

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

Genotyping Report

Date: 5 May 2010

FMDV type O

Country: Japan

Period: 2010

No. of isolates: 1



The contents of this report are copyright and should not be reproduced without permission

© Institute for Animal Health

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 05/05/2010
WRLFMD Ref No: JPN/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: O/JP/1/2010	
Location: not known, Japan	Topotype: SEA
Date collected: not known	Genotype/strain: Mya-98
Date received by WRLFMD: 27/04/2010	Sequence filename: JPN10-AA.SEQ
Date received for sequencing: n/a	Date sequence last updated: 28/04/2010
Species: not known	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: 2359
	Min. no. of nt for comparison: 300
	Total turn-around time: 8 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	634	0	99.22	0.78	SEA	Mya-98
2	O/HKN/14/2010	HKN10-14	639	634	0	99.22	0.78	SEA	Mya-98
3	O/HKN/15/2010	HKN10-15	639	634	0	99.22	0.78	SEA	Mya-98
4	O/HKN/7/2010	HKN10-07	639	634	0	99.22	0.78	SEA	Mya-98
5	O/HKN/8/2010	HKN10-08	639	634	0	99.22	0.78	SEA	Mya-98
6	O/HKN/10/2010	HKN10-10	639	633	0	99.06	0.94	SEA	Mya-98
7	O/HKN/11/2010	HKN10-11	639	633	0	99.06	0.94	SEA	Mya-98
8	O/HKN/12/2010	HKN10-12	639	633	0	99.06	0.94	SEA	Mya-98
9	O/HKN/9/2010	HKN10-09	639	633	0	99.06	0.94	SEA	Mya-98
10	O/Ganghwa/SKR/2010	SKR10-AB	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	594	0	92.96	7.04	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	570	0	89.20	10.80	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	542	0	84.82	15.18	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	542	0	84.82	15.18	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	542	0	84.82	15.18	ME-SA	PanAsia-2
6	O/ETH/3/2004 (FJ798109)	ETH04-03	639	539	0	84.35	15.65	EA-3	unnamed
7	O/UKG/35/2001 (AJ539141)	UKG01-35	639	538	0	84.19	15.81	ME-SA	PanAsia
8	O/ETH/1/2007 (FJ798137)	ETH07-01	639	535	0	83.72	16.28	EA-3	unnamed
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	533	0	83.41	16.59	ME-SA	Ind-2001a
10	O/IND/53/79 (AF292107)	IND79A53	639	532	0	83.26	16.74	ME-SA	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.1

© Institute for Animal Health

Report on FMDV O in Japan in 2010

VP1 sequence received from the National Institute for Animal Health, Tokyo, Japan, on 27/04/2010

Software: MEGA 4.0
 No. of Taxa : 241
 Data File : n:\evd\meg\db\fmdv\o\JPN2010a.meg
 Data Title : O Japan 2010
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64843)
 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 & F. Hamid, 5 May 2010

© Institute for Animal Health

