

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

Genotyping Report

Report Date for this Batch: 9 July 2013

FMDV type O

Country: Bhutan

Period: 2013

No. of samples: 1

BATCH: WRLFMD/2013/00016



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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: 09/07/2013
WRLFMD Ref No: BHU/1/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00016	Checked by: D.P. King
Sender Ref: 409	
Location: Chukha, Bhutan	Topotype: ME-SA
Date collected: 06/06/2013	Genotype/strain: Ind-2001d
Date received by WRLFMD: 27/06/2013	Sequence filename: BHU13-01.SEQ
Date received for sequencing: 05/07/2013	Date sequence last updated: 09/07/2013
Species: Bovine	No. of Nt determined: 639
Material used: BTy1 03/07/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3684
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 12 days
	Sequencing time: 4 days
Comments:	

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/BHU/18/2009	BHU09-18	639	618	0	96.71	3.29	ME-SA	Ind-2001d
2	O/BHU/2/2009	BHU09-02	639	618	0	96.71	3.29	ME-SA	Ind-2001d
3	O/BHU/26/2009	BHU09-26	639	618	0	96.71	3.29	ME-SA	Ind-2001d
4	O/BHU/3/2009	BHU09-03	639	618	0	96.71	3.29	ME-SA	Ind-2001d
5	O/BHU/4/2009	BHU09-04	639	618	0	96.71	3.29	ME-SA	Ind-2001d
6	O/BHU/5/2009	BHU09-05	639	618	0	96.71	3.29	ME-SA	Ind-2001d
7	O/BHU/6/2009	BHU09-06	639	618	0	96.71	3.29	ME-SA	Ind-2001d
8	O/IND/148/2010* (KC506474)	IND10148	639	618	0	96.71	3.29	ME-SA	Ind-2001b
9	O/IND/182/2010* (KC506478)	IND10182	639	618	0	96.71	3.29	ME-SA	Ind-2001b
10	O/IND/220/2010* (KC506481)	IND10220	639	618	0	96.71	3.29	ME-SA	Ind-2001b

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/BHU/3/2009	BHU09-03	639	618	0	96.71	3.29	ME-SA	Ind-2001d
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	592	0	92.64	7.36	ME-SA	Ind-2001a
3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	589	0	92.18	7.82	ME-SA	Ind-2001b
4	O/UAE/4/2008	UAE08-04	636	579	0	91.04	8.96	ME-SA	Ind-2001c
5	O/IRN/31/2009	IRN09-31	639	573	0	89.67	10.33	ME-SA	PanAsia-2 ^{FAR-09}
6	O/UKG/35/2001 (AJ539141)	UKG01-35	639	569	0	89.05	10.95	ME-SA	PanAsia
7	O/IRN/61/2001 (DQ164896)	IRN01-61	638	568	1	89.03	10.97	ME-SA	Irn-2001
8	O/IRN/18/2010	IRN10-18	639	568	0	88.89	11.11	ME-SA	PanAsia-2 ^{BAL-09}
9	O/PAK/16/2010	PAK10-16	639	568	0	88.89	11.11	ME-SA	PanAsia-2 ^{PUN-10}
10	O/IRN/8/2005	IRN05-08	639	567	0	88.73	11.27	ME-SA	PanAsia-2

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV O in Bhutan in 2013

Batch: WRLFMD/2013/00016

◆ indicates viruses in this batch

Software: MEGA 5.2

Analysis

Analysis ----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

Test of Phylogeny ----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment ----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 642

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, K. Bachanek-Bankowska & J. Wadsworth,
09 July 2013

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