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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00003
Sender Details:

Date Received: 18th January 2012
Country of Origin: Japan
Date Reported: 21st February 2012

Dear Dr Kenichi Sakamoto

Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

Results Approved By:

Official Stamp:

Date:

21/2/12

A UKAS accredited testing laboratory No. 4025.

To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: gareth.shimmon@iah.ac.uk. IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

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

Genotyping Report (for information only – not to be reported)

Report Date for this Batch: 20 February 2012

FMDV type O

Country: Japan

Period: 2010

No. of samples: 1

BATCH: WRLFMD/2012/00003



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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: 03/02/2012
WRLFMD Ref No: JPN/1/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00003	Checked by: D.P. King
Sender Ref: O/JPN/2010	
Location: Miyazaki Prefecture, Japan	Topotype: SEA
Date collected: 17/04/2010	Genotype/strain: Mya-98
Date received by WRLFMD: 18/01/2012	Sequence filename: JPN10-01.SEQ
Date received for sequencing: 30/01/2012	Date sequence last updated: 03/02/2012
Species: Cattle	No. of Nt determined: 639
Material used: RS3 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3206
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 16 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/JPN/MZ1/2010 (AB618503)	JPN10-AA	639	639	0	100	0	SEA	Mya-98
2	O/TZ/CHA/2010 (HQ652081)	CHA10-AW	639	636	0	99.53	0.47	SEA	Mya-98
3	O/CHA/31/2010* (JF792356)	CHA10-AB	639	635	0	99.37	0.63	SEA	Mya-98
4	O/BY/CHA/2010 (JN998085)	CHA10-AX	639	634	0	99.22	0.78	SEA	Mya-98
5	O/HKN/13/2010	HKN10-13	639	634	0	99.22	0.78	SEA	Mya-98
6	O/HKN/14/2010	HKN10-14	639	634	0	99.22	0.78	SEA	Mya-98
7	O/HKN/15/2010	HKN10-15	639	634	0	99.22	0.78	SEA	Mya-98
8	O/HKN/7/2010 (JQ070303)	HKN10-07	639	634	0	99.22	0.78	SEA	Mya-98
9	O/HKN/8/2010	HKN10-08	639	634	0	99.22	0.78	SEA	Mya-98
10	O/HKN/10/2010	HKN10-10	639	633	0	99.06	0.94	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/PAK/16/2010	PAK10-16	639	540	0	84.51	15.49	ME-SA	PanAsia-2 ^{PUN-10}
7	O/ETH/3/2004 (FJ798109)	ETH04-03	639	539	0	84.35	15.65	EA-3	unnamed
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	538	0	84.19	15.81	ME-SA	PanAsia
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	536	0	83.88	16.12	ME-SA	PanAsia-2 ^{TER-08}
10	O/ETH/1/2007 (FJ798137)	ETH07-01	639	535	0	83.72	16.28	EA-3	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV O in Japan in 2010

Batch: WRLFMD/2012/00003

◆ indicates viruses in this batch

Software: MEGA 5.0

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

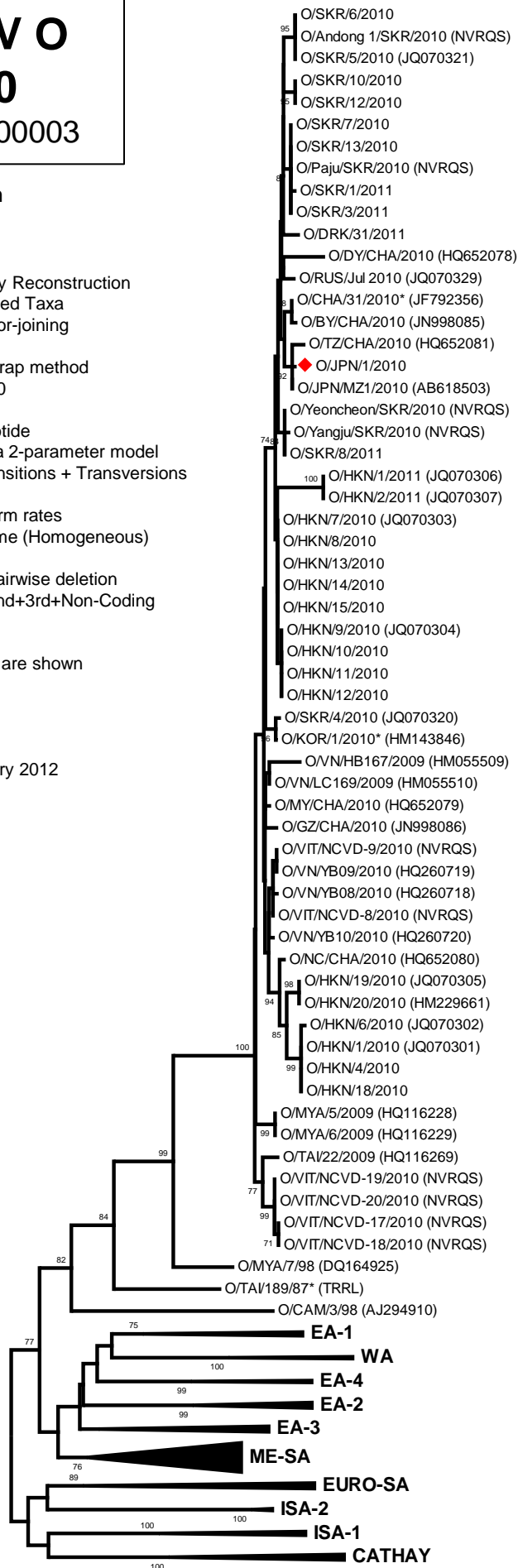
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 20 February 2012

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Mya-98

SEA

Cam-94

0.02