535	0	83.72	16.28	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	532	0	83.26	16.74	ME-SA	PanAsia-2
6	O/UAE/4/2008 (KM921876)	UAE08-04	636	529	0	83.18	16.82	ME-SA	Ind-2001c
7	O/TUR/257/2008* (FMDI)	TUR08-AD	639	531	0	83.10	16.90	ME-SA	PanAsia-2 ^{TER-08}
8	O/ETH/3/2004 (FJ798109)	ETH04-03	639	530	0	82.94	17.06	EA-3	unnamed
9	O/IRN/31/2009	IRN09-31	639	530	0	82.94	17.06	ME-SA	PanAsia-2 ^{FAR-09}
10	O/TUR/264/2009* (FMDI)	TUR09-AK	639	530	0	82.94	17.06	ME-SA	PanAsia-2 ^{SAN-09}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O WRLFMD Ref No: SKR/7/2016 Batch No: WRLFMD/2016/00006 Sender Ref: 2016-0001-02, GJ-02 Location: Youngsu 6 Gil, Gimje, Jeonbuk, Republic of Korea Date collected: 12/01/2016 Date received by WRLFMD: 01/02/2016 Date received for sequencing: 19/02/2016 Species: Pig Material used: RS1 09/02/2016 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 24/02/2016 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: SEA Genotype/strain: Mya-98 Sequence filename: SKR16-07.SEQ Date sequence last updated: 24/02/2016 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4225 Min. no. of nt for comparison: 600 Total turn-around time: 23 days Sequencing time: 5 days
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7	O/SKR/6/2016	SKR16-06	639	639	0	100.00	0.00	SEA	Mya-98
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Report on FMDV O in the Republic of Korea in 2016

Batch: WRLFMD/2016/00006

◆ 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

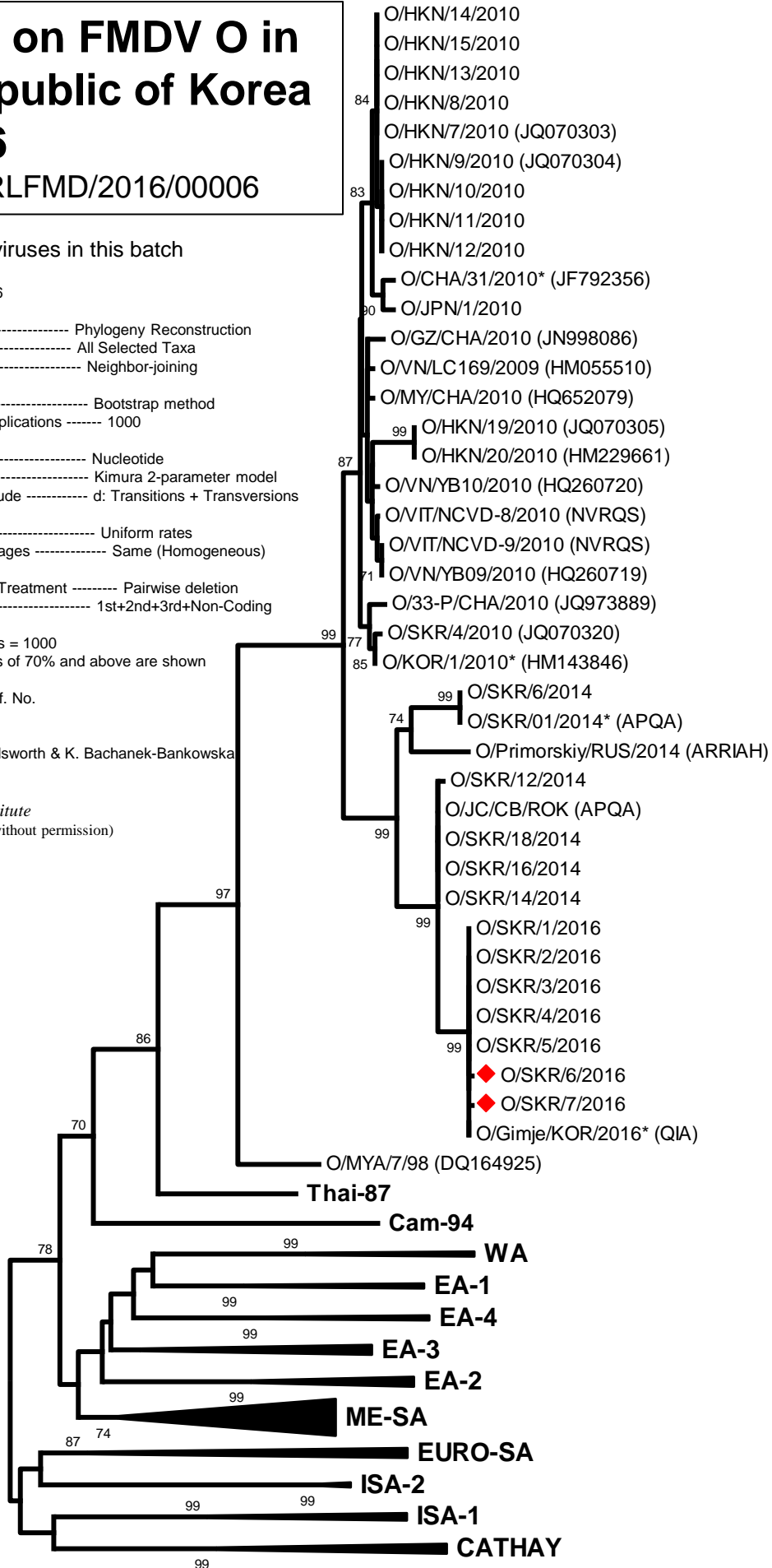
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska
24 February 2016

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Mya-98

SEA

0.02