

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

## Genotyping Report

Report Date for this Batch: 16 October 2015

FMDV type A

Country: Saudi Arabia

Period: 2015

No. of samples: 2

BATCH: WRLFMD/2015/00025



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: A WRLFMD Ref No: SAU/1/2015 Batch No: WRLFMD/2015/00025 Sender Ref: 957 Location: Izdahair District, Riyadh, Saudi Arabia Date collected: 02/09/2015 Date received by WRLFMD: 15/09/2015 Date received for sequencing: 13/10/2015 Species: Cattle Material used: BTy1 29/09/2015 Region sequenced: VPI RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 16/10/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ASIA Genotype/strain: unnamed Sequence filename: SAU15-01.SEQ Date sequence last updated: 16/10/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2064 Min. no. of nt for comparison: 600 Total turn-around time: 31 days Sequencing time: 3 days
Comments:	

### Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/SAU/2/2015	SAU15-02	639	639	0	100.00	0.00	ASIA	unnamed
2	A/IND/249/2004* (HQ832582)	IND04-AF	639	597	0	93.43	6.57	ASIA	unnamed
3	A/IND/243/04* (FJ617245)	IND04-AA	639	596	0	93.27	6.73	ASIA	unnamed
4	A/IND/249/2004* (HQ127680)	IND04-AD	639	596	0	93.27	6.73	ASIA	unnamed
5	A/BHU/41/2002 (EU414525)	BHU02-41	639	595	0	93.11	6.89	ASIA	unnamed
6	A/BHU/8/2003	BHU03-08	639	595	0	93.11	6.89	ASIA	unnamed
7	A/IND/161/2003* (HQ832578)	IND03-AD	639	595	0	93.11	6.89	ASIA	unnamed
8	A/IND/281/2003* (HQ832579)	IND03-AE	639	595	0	93.11	6.89	ASIA	unnamed
9	A/IND/447/2005* (HQ832583)	IND05-AR	639	595	0	93.11	6.89	ASIA	unnamed
10	A/BHU/27/2003 (FJ755013)	BHU03-27	639	594	0	92.96	7.04	ASIA	unnamed

### Most Closely Related Reference Viruses

(see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](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	A22/IRQ/64 (AY593763)	IRQ64-A	639	541	0	84.66	15.34	ASIA	A22
2	A/IRN/1/96 (EF208771)	IRN96-01	638	538	1	84.33	15.67	ASIA	Iran-96
3	A/IRN/2/87 (EF208770)	IRN87-02	636	533	0	83.81	16.19	ASIA	Iran-87
4	A15/Bangkok/TAI/60 (AY593755)	TAI60-D	639	529	0	82.79	17.21	ASIA	A15
5	A12/UK/119/32 (M10975)	UKG32119	639	528	0	82.63	17.37	EURO-SA	A12
6	A/IRN/22/99 (EF208772)	IRN99-22	636	524	0	82.39	17.61	ASIA	Iran-99
7	A/AFG/10/2010	AFG10-10	639	525	0	82.16	17.84	ASIA	Iran-05 <sup>HER-10</sup>
8	A/IRN/9/2011	IRN11-09	639	525	0	82.16	17.84	ASIA	Iran-05 <sup>QAZ-11</sup>
9	A/TAI/118/87* (EF208777)	TAI87-AD	636	522	0	82.08	17.92	ASIA	Thai-87
10	A/IRN/1/2011	IRN11-01	639	524	0	82.00	18.00	ASIA	Iran-05 <sup>FAR-11</sup>

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: A WRLFMD Ref No: SAU/2/2015 Batch No: WRLFMD/2015/00025 Sender Ref: 957 Location: Izdahair District, Riyadh, Saudi Arabia Date collected: 02/09/2015 Date received by WRLFMD: 15/09/2015 Date received for sequencing: 13/10/2015 Species: Cattle Material used: BTy1 29/09/2015 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 16/10/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ASIA Genotype/strain: unnamed Sequence filename: SAU15-02.SEQ Date sequence last updated: 16/10/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2064 Min. no. of nt for comparison: 600 Total turn-around time: 31 days Sequencing time: 3 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/SAU/1/2015	SAU15-01	639	639	0	100.00	0.00	ASIA	unnamed
2	A/IND/249/2004* (HQ832582)	IND04-AF	639	597	0	93.43	6.57	ASIA	unnamed
3	A/IND/243/04* (FJ617245)	IND04-AA	639	596	0	93.27	6.73	ASIA	unnamed
4	A/IND/249/2004* (HQ127680)	IND04-AD	639	596	0	93.27	6.73	ASIA	unnamed
5	A/BHU/41/2002 (EU414525)	BHU02-41	639	595	0	93.11	6.89	ASIA	unnamed
6	A/BHU/8/2003	BHU03-08	639	595	0	93.11	6.89	ASIA	unnamed
7	A/IND/161/2003* (HQ832578)	IND03-AD	639	595	0	93.11	6.89	ASIA	unnamed
8	A/IND/281/2003* (HQ832579)	IND03-AE	639	595	0	93.11	6.89	ASIA	unnamed
9	A/IND/447/2005* (HQ832583)	IND05-AR	639	595	0	93.11	6.89	ASIA	unnamed
10	A/BHU/27/2003 (FJ755013)	BHU03-27	639	594	0	92.96	7.04	ASIA	unnamed
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A22/IRQ/64 (AY593763)	IRQ64-A	639	541	0	84.66	15.34	ASIA	A22
2	A/IRN/1/96 (EF208771)	IRN96-01	638	538	1	84.33	15.67	ASIA	Iran-96
3	A/IRN/2/87 (EF208770)	IRN87-02	636	533	0	83.81	16.19	ASIA	Iran-87
4	A15/Bangkok/TAI/60 (AY593755)	TAI60-D	639	529	0	82.79	17.21	ASIA	A15
5	A12/UK/119/32 (M10975)	UKG32119	639	528	0	82.63	17.37	EURO-SA	A12
6	A/IRN/22/99 (EF208772)	IRN99-22	636	524	0	82.39	17.61	ASIA	Iran-99
7	A/AFG/10/2010	AFG10-10	639	525	0	82.16	17.84	ASIA	Iran-05 <sup>HER-10</sup>
8	A/IRN/9/2011	IRN11-09	639	525	0	82.16	17.84	ASIA	Iran-05 <sup>QAZ-11</sup>
9	A/TAI/118/87* (EF208777)	TAI87-AD	636	522	0	82.08	17.92	ASIA	Thai-87
10	A/IRN/1/2011	IRN11-01	639	524	0	82.00	18.00	ASIA	Iran-05 <sup>FAR-11</sup>

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 A in Saudi Arabia in 2015

Batch: WRLFMD/2015/00025

◆ 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 : 639

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,  
16 October 2015

© The Pirbright Institute

(not to be reproduced without permission)

