

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

Genotyping Report

Report Date for this Batch: 19 July 2010

FMDV type O

Country: Russian Federation

Period: 2010

No. of isolates: 1 (VP1 sequence only)

VP1 sequence received from ARRIAH, Vladimir, Russian Federation.



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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: 19/07/2010
WRLFMD Ref No: none	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: O/Russia/2010	
Location: Zabajkalsky kray, Chita region, Russian Federation	Topotype: SEA
Date collected: 2010	Genotype/strain: Mya-98
Date received by WRLFMD: 19/07/2010	Sequence filename: RUS10-AA.SEQ
Date received for sequencing: n/a	Date sequence last updated: 19/07/2010
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: 2153
	Min. no. of nt for comparison: 600
	Total turn-around time: 0 days
	Sequencing time: n/a
Comments: VP1 sequence received from ARRIAH, Vladimir, Russian Federation.	

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	98.9	1.1	SEA	Mya-98
7	O/HKN/11/2010	HKN10-11	639	632	0	98.9	1.1	SEA	Mya-98
8	O/HKN/12/2010	HKN10-12	639	632	0	98.9	1.1	SEA	Mya-98
9	O/HKN/9/2010	HKN10-09	639	632	0	98.9	1.1	SEA	Mya-98
10	O/JPN/2010 (NIAH)	JPN10-AA	639	632	0	98.9	1.1	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	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	541	0	84.66	15.34	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	541	0	84.66	15.34	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	541	0	84.66	15.34	ME-SA	PanAsia-2
6	O/ETH/3/2004 (FJ798109)	ETH04-03	639	538	0	84.19	15.81	EA-3	unnamed
7	O/UKG/35/2001 (AJ539141)	UKG01-35	639	537	0	84.04	15.96	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	535	0	83.72	16.28	ME-SA	Ind-2001a
10	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	533	0	83.41	16.59	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 Russia in 2010

VP1 sequence received from ARRIAH, Vladimir, Russian Federation, 19/07/2010.

Software: MEGA 4.0
 No. of Taxa : 244
 Data File : n:\evd\meg\db\fmdv\o\RUS2010a.meg
 Data Title : O Russia 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, 19 July 2010

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