

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

Genotyping Report

Date: 12 April 2010

FMDV type O

Country: Republic of Korea

Period: 2010

No. of isolates: 1 (VP1 sequence only)



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

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Serotype: O WRLFMD Ref No: none Batch No: n/a Sender Ref: O/Ganghwa/KOR/2010 Location: Geumwol-ri 307, Seonwon-myeon, Ganghwa-gun, Inch'on-Jikhalsi, Republic of South Korea Date collected: 08/04/2010 Date received by WRLFMD: 12/04/2010 Date received for sequencing: n/a Species: Cattle Material used: Not known Region sequenced: VP1 RT-PCR primers: Not known	Report date: 12/04/2010 Reported by: N.J. Knowles Checked by: D.P. King Topotype: SEA Genotype/strain: Mya-98 Sequence filename: SKR10-AB.SEQ Date sequence last updated: n/a No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2326 Min. no. of nt for comparison: 300 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/HKN/10/2010	HKN10-10	639	632	0	98.90	1.10	SEA	Mya-98
7	O/HKN/11/2010	HKN10-11	639	632	0	98.90	1.10	SEA	Mya-98
8	O/HKN/12/2010	HKN10-12	639	632	0	98.90	1.10	SEA	Mya-98
9	O/HKN/9/2010	HKN10-09	639	632	0	98.90	1.10	SEA	Mya-98
10	O/MYA/5/2009	MYA09-05	639	630	0	98.59	1.41	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	599	0	93.74	6.26	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	574	0	89.83	10.17	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	546	0	85.45	14.55	ME-SA	unnamed
4	O/IRN/8/2005	IRN05-08	639	545	0	85.29	14.71	ME-SA	PanAsia-2
5	O/CAM/3/98 (AJ294910)	CAM98-03	639	543	0	84.98	15.02	SEA	Cam-94
6	O/UKG/35/2001 (AJ539141)	UKG01-35	639	542	0	84.82	15.18	ME-SA	PanAsia
7	O/ETH/3/2004 (FJ798109)	ETH04-03	639	537	0	84.04	15.96	EA-3	unnamed
8	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	537	0	84.04	15.96	ME-SA	unnamed
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	535	0	83.72	16.28	ME-SA	Ind-2001a
10	O/IND/53/79 (AF292107)	IND79A53	639	534	0	83.57	16.43	ME-SA	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.1

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Report on FMDV O in South Korea in 2010

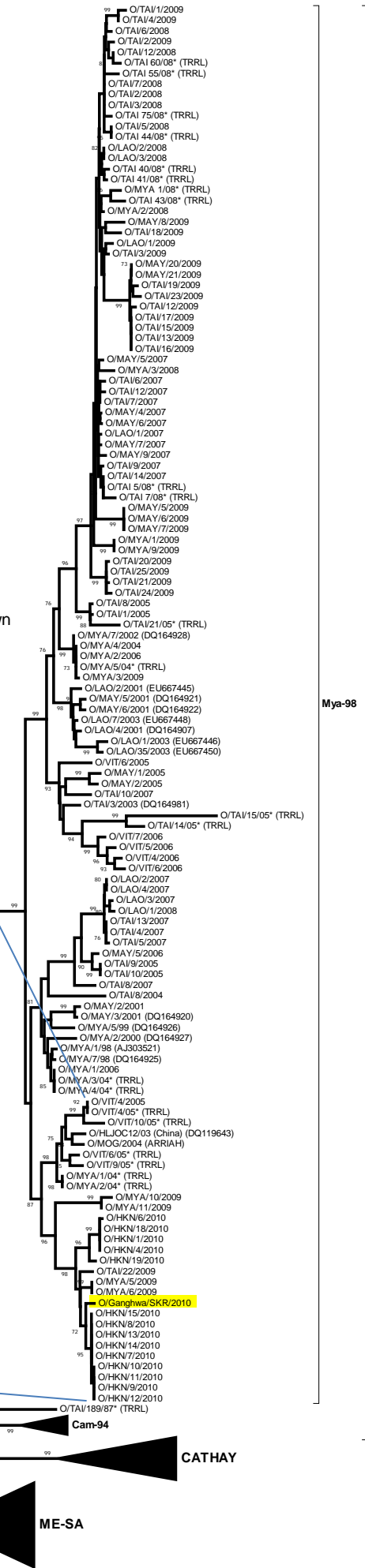
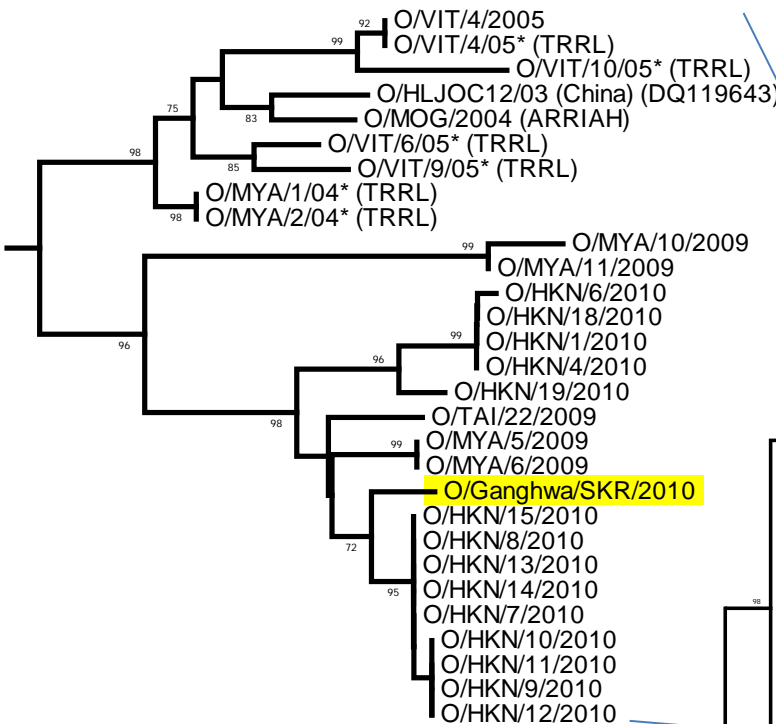
VP1 sequence received from National Veterinary Research and Quarantine Service, Anyang, Gyeonggi 430-824, Republic of Korea.

Software: MEGA 4.0
 No. of Taxa : 239
 Data File : n:\levd\meg\db\fmdv\o\SKR2010a.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, F.Hamid & J. Wadsworth, 12 April 2010

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0.005

0.02