

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

## Genotyping Report

Report Date for this Batch: 30 November 2010

FMDV type O

Country: Republic of Korea

Period: 2010

No. of isolates: 1 (sequence only)

VP1 sequence received from National Veterinary Research and Quarantine Service (NVRQS), Anyang, Gyeonggi 430-824, Republic of Korea, 30/11/2010



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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: 30/11/2010
WRLFMD Ref No: O/Andong 1/SKR/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: J.M. Hammond
Sender Ref: O KOR 1 Andong 2010	
Location: Waryong-myun, Andong city, Kyongsang-Bukdo, Republic of Korea	Topotype: SEA
Date collected: 28/11/2010	Genotype/strain: Mya-98
Date received by WRLFMD: 30/11/2010	Sequence filename: SKR10-AC.SEQ
Date received for sequencing: n/a	Date sequence last updated: 30/11/2010
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: 2496
	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/HKN/13/2010	HKN10-13	639	633	0	99.06	0.94	SEA	Mya-98
2	O/HKN/14/2010	HKN10-14	639	633	0	99.06	0.94	SEA	Mya-98
3	O/HKN/15/2010	HKN10-15	639	633	0	99.06	0.94	SEA	Mya-98
4	O/HKN/7/2010	HKN10-07	639	633	0	99.06	0.94	SEA	Mya-98
5	O/HKN/8/2010	HKN10-08	639	633	0	99.06	0.94	SEA	Mya-98
6	O/RUS/Jul 2010 (ARRIAH)	RUS10-AA	639	633	0	99.06	0.94	SEA	Mya-98
7	O/HKN/10/2010	HKN10-10	639	632	0	98.9	1.1	SEA	Mya-98
8	O/HKN/11/2010	HKN10-11	639	632	0	98.9	1.1	SEA	Mya-98
9	O/HKN/12/2010	HKN10-12	639	632	0	98.9	1.1	SEA	Mya-98
10	O/HKN/9/2010	HKN10-09	639	632	0	98.9	1.1	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	593	0	92.80	7.20	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	569	0	89.05	10.95	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	539	0	84.35	15.65	ME-SA	PanAsia-2
6	O/PAK/16/2010	PAK10-16	639	538	0	84.19	15.81	ME-SA	PanAsia-2 <sup>PUN-10</sup>
7	O/ETH/3/2004 (FJ798109)	ETH04-03	639	536	0	83.88	16.12	EA-3	unnamed
8	O/IRN/88/2009	IRN09-88	639	536	0	83.88	16.12	ME-SA	PanAsia-2 <sup>ANT-10</sup>
9	O/IRN/31/2009	IRN09-31	639	535	0	83.72	16.28	ME-SA	PanAsia-2 <sup>FAR-09</sup>
10	O/TUR/257/2008* (FMDI)	TUR08-AD	639	535	0	83.72	16.28	ME-SA	PanAsia-2 <sup>TER-08</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v3.11

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# Report on FMDV O in South Korea in 2010

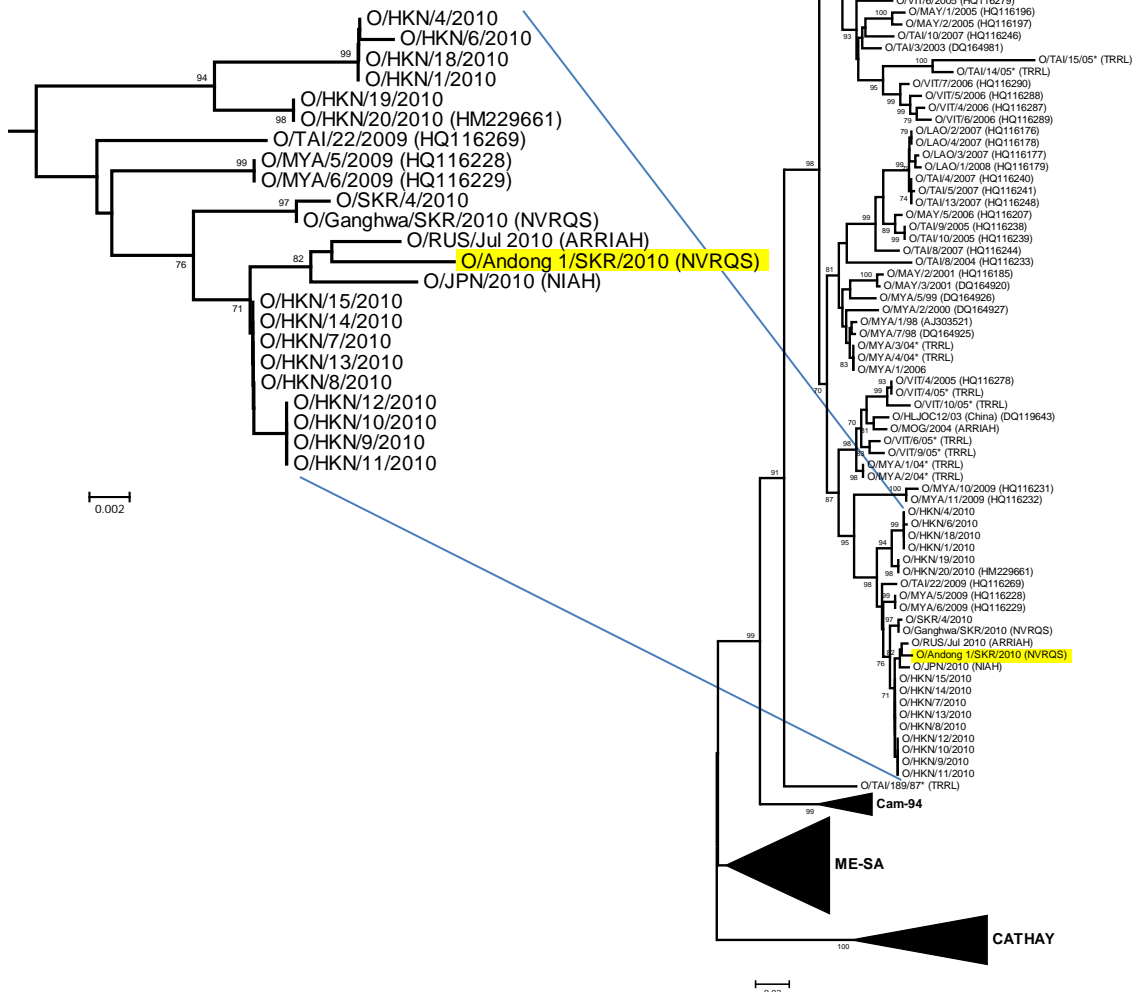
VP1 sequence received from National Veterinary Research and Quarantine Service (NVRQS), Anyang, Gyeonggi 430-824, Republic of Korea, 30/11/2010

Software: MEGA 4.0  
 No. of Taxa : 257  
 Data File : n:\levd\meg\db\fmvd\o\SKR2010c.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=43139)  
 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, 30 November 2010

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Mya-98

SEA