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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2011/00025

Sender Details:



Date Received: 21st May 2011

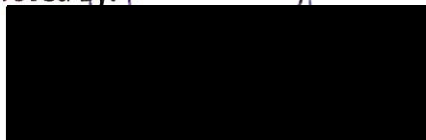
Country of Origin: Republic of Korea (South Korea)

Date Reported: 10th June 2011

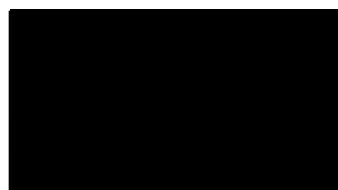
Dear Dr Lee Kwang-Nyeong,

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:

10 / 6 / 11

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: elizabeth.wilson@bbsrc.ac.uk)

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

Genotyping Report

Report Date for this Batch: 9 June 2011

FMDV type O

Country: Republic of Korea (South Korea)

Period: 2010-2011

No. of samples: 3

BATCH: WRLFMD/2011/00025



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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O	Report date: 09/06/2011
WRLFMD Ref No: SKR/12/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2011/00025	Checked by: V. Mioulet
Sender Ref: 85-1	
Location: Not given, Republic of Korea,	Topotype: SEA
Date collected: 27/12/2010	Genotype/strain: Mya-98
Date received by WRLFMD: 21/05/2011	Sequence filename: SKR10-12.SEQ
Date received for sequencing: 26/05/2011	Date sequence last updated: 27/05/2011
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2998
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 19 days
	Sequencing time: 14 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/SKR/10/2010	SKR10-10	639	639	0	100.00	0.00	SEA	Mya-98
2	O/Paju/SKR/2010 (NVRQS)	SKR10-AF	639	634	0	99.22	0.78	SEA	Mya-98
3	O/SKR/13/2010	SKR10-13	639	634	0	99.22	0.78	SEA	Mya-98
4	O/SKR/3/2011	SKR11-03	639	634	0	99.22	0.78	SEA	Mya-98
5	O/SKR/7/2010	SKR10-07	639	634	0	99.22	0.78	SEA	Mya-98
6	O/SKR/8/2011	SKR11-08	639	634	0	99.22	0.78	SEA	Mya-98
7	O/Yeoncheon/SKR/2010 (NVRQS)	SKR10-AE	639	634	0	99.22	0.78	SEA	Mya-98
8	O/Andong 1/SKR/2010 (NVRQS)	SKR10-AC	639	633	0	99.06	0.94	SEA	Mya-98
9	O/HKN/13/2010	HKN10-13	639	633	0	99.06	0.94	SEA	Mya-98
10	O/HKN/14/2010	HKN10-14	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	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/PAK/16/2010	PAK10-16	639	540	0	84.51	15.49	ME-SA	PanAsia-2 ^{PUN-10}
6	O/IRN/8/2005	IRN05-08	639	539	0	84.35	15.65	ME-SA	PanAsia-2
7	O/UKG/35/2001 (AJ539141)	UKG01-35	639	539	0	84.35	15.65	ME-SA	PanAsia
8	O/TUR/257/2008* (FMDI)	TUR08-AD	639	537	0	84.04	15.96	ME-SA	PanAsia-2 ^{TER-08}
9	O/ETH/3/2004 (FJ798109)	ETH04-03	639	536	0	83.88	16.12	EA-3	unnamed
10	O/IRN/88/2009	IRN09-88	639	536	0	83.88	16.12	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O WRLFMD Ref No: SKR/13/2010 Batch No: WRLFMD/2011/00025 Sender Ref: 88-1 Location: Not given, Republic of Korea, Date collected: 27/12/2010 Date received by WRLFMD: 21/05/2011 Date received for sequencing: 26/05/2011 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 09/06/2011 Reported by: N.J. Knowles Checked by: V. Mioulet Topotype: SEA Genotype/strain: Mya-98 Sequence filename: SKR10-13.SEQ Date sequence last updated: 27/05/2011 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2998 Min. no. of nt for comparison: 600 Total turn-around time: 19 days Sequencing time: 14 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/Paju/SKR/2010 (NVRQS)	SKR10-AF	639	639	0	100.00	0.00	SEA	Mya-98
2	O/SKR/3/2011	SKR11-03	639	639	0	100.00	0.00	SEA	Mya-98
3	O/SKR/7/2010	SKR10-07	639	639	0	100.00	0.00	SEA	Mya-98
4	O/SKR/1/2011	SKR11-01	639	638	0	99.84	0.16	SEA	Mya-98
5	O/SKR/8/2011	SKR11-08	639	635	0	99.37	0.63	SEA	Mya-98
6	O/Yeoncheon/SKR/2010 (NVRQS)	SKR10-AE	639	635	0	99.37	0.63	SEA	Mya-98
7	O/Andong 1/SKR/2010 (NVRQS)	SKR10-AC	639	634	0	99.22	0.78	SEA	Mya-98
8	O/HKN/13/2010	HKN10-13	639	634	0	99.22	0.78	SEA	Mya-98
9	O/HKN/14/2010	HKN10-14	639	634	0	99.22	0.78	SEA	Mya-98
10	O/HKN/15/2010	HKN10-15	639	634	0	99.22	0.78	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	596	0	93.27	6.73	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	572	0	89.51	10.49	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	544	0	85.13	14.87	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	544	0	85.13	14.87	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	541	0	84.66	15.34	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/TUR/257/2008* (FMDI)	TUR08-AD	639	538	0	84.19	15.81	ME-SA	PanAsia-2 ^{TER-08}
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	538	0	84.19	15.81	ME-SA	PanAsia
10	O/IRN/88/2009	IRN09-88	639	537	0	84.04	15.96	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*. not a WRLFMD reference number

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Serotype: O	Report date: 09/06/2011
WRLFMD Ref No: SKR/8/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2011/00025	Checked by: V. Mioulet
Sender Ref: 107-1	
Location: Not given, Republic of Korea,	Topotype: SEA
Date collected: 02/01/2011	Genotype/strain: Mya-98
Date received by WRLFMD: 21/05/2011	Sequence filename: SKR11-08.SEQ
Date received for sequencing: 26/05/2011	Date sequence last updated: 27/05/2011
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2998
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 19 days
	Sequencing time: 14 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/Yeoncheon/SKR/2010 (NVRQS)	SKR10-AE	639	639	0	100.00	0.00	SEA	Mya-98
2	O/Yangju/SKR/2010 (NVRQS)	SKR10-AD	639	638	0	99.84	0.16	SEA	Mya-98
3	O/HKN/13/2010	HKN10-13	639	636	0	99.53	0.47	SEA	Mya-98
4	O/HKN/14/2010	HKN10-14	639	636	0	99.53	0.47	SEA	Mya-98
5	O/HKN/15/2010	HKN10-15	639	636	0	99.53	0.47	SEA	Mya-98
6	O/HKN/7/2010	HKN10-07	639	636	0	99.53	0.47	SEA	Mya-98
7	O/HKN/8/2010	HKN10-08	639	636	0	99.53	0.47	SEA	Mya-98
8	O/HKN/10/2010	HKN10-10	639	635	0	99.37	0.63	SEA	Mya-98
9	O/HKN/11/2010	HKN10-11	639	635	0	99.37	0.63	SEA	Mya-98
10	O/HKN/12/2010	HKN10-12	639	635	0	99.37	0.63	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	596	0	93.27	6.73	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	574	0	89.83	10.17	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	544	0	85.13	14.87	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	544	0	85.13	14.87	ME-SA	unnamed
5	O/IRN/8/2005	IRN05-08	639	544	0	85.13	14.87	ME-SA	PanAsia-2
6	O/PAK/16/2010	PAK10-16	639	543	0	84.98	15.02	ME-SA	PanAsia-2 ^{PUN-10}
7	O/ETH/3/2004 (FJ798109)	ETH04-03	639	541	0	84.66	15.34	EA-3	unnamed
8	O/TUR/257/2008* (FMDI)	TUR08-AD	639	540	0	84.51	15.49	ME-SA	PanAsia-2 ^{TER-08}
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	540	0	84.51	15.49	ME-SA	PanAsia
10	O/IRN/88/2009	IRN09-88	639	539	0	84.35	15.65	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV O in the Republic of Korea (South Korea) in 2010-2011

Batch: WRLFMD/2011/00025

◆ 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 : 639

No Of Bootstrap Repts = 1000

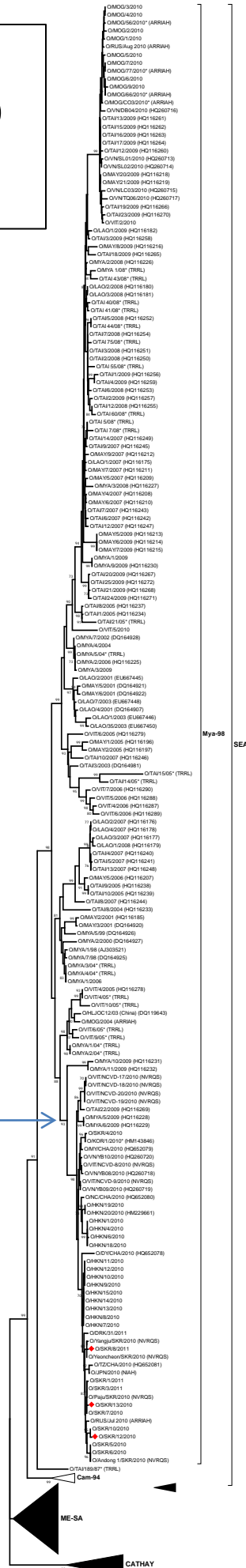
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 09 June 2011

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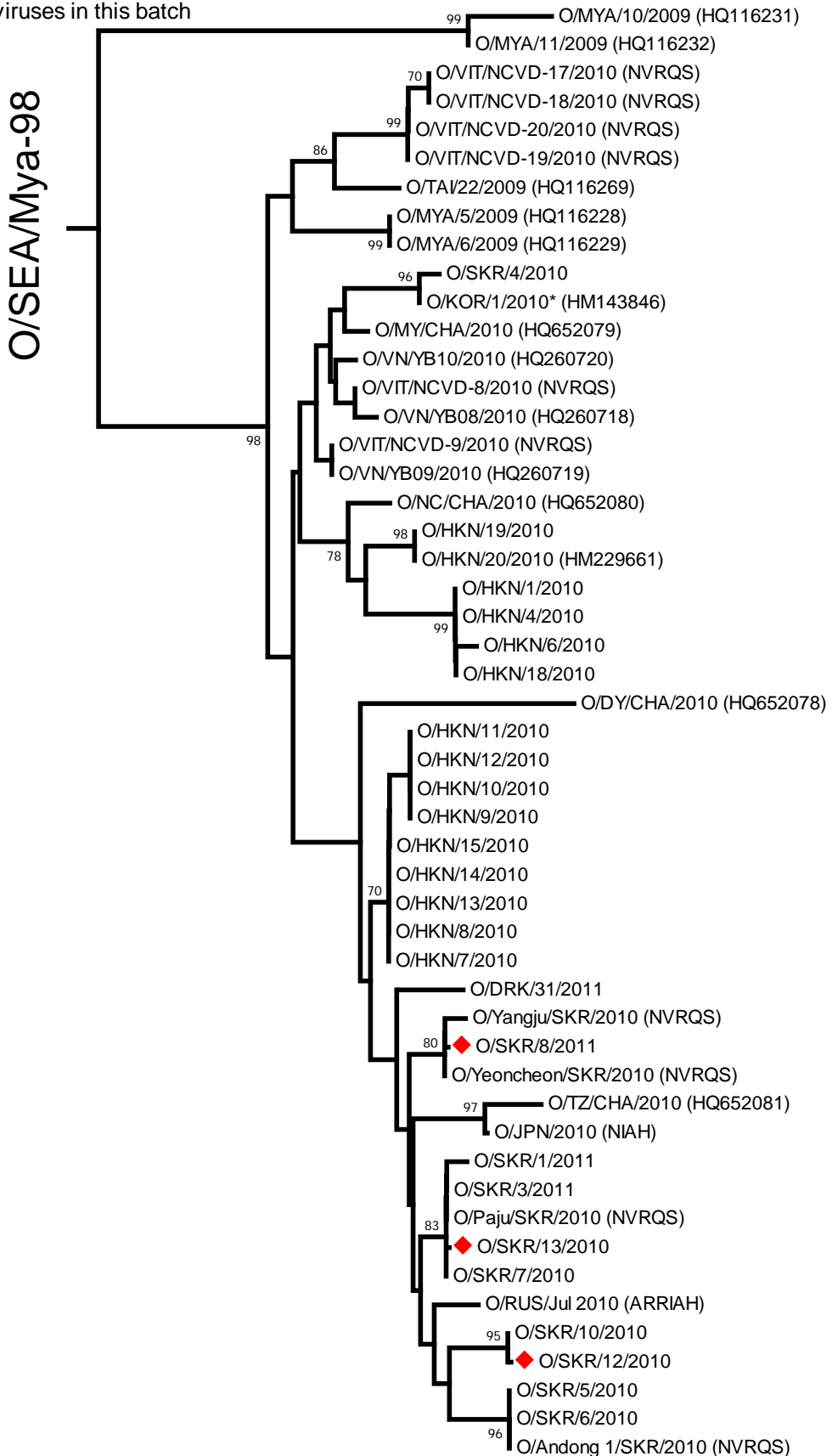
see next page →



Report on FMDV O in the Republic of Korea in 2010-2011

Batch: WRLFMD/2011/00025

◆ indicates viruses in this batch



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