

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

Genotyping Report

Report Date for this Batch: 18 December 2013

FMDV type O

Country: Saudi Arabia

Period: 2013

No. of samples: 3

BATCH: WRLFMD/2013/00026



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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O WRLFMD Ref No: SAU/6/2013 Batch No: WRLFMD/2013/00026 Sender Ref: G134 (AN1) Location: Durma, Riyadh, Central region, Saudi Arabia Date collected: 22/11/2013 Date received by WRLFMD: 29/11/2013 Date received for sequencing: 13/12/2013 Species: Cattle Material used: BTy1 05/12/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 18/12/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: Ind-2001 ^{KAR-13} Sequence filename: SAU13-06.SEQ Date sequence last updated: 18/12/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3727 Min. no. of nt for comparison: 600 Total turn-around time: 19 days Sequencing time: 5 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/SAU/7/2013	SAU13-07	639	639	0	100.00	0.00	ME-SA	Ind-2001 ^{KAR-13}
2	O/SAU/8/2013	SAU13-08	639	639	0	100.00	0.00	ME-SA	Ind-2001 ^{KAR-13}
3	O/SAU/3/2013	SAU13-03	639	635	0	99.37	0.63	ME-SA	Ind-2001 ^{KAR-13}
4	O/SAU/4/2013	SAU13-04	639	635	0	99.37	0.63	ME-SA	Ind-2001 ^{KAR-13}
5	O/SAU/1/2013	SAU13-01	639	634	0	99.22	0.78	ME-SA	Ind-2001 ^{KAR-13}
6	O/LIB/1/2013	LIB13-01	639	630	0	98.59	1.41	ME-SA	Ind-2001 ^{KAR-13}
7	O/LIB/4/2013	LIB13-04	639	630	0	98.59	1.41	ME-SA	Ind-2001 ^{KAR-13}
8	O/LIB/5/2013	LIB13-05	639	630	0	98.59	1.41	ME-SA	Ind-2001 ^{KAR-13}
9	O/LIB/7/2013	LIB13-07	639	630	0	98.59	1.41	ME-SA	Ind-2001 ^{KAR-13}
10	O/LIB/2/2013	LIB13-02	639	629	0	98.44	1.56	ME-SA	Ind-2001 ^{KAR-13}
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/1/2013	BHU13-01	639	621	0	97.18	2.82	ME-SA	Ind-2001 ^{KAR-13}
2	O/BHU/3/2009	BHU09-03	639	614	0	96.09	3.91	ME-SA	Ind-2001d
3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	588	0	92.02	7.98	ME-SA	Ind-2001b
4	O/KUW/3/97 (DQ164904)	KUW97-03	639	585	0	91.55	8.45	ME-SA	Ind-2001a
5	O/UAE/4/2008	UAE08-04	636	575	0	90.41	9.59	ME-SA	Ind-2001c
6	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 ^{FAR-09}
7	O/IRN/8/2005	IRN05-08	639	574	0	89.83	10.17	ME-SA	PanAsia-2
8	O/PAK/16/2010	PAK10-16	639	570	0	89.20	10.80	ME-SA	PanAsia-2 ^{PUN-10}
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	570	0	89.20	10.80	ME-SA	PanAsia
10	O/IRN/18/2010	IRN10-18	639	569	0	89.05	10.95	ME-SA	PanAsia-2 ^{BAL-09}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O WRLFMD Ref No: SAU/7/2013 Batch No: WRLFMD/2013/00026 Sender Ref: G169 (AN2) Location: Durma, Riyadh, Central region, Saudi Arabia Date collected: 27/11/2013 Date received by WRLFMD: 29/11/2013 Date received for sequencing: 13/12/2013 Species: Cattle Material used: BTy1 05/12/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 18/12/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: Ind-2001 ^{KAR-13} Sequence filename: SAU13-07.SEQ Date sequence last updated: 18/12/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3727 Min. no. of nt for comparison: 600 Total turn-around time: 19 days Sequencing time: 5 days
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Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/SAU/6/2013	SAU13-06	639	639	0	100.00	0.00	ME-SA	Ind-2001 ^{KAR-13}
2	O/SAU/8/2013	SAU13-08	639	639	0	100.00	0.00	ME-SA	Ind-2001 ^{KAR-13}
3	O/SAU/3/2013	SAU13-03	639	635	0	99.37	0.63	ME-SA	Ind-2001 ^{KAR-13}
4	O/SAU/4/2013	SAU13-04	639	635	0	99.37	0.63	ME-SA	Ind-2001 ^{KAR-13}
5	O/SAU/1/2013	SAU13-01	639	634	0	99.22	0.78	ME-SA	Ind-2001 ^{KAR-13}
6	O/LIB/1/2013	LIB13-01	639	630	0	98.59	1.41	ME-SA	Ind-2001 ^{KAR-13}
7	O/LIB/4/2013	LIB13-04	639	630	0	98.59	1.41	ME-SA	Ind-2001 ^{KAR-13}
8	O/LIB/5/2013	LIB13-05	639	630	0	98.59	1.41	ME-SA	Ind-2001 ^{KAR-13}
9	O/LIB/7/2013	LIB13-07	639	630	0	98.59	1.41	ME-SA	Ind-2001 ^{KAR-13}
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3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	588	0	92.02	7.98	ME-SA	Ind-2001b
4	O/KUW/3/97 (DQ164904)	KUW97-03	639	585	0	91.55	8.45	ME-SA	Ind-2001a
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7	O/IRN/8/2005	IRN05-08	639	574	0	89.83	10.17	ME-SA	PanAsia-2
8	O/PAK/16/2010	PAK10-16	639	570	0	89.20	10.80	ME-SA	PanAsia-2 ^{PUN-10}
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	570	0	89.20	10.80	ME-SA	PanAsia
10	O/IRN/18/2010	IRN10-18	639	569	0	89.05	10.95	ME-SA	PanAsia-2 ^{BAL-09}

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Serotype: O WRLFMD Ref No: SAU/8/2013 Batch No: WRLFMD/2013/00026 Sender Ref: G348 (AN3) Location: Durma, Riyadh, Central region, Saudi Arabia Date collected: 27/11/2013 Date received by WRLFMD: 29/11/2013 Date received for sequencing: 13/12/2013 Species: Cattle Material used: BTy2 05/12/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 18/12/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: Ind-2001 ^{KAR-13} Sequence filename: SAU13-08.SEQ Date sequence last updated: 18/12/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3727 Min. no. of nt for comparison: 600 Total turn-around time: 19 days Sequencing time: 5 days
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3	O/SAU/3/2013	SAU13-03	639	635	0	99.37	0.63	ME-SA	Ind-2001 ^{KAR-13}
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9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	570	0	89.20	10.80	ME-SA	PanAsia
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Report on FMDV O in Saudi Arabia in 2013

Batch: WRLFMD/2013/00026

◆ indicates viruses in this batch

Software: MEGA 5.2

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,
18 December 2013

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