

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

Genotyping Report

Report Date for this Batch: 17 December 2015

FMDV type O

Country: Myanmar

Period: 2015

No. of samples: 2

BATCH: WRLFMD/2015/00035



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

© The Pirbright Institute

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 17/12/2015
WRLFMD Ref No: MYA/1/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00035	Checked by: K. Bachanek-Bankowska
Sender Ref: MYA 2/15R3	
Location: Mahlaing, Mandalay State, Myanmar	Topotype: SEA
Date collected: 29/10/2015	Genotype/strain: Mya-98
Date received by WRLFMD: 26/11/2015	Sequence filename: MYA15-01.SEQ
Date received for sequencing: 09/12/2015	Date sequence last updated: 10/12/2015
Species: Bovine	No. of Nt determined: 639
Material used: BTy1 04/12/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4191
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 21 days
	Sequencing time: 8 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/MAY/11/2012	MAY12-11	639	609	0	95.31	4.69	SEA	Mya-98
2	O/MAY/12/2012	MAY12-12	639	609	0	95.31	4.69	SEA	Mya-98
3	O/MAY/13/2012	MAY12-13	639	609	0	95.31	4.69	SEA	Mya-98
4	O/MAY/14/2012	MAY12-14	639	609	0	95.31	4.69	SEA	Mya-98
5	O/MAY/15/2012	MAY12-15	639	609	0	95.31	4.69	SEA	Mya-98
6	O/MAY/16/2012	MAY12-16	639	609	0	95.31	4.69	SEA	Mya-98
7	O/MAY/17/2012	MAY12-17	639	609	0	95.31	4.69	SEA	Mya-98
8	O/MAY/10/2012	MAY12-10	639	608	0	95.15	4.85	SEA	Mya-98
9	O/MAY/6/2012	MAY12-06	639	606	0	94.84	5.16	SEA	Mya-98
10	O/33-P/CHA/2010 (JQ973889)	CHA10-BA	639	598	0	93.58	6.42	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	589	0	92.18	7.82	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	568	0	88.89	11.11	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	539	0	84.35	15.65	SEA	Cam-94
4	O/PAK/16/2010	PAK10-16	639	534	0	83.57	16.43	ME-SA	PanAsia-2 ^{PUN-10}
5	O/TUR/257/2008* (FMDI)	TUR08-AD	639	534	0	83.57	16.43	ME-SA	PanAsia-2 ^{TER-08}
6	O/IRN/31/2009	IRN09-31	639	533	0	83.41	16.59	ME-SA	PanAsia-2 ^{FAR-09}
7	O/IRN/88/2009	IRN09-88	639	533	0	83.41	16.59	ME-SA	PanAsia-2 ^{ANT-10}
8	O/IRN/18/2010	IRN10-18	639	532	0	83.26	16.74	ME-SA	PanAsia-2 ^{BAL-09}
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	532	0	83.26	16.74	ME-SA	PanAsia
10	O/IND/R2/75* (AF204276)	IND75--A	639	531	0	83.10	16.90	ME-SA	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

© *The Pirbright Institute* (not to be reproduced without permission)

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: MYA/5/2015 Batch No: WRLFMD/2015/00035 Sender Ref: MYA 16/15R3 Location: Narhtogyi, Mandalay State, Myanmar Date collected: 29/10/2015 Date received by WRLFMD: 26/11/2015 Date received for sequencing: 09/12/2015 Species: Bovine Material used: BTy1 04/12/2015 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 17/12/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: SEA Genotype/strain: Mya-98 Sequence filename: MYA15-05.SEQ Date sequence last updated: 10/12/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4191 Min. no. of nt for comparison: 600 Total turn-around time: 21 days Sequencing time: 8 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/MYA/1/04* (TRRL)	MYA04-AA	639	597	0	93.43	6.57	SEA	Mya-98
2	O/MYA/2/04* (TRRL)	MYA04-AB	639	597	0	93.43	6.57	SEA	Mya-98
3	O/MAY/11/2012	MAY12-11	639	595	0	93.11	6.89	SEA	Mya-98
4	O/MAY/12/2012	MAY12-12	639	595	0	93.11	6.89	SEA	Mya-98
5	O/MAY/13/2012	MAY12-13	639	595	0	93.11	6.89	SEA	Mya-98
6	O/MAY/14/2012	MAY12-14	639	595	0	93.11	6.89	SEA	Mya-98
7	O/MAY/15/2012	MAY12-15	639	595	0	93.11	6.89	SEA	Mya-98
8	O/MAY/16/2012	MAY12-16	639	595	0	93.11	6.89	SEA	Mya-98
9	O/MAY/17/2012	MAY12-17	639	595	0	93.11	6.89	SEA	Mya-98
10	O/MYA/5/2009 (HQ116228)	MYA09-05	639	595	0	93.11	6.89	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	583	0	91.24	8.76	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	560	0	87.64	12.36	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	540	0	84.51	15.49	SEA	Cam-94
4	O/IND/R/2/75* (AF204276)	IND75--A	639	529	0	82.79	17.21	ME-SA	unnamed
5	O/PAK/16/2010	PAK10-16	639	528	0	82.63	17.37	ME-SA	PanAsia-2 ^{PUN-10}
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	527	0	82.47	17.53	ME-SA	PanAsia-2 ^{TER-08}
7	O/BHU/3/2009 (KM921814)	BHU09-03	639	525	0	82.16	17.84	ME-SA	Ind-2001d
8	O/ETH/1/2007 (FJ798137)	ETH07-01	639	525	0	82.16	17.84	EA-3	unnamed
9	O/IND/53/79 (AF292107)	IND79A53	639	525	0	82.16	17.84	ME-SA	unnamed
10	O/IRN/18/2010	IRN10-18	639	524	0	82.00	18.00	ME-SA	PanAsia-2 ^{BAL-09}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

© The Pirbright Institute (not to be reproduced without permission)

Report on FMDV O in Myanmar in 2015

Batch: WRLFMD/2015/00035

◆ indicates viruses in this batch

Software: MEGA 6.06

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

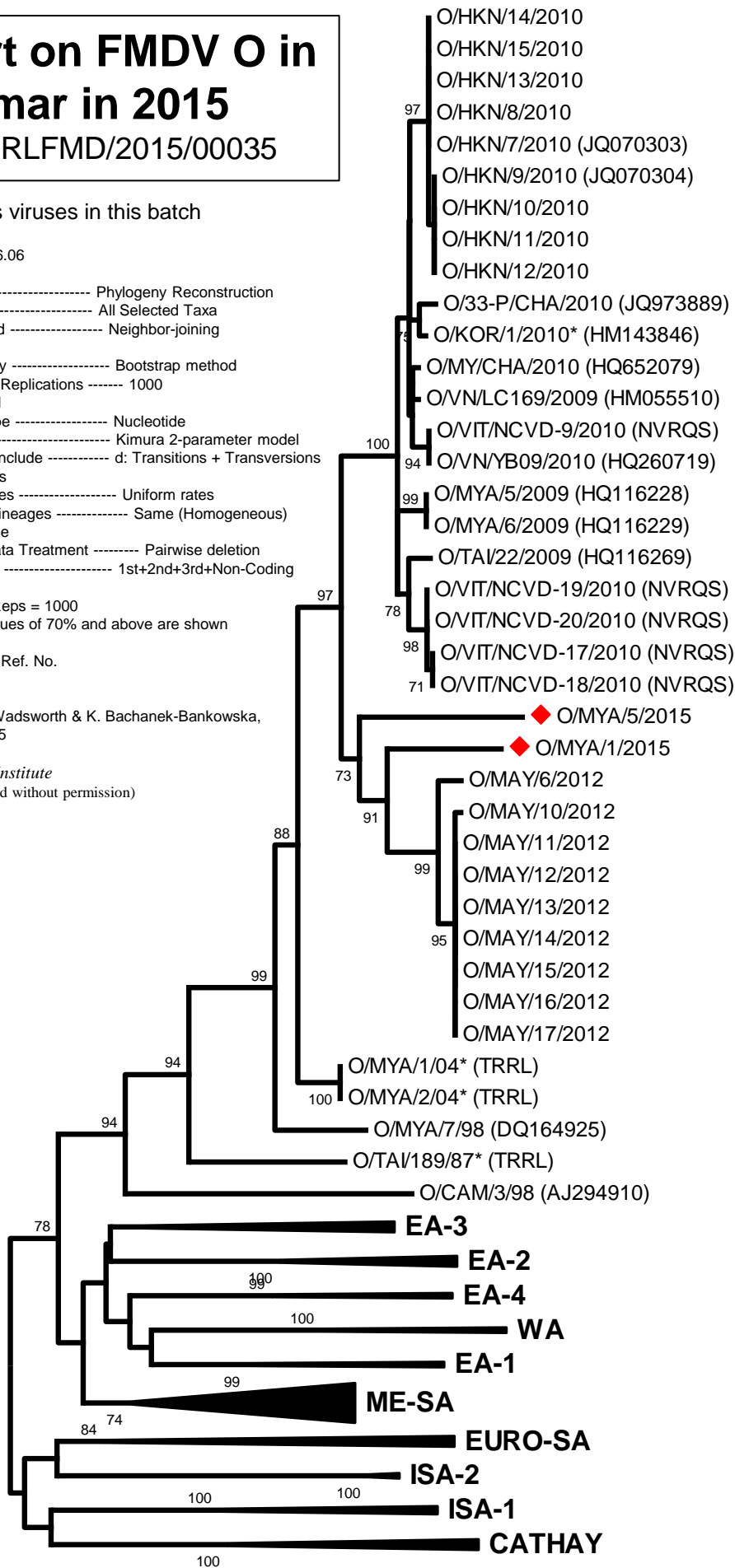
No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
17 December 2015

© The Pirbright Institute
(not to be reproduced without permission)



Mya-98

SEA

Cam-94

0.02