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

Genotyping Report

Date: 5 June 2010

FMDV type O
Country: Mongolia
Period: 2010
No. of isolates: 1 (VP1 sequence received from ARRIAH)

BATCH: n/a

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 05/06/2010
WRLFMD Ref No: none	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.J. Paton
Sender Ref: O/Mongolia/CO3/2010	
Location: Dornod, Mongolia	Topotype: SEA
Date collected: 2010	Genotype/strain: Mya-98
Date received by WRLFMD: 04/06/2010	Sequence filename: MOG10-AA.SEQ
Date received for sequencing: n/a	Date sequence last updated: 05/06/2010
Species: Cattle	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: 2446
	Min. no. of nt for comparison: 300
	Total turn-around time: 1 days
	Sequencing time: n/a

Comments: VP1 sequenced received from ARRIAH.

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/TAI/13/2009	TAI09-13	639	635	0	99.37	0.63	SEA	Mya-98
2	O/TAI/15/2009	TAI09-15	639	635	0	99.37	0.63	SEA	Mya-98
3	O/TAI/16/2009	TAI09-16	639	635	0	99.37	0.63	SEA	Mya-98
4	O/TAI/17/2009	TAI09-17	639	635	0	99.37	0.63	SEA	Mya-98
5	O/MAY/20/2009	MAY09-20	639	633	0	99.06	0.94	SEA	Mya-98
6	O/MAY/21/2009	MAY09-21	639	633	0	99.06	0.94	SEA	Mya-98
7	O/TAI/12/2009	TAI09-12	639	633	0	99.06	0.94	SEA	Mya-98
8	O/TAI/19/2009	TAI09-19	639	632	0	98.90	1.10	SEA	Mya-98
9	O/TAI/23/2009	TAI09-23	639	631	0	98.75	1.25	SEA	Mya-98
10	O/MYA/2/2008	MYA08-02	639	623	0	97.50	2.50	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	584	0	91.39	8.61	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	564	0	88.26	11.74	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	548	0	85.76	14.24	ME-SA	unnamed
4	O/PAK/16/2003 (DQ165068)	PAK03-16	639	546	0	85.45	14.55	ME-SA	Pak-98
5	O/CAM/3/98 (AJ294910)	CAM98-03	639	545	0	85.29	14.71	SEA	Cam-94
6	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	544	0	85.13	14.87	ME-SA	unnamed
7	O/IND/53/79 (AF292107)	IND79A53	639	537	0	84.04	15.96	ME-SA	unnamed
8	O/KUW/3/97 (DQ164904)	KUW97-03	639	537	0	84.04	15.96	ME-SA	Ind-2001a
9	O/UAE/4/2008	UAE08-04	636	534	0	83.96	16.04	ME-SA	Ind-2001c
10	O/IRN/8/2005	IRN05-08	639	536	0	83.88	16.12	ME-SA	PanAsia-2

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v3.1

Report on FMDV O in Mongolia in 2010

VP1 sequence received from the All-Russian Research Institute for Animal Health (ARRIAH), 04/06/2010

Software: MEGA 4.0
No. of Taxa : 243
Data File : n:\evd\meg\db\fmdv\o\MOG2010a.meg
Data Title : O Mongolia 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, 05 June 2010