

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

&

Federal Governmental Budgetary Institution,
Federal Centre for Animal Health (FGBI-ARRIAH)

&

ICAR Project Directorate on Foot-and-Mouth Disease (PD-FMD)

Genotyping Report

Report Date for this Batch: 25 January 2016

FMDV type A

Country: Armenia

Period: 2015

No. of sequences: 3 (VP1)

Originator

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]



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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	Report date: 23/01/2016
WRLFMD Ref No: ARM/1/2015	Reported by: N.J. Knowles
Batch No: WRLMEG/2015/00021	Checked by: D.P. King
Sender Ref: A/ARRIAH/1/25-12-2015	
Location: Armavir, Arazap, Armenia	Topotype: ASIA
Date collected: 25/12/2015	Genotype/strain: G-VII
Date received by WRLFMD: 28/12/2015	Sequence filename: ARM15-AA.SEQ
Date received for sequencing:	Date sequence last updated: 04/01/2016
Species: not known	No. of Nt determined: 639
Material used: not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not known	Total no. of comparisons: 2100
	Min. no. of nt for comparison: 600
	Total turn-around time: 26 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/ARM/3/2015 (ARRIAH)	ARM15-AC	639	639	0	100.00	0.00	ASIA	G-VII
2	A/ARM/2/2015 (ARRIAH)	ARM15-AB	639	638	0	99.84	0.16	ASIA	G-VII
3	A/IRN/12/2015	IRN15-12	639	638	0	99.84	0.16	ASIA	G-VII
4	A/Van/TUR/203/2015* (FMDI)	TUR15-AA	639	636	0	99.53	0.47	ASIA	G-VII
5	A/IRN/8/2015	IRN15-08	639	634	0	99.22	0.78	ASIA	G-VII
6	A/PD78/IND/2015* (PD-FMD)	IND15-AA	639	633	0	99.06	0.94	ASIA	G-VII
7	A/SAU/3/2015	SAU15-03	639	632	0	98.90	1.10	ASIA	G-VII
8	A/SAU/4/2015	SAU15-04	639	632	0	98.90	1.10	ASIA	G-VII
9	A/SAU/1/2015 (KU127247)	SAU15-01	639	631	0	98.75	1.25	ASIA	G-VII
10	A/SAU/2/2015	SAU15-02	639	631	0	98.75	1.25	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	576	0	90.14	9.86	ASIA	G-VII
2	A22/IRQ/64 (AY593763)	IRQ64--A	639	543	0	84.98	15.02	ASIA	A ₂₂
3	A/IRN/1/96 (EF208771)	IRN96-01	638	542	1	84.95	15.05	ASIA	Iran-96
4	A/IRN/2/87 (EF208770)	IRN87-02	636	532	0	83.65	16.35	ASIA	Iran-87
5	A12/UK/119/32 (M10975)	UKG32119	639	532	0	83.26	16.74	EURO-SA	A ₁₂
6	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	529	0	82.79	17.21	ASIA	A ₁₅
7	A/IRN/22/99 (EF208772)	IRN99-22	636	525	0	82.55	17.45	ASIA	Iran-99
8	A/IRN/9/2011	IRN11-09	639	527	0	82.47	17.53	ASIA	Iran-05 ^{QAZ-11}
9	A/AFG/10/2010	AFG10-10	639	525	0	82.16	17.84	ASIA	Iran-05 ^{HER-10}
10	A/TUR/1/2008 (FJ755133)	TUR08-01	639	525	0	82.16	17.84	ASIA	Iran-05 ^{ARD-07}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: A	Report date: 23/01/2016
WRLFMD Ref No: ARM/2/2015	Reported by: N.J. Knowles
Batch No: WRLMEG/2015/00021	Checked by: D.P. King
Sender Ref: A/ARRIAH/2/25-12-2015	
Location: Armavir, Arazap, Armenia	Topotype: ASIA
Date collected: 25/12/2015	Genotype/strain: G-VII
Date received by WRLFMD: 28/12/2015	Sequence filename: ARM15-AB.SEQ
Date received for sequencing:	Date sequence last updated: 04/01/2016
Species: not known	No. of Nt determined: 639
Material used: not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not known	Total no. of comparisons: 2100
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2	A/ARM/3/2015 (ARRIAH)	ARM15-AC	639	638	0	99.84	0.16	ASIA	G-VII
3	A/IRN/12/2015	IRN15-12	639	637	0	99.69	0.31	ASIA	G-VII
4	A/Van/TUR/203/2015* (FMDI)	TUR15-AA	639	635	0	99.37	0.63	ASIA	G-VII
5	A/IRN/8/2015	IRN15-08	639	633	0	99.06	0.94	ASIA	G-VII
6	A/PD78/IND/2015* (PD-FMD)	IND15-AA	639	632	0	98.90	1.10	ASIA	G-VII
7	A/SAU/1/2015 (KU127247)	SAU15-01	639	632	0	98.90	1.10	ASIA	G-VII
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10	A/SAU/4/2015	SAU15-04	639	631	0	98.75	1.25	ASIA	G-VII
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1	A/IND/40/2000* (1999;AF390646)	IND00-40	639	577	0	90.30	9.70	ASIA	G-VII
2	A22/IRQ/64 (AY593763)	IRQ64--A	639	544	0	85.13	14.87	ASIA	A ₂₂
3	A/IRN/1/96 (EF208771)	IRN96-01	638	543	1	85.11	14.89	ASIA	Iran-96
4	A/IRN/2/87 (EF208770)	IRN87-02	636	533	0	83.81	16.19	ASIA	Iran-87
5	A12/UK/119/32 (M10975)	UKG32119	639	531	0	83.10	16.90	EURO-SA	A ₁₂
6	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	530	0	82.94	17.06	ASIA	A15
7	A/IRN/22/99 (EF208772)	IRN99-22	636	526	0	82.70	17.30	ASIA	Iran-99
8	A/IRN/9/2011	IRN11-09	639	528	0	82.63	17.37	ASIA	Iran-05 ^{QAZ-11}
9	A/AFG/10/2010	AFG10-10	639	526	0	82.32	17.68	ASIA	Iran-05 ^{HER-10}
10	A/TUR/1/2008 (FJ755133)	TUR08-01	639	526	0	82.32	17.68	ASIA	Iran-05 ^{ARD-07}

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8	A/SAU/4/2015	SAU15-04	639	632	0	98.90	1.10	ASIA	G-VII
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nt, nucleotides

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Report on FMDV A in Armenia in 2015

Batch: WRLMEG/2015/00021

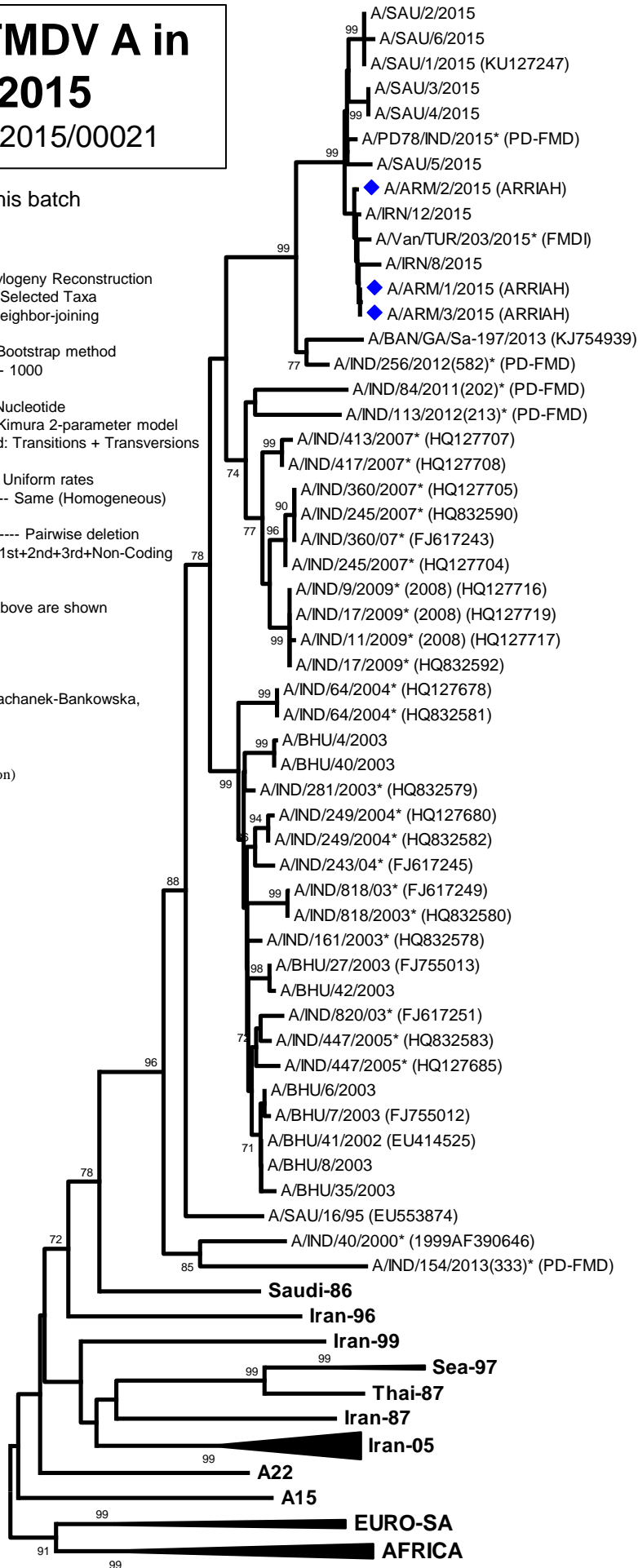
◆ indicates viruses in this batch

Software: MEGA 6.06
 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 & K. Bachanek-Bankowska,
 23 January 2016

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G-VII (G-18)

ASIA