

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

Genotyping Report

Report Date for this Batch: 16 December 2010

FMDV type O

Country: Republic of Korea

Period: 2010

No. of isolates: 2 (VP1 sequences)

VP1 sequences received from Foreign Animal Disease Research Division, National
Veterinary Research and Quarantine Service, Republic of Korea, 16/12/2010.



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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O	Report date: 16/12/2010
WRLFMD Ref No: Yangju/SKR/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: Yangju	
Location: Sangsu-ri, Nam-myun, Yangju city, Gyeonggi-Do, Republic of Korea	Topotype: SEA
Date collected: 14/12/2010	Genotype/strain: Mya-98
Date received by WRLFMD: 16/12/2010	Sequence filename: SKR10-AD.SEQ
Date received for sequencing: n/a	Date sequence last updated: 16/12/2010
Species: Pigs	No. of Nt determined: 639
Material used: Not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: Not known	Total no. of comparisons: 2512
	Min. no. of nt for comparison: 600
	Total turn-around time: 0 days
	Sequencing time: n/a
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/Yeoncheon/SKR/2010 (NVRQS)	SKR10-AE	639	638	0	99.84	0.16	SEA	Mya-98
2	O/HKN/13/2010	HKN10-13	639	635	0	99.37	0.63	SEA	Mya-98
3	O/HKN/14/2010	HKN10-14	639	635	0	99.37	0.63	SEA	Mya-98
4	O/HKN/15/2010	HKN10-15	639	635	0	99.37	0.63	SEA	Mya-98
5	O/HKN/7/2010	HKN10-07	639	635	0	99.37	0.63	SEA	Mya-98
6	O/HKN/8/2010	HKN10-08	639	635	0	99.37	0.63	SEA	Mya-98
7	O/HKN/10/2010	HKN10-10	639	634	0	99.22	0.78	SEA	Mya-98
8	O/HKN/11/2010	HKN10-11	639	634	0	99.22	0.78	SEA	Mya-98
9	O/HKN/12/2010	HKN10-12	639	634	0	99.22	0.78	SEA	Mya-98
10	O/HKN/9/2010	HKN10-09	639	634	0	99.22	0.78	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	595	0	93.11	6.89	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	574	0	89.83	10.17	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	543	0	84.98	15.02	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	543	0	84.98	15.02	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	543	0	84.98	15.02	ME-SA	PanAsia-2
6	O/PAK/16/2010	PAK10-16	639	542	0	84.82	15.18	ME-SA	PanAsia-2 ^{PUN-10}
7	O/ETH/3/2004 (FJ798109)	ETH04-03	639	540	0	84.51	15.49	EA-3	unnamed
8	O/TUR/257/2008* (FMDI)	TUR08-AD	639	539	0	84.35	15.65	ME-SA	PanAsia-2 ^{TER-08}
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	539	0	84.35	15.65	ME-SA	PanAsia
10	O/IRN/88/2009	IRN09-88	639	538	0	84.19	15.81	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O WRLFMD Ref No: Yeoncheon/SKR/2010 Batch No: n/a Sender Ref: Yeoncheon Location: Nogo-ri, Baekhak-myun, Yeoncheon-gun, Gyeonggi-do, Republic of Korea Date collected: 14/12/2010 Date received by WRLFMD: 16/12/2010 Date received for sequencing: n/a Species: Pigs Material used: Not known Region sequenced: VP1 RT-PCR primers: Not known	Report date: 16/12/2010 Reported by: N.J. Knowles Checked by: D.P. King Topotype: SEA Genotype/strain: Mya-98 Sequence filename: SKR10-AE.SEQ Date sequence last updated: 16/12/2010 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2512 Min. no. of nt for comparison: 600 Total turn-around time: 0 days Sequencing time: n/a
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3	O/HKN/14/2010	HKN10-14	639	636	0	99.53	0.47	SEA	Mya-98
4	O/HKN/15/2010	HKN10-15	639	636	0	99.53	0.47	SEA	Mya-98
5	O/HKN/7/2010	HKN10-07	639	636	0	99.53	0.47	SEA	Mya-98
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7	O/ETH/3/2004 (FJ798109)	ETH04-03	639	541	0	84.66	15.34	EA-3	unnamed
8	O/TUR/257/2008* (FMDI)	TUR08-AD	639	540	0	84.51	15.49	ME-SA	PanAsia-2 ^{TER-08}
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nt, nucleotides

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Report on FMDV O in the Republic of Korea in 2010

VP1 sequences received from National Veterinary Research and Quarantine Service (NVRQS), Anyang, Gyeonggi 430-824, Republic of Korea, 16/12/2010

Software: MEGA 4.0
 No. of Taxa : 259
 Data File : n:\evd\meg\db\fmv\o\SKR2010d.meg
 Data Title : O South Korea 2010
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)
 Include Sites : =====
 ->Gaps/Missing Data : Pairwise Deletion
 ->Codon Positions : 1st+2nd+3rd+Noncoding
 Substitution Model : =====
 ->Model : Nucleotide: Kimura 2-parameter
 ->Substitutions to Include : d: Transitions + Transversions
 ->Pattern among Lineages : Same (Homogeneous)
 ->Rates among sites : Uniform rates
 No. of Sites : 639
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 16 December 2010

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