

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

## Genotyping Report

Report Date for this Batch: 24 July 2014

FMDV type O

Country: Republic of Korea

Period: 2014

No. of sequences: 1 (VP1)

Originator: [REDACTED] Foot-and-Mouth Disease Division,  
Animal and Plant Quarantine Agency, Ministry of Agriculture, Food  
and Rural Affairs, Republic of Korea.



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IAH-P-EP-MEG-FOR-005-3

Page 1 of 1

Serotype: O WRLFMD Ref No: SKR/01/2014* Batch No: WRLMEG/2014/00022 Sender Ref: SKR/01/2014 Location: Uiseoung-Gun, Gyeongbuk-Do (Province), Republic of Korea (South Korea) Date collected: 23/07/2014 Date received by WRLFMD: 24/07/2014 Date received for sequencing: n/a Species: Pigs Material used: not known Region sequenced: VP1 RT-PCR primers: Not known	Report date: 24/07/2014 Reported by: N.J. Knowles Checked by: J. Wadsworth Topotype: SEA Genotype/strain: Mya-98 Sequence filename: SKR14-AA.SEQ Date sequence last updated: 24/07/2014 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3904 Min. no. of nt for comparison: 600 Total turn-around time: 0 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/Primorskiy/RUS/2014 (ARRIAH)	RUS14-AD	639	619	0	96.87	3.13	SEA	Mya-98
2	O/GZ-MT/CHA/2013 (KJ646655)	CHA13-AP	639	617	0	96.56	3.44	SEA	Mya-98
3	O/HKN/13/2010	HKN10-13	639	612	0	95.77	4.23	SEA	Mya-98
4	O/HKN/14/2010	HKN10-14	639	612	0	95.77	4.23	SEA	Mya-98
5	O/HKN/15/2010	HKN10-15	639	612	0	95.77	4.23	SEA	Mya-98
6	O/HKN/7/2010 (JQ070303)	HKN10-07	639	612	0	95.77	4.23	SEA	Mya-98
7	O/HKN/8/2010	HKN10-08	639	612	0	95.77	4.23	SEA	Mya-98
8	O/HKN/10/2010	HKN10-10	639	611	0	95.62	4.38	SEA	Mya-98
9	O/HKN/11/2010	HKN10-11	639	611	0	95.62	4.38	SEA	Mya-98
10	O/HKN/12/2010	HKN10-12	639	611	0	95.62	4.38	SEA	Mya-98
Most Closely Related Reference Viruses									
(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/MYA/7/98 (DQ164925)	MYA98-07	639	584	0	91.39	8.61	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	564	0	88.26	11.74	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	541	0	84.66	15.34	ME-SA	unnamed
4	O/IRN/8/2005	IRN05-08	639	534	0	83.57	16.43	ME-SA	PanAsia-2
5	O/ETH/3/2004 (FJ798109)	ETH04-03	639	531	0	83.10	16.90	EA-3	unnamed
6	O/PAK/16/2010	PAK10-16	639	531	0	83.10	16.90	ME-SA	PanAsia-2 <sup>PUN-10</sup>
7	O/CAM/3/98 (AJ294910)	CAM98-03	639	530	0	82.94	17.06	SEA	Cam-94
8	O/TUR/257/2008* (FMDI)	TUR08-AD	639	529	0	82.79	17.21	ME-SA	PanAsia-2 <sup>TER-08</sup>
9	O/TUR/264/2009* (FMDI)	TUR09-AK	639	529	0	82.79	17.21	ME-SA	PanAsia-2 <sup>SAN-09</sup>
10	O/IRN/31/2009	IRN09-31	639	528	0	82.63	17.37	ME-SA	PanAsia-2 <sup>FAR-09</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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# Report on FMDV O in the Republic of Korea in 2014

Batch: WRLMEG/2014/00022

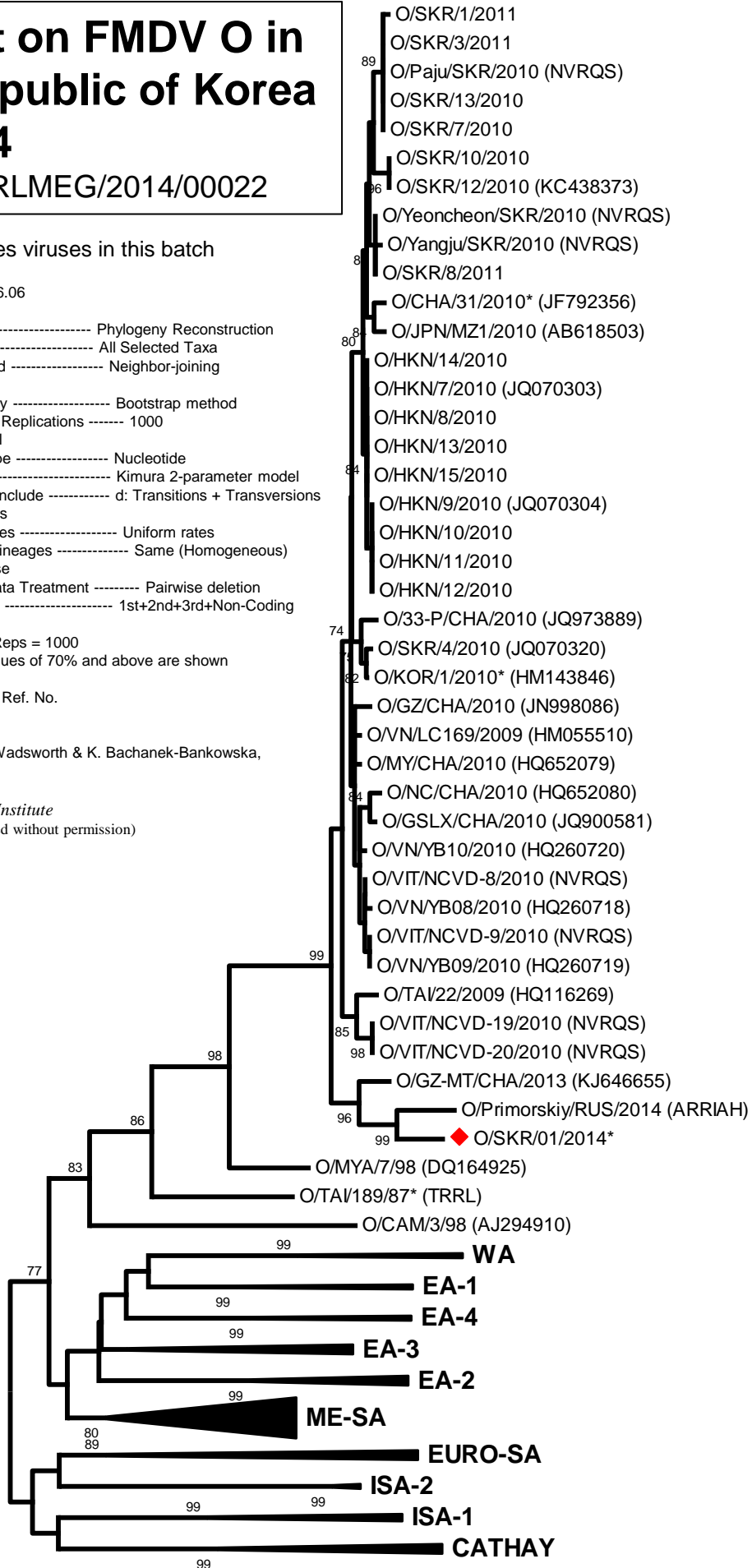
◆ indicates viruses in this batch

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 July 2014

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Mya-98

SEA

Cam-94

0.02