

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

Genotyping Report

Report Date for this Batch: 16 November 2015

FMDV type A

Country: Saudi Arabia

Period: 2015

No. of samples: 2

BATCH: WRLFMD/2015/00028



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: A WRLFMD Ref No: SAU/3/2015 Batch No: WRLFMD/2015/00028 Sender Ref: 28415 Location: Haradh Road, Al Kharj, Central region, Saudi Arabia Date collected: 09/10/2015 Date received by WRLFMD: 19/10/2015 Date received for sequencing: 10/11/2015 Species: Cattle Material used: BTy1 22/10/2015 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 15/11/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ASIA Genotype/strain: G-VII Sequence filename: SAU15-03.SEQ Date sequence last updated: 15/11/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2071 Min. no. of nt for comparison: 600 Total turn-around time: 27 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	A/SAU/4/2015	SAU15-04	639	639	0	100.00	0.00	ASIA	G-VII
2	A/SAU/1/2015	SAU15-01	639	631	0	98.75	1.25	ASIA	G-VII
3	A/SAU/2/2015	SAU15-02	639	631	0	98.75	1.25	ASIA	G-VII
4	A/SAU/5/2015	SAU15-05	639	629	0	98.44	1.56	ASIA	G-VII
5	A/SAU/6/2015	SAU15-06	639	629	0	98.44	1.56	ASIA	G-VII
6	A/Van/TUR/203/2015* (FMDI)	TUR15-AA	639	629	0	98.44	1.56	ASIA	G-VII
7	A/BAN/GA/Sa-197/2013 (KJ754939)	BAN13-AB	639	608	0	95.15	4.85	ASIA	G-VII
8	A/IND/161/2003* (HQ832578)	IND03-AD	639	596	0	93.27	6.73	ASIA	G-VII
9	A/IND/249/2004* (HQ832582)	IND04-AF	639	596	0	93.27	6.73	ASIA	G-VII
10	A/IND/243/04* (FJ617245)	IND04-AA	639	595	0	93.11	6.89	ASIA	G-VII

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	A/IND/40/2000* (1999:AF390646)	IND00-40	639	573	0	89.67	10.33	ASIA	G-VII
2	A/IRN/1/96 (EF208771)	IRN96-01	638	540	1	84.64	15.36	ASIA	Iran-96
3	A22/IRQ/64 (AY593763)	IRQ64-A	639	538	0	84.19	15.81	ASIA	A22
4	A/IRN/2/87 (EF208770)	IRN87-02	636	531	0	83.49	16.51	ASIA	Iran-87
5	A/IRN/9/2011	IRN11-09	639	528	0	82.63	17.37	ASIA	Iran-05 ^{QAZ-11}
6	A12/UK/119/32 (M10975)	UKG32119	639	528	0	82.63	17.37	EURO-SA	A12
7	A15/Bangkok/TAI/60 (AY593755)	TAI60-D	639	528	0	82.63	17.37	ASIA	A15
8	A/IRN/22/99 (EF208772)	IRN99-22	636	525	0	82.55	17.45	ASIA	Iran-99
9	A/TAI/118/87* (EF208777)	TAI87-AD	636	522	0	82.08	17.92	ASIA	Thai-87
10	A/AFG/10/2010	AFG10-10	639	524	0	82.00	18.00	ASIA	Iran-05 ^{HER-10}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: A WRLFMD Ref No: SAU/4/2015 Batch No: WRLFMD/2015/00028 Sender Ref: 28339 Location: Haradh Road, Al Kharj, Central region, Saudi Arabia Date collected: 09/10/2015 Date received by WRLFMD: 19/10/2015 Date received for sequencing: 10/11/2015 Species: Cattle Material used: BTy1 22/10/2015 & BTy2 31/10/2015 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 15/11/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ASIA Genotype/strain: G-VII Sequence filename: SAU15-04.SEQ Date sequence last updated: 15/11/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2071 Min. no. of nt for comparison: 600 Total turn-around time: 27 days Sequencing time: 5 days
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Report on FMDV A in Saudi Arabia in 2015

Batch: WRLFMD/2015/00028

◆ 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

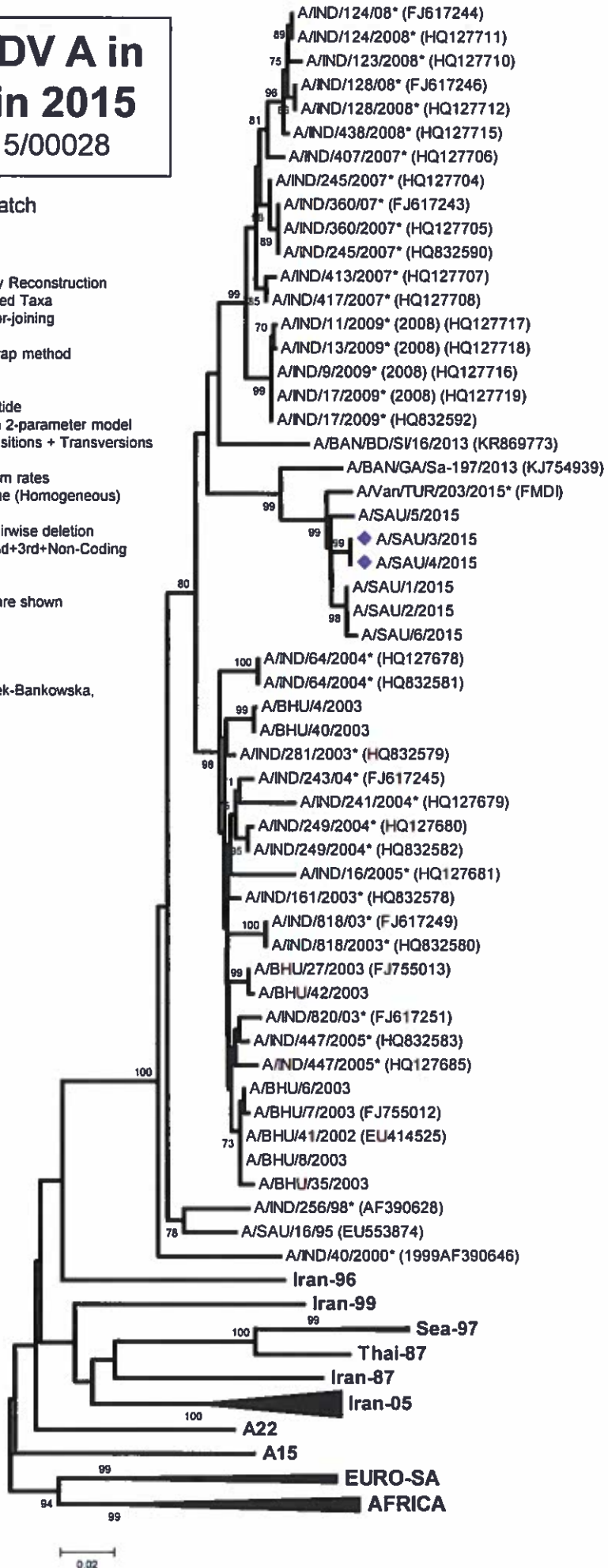
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
16 November 2015

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G-VII

ASIA