

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

Joint Genotyping Report with the Sap Institute, Ankara, Turkey

Report Date for this Batch: 10 November 2015

FMDV type A

Country: Turkey

Period: 2015

No. of sequences: 1 (VP1)

Originator: [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: 10/11/2015
WRLFMD Ref No: Van/TUR/203/2015*	Reported by: N.J. Knowles
Batch No: WRLMEG/2015/00019	Checked by: K. Bachanek-Bankowska
Sender Ref: A/Van/203/2015	
Location: Van, Turkey	Topotype: ASIA
Date collected: 2015	Genotype/strain: genotype VII
Date received by WRLFMD: 09/11/2015	Sequence filename: TUR15-AA.SEQ
Date received for sequencing: n/a	Date sequence last updated: 10/11/2015
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: 2067
	Min. no. of nt for comparison: 600
	Total turn-around time: 1 day
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	628	0	98.28	1.72	ASIA	genotype VII
2	A/SAU/2/2015	SAU15-02	639	628	0	98.28	1.72	ASIA	genotype VII
3	A/BAN/GA/Sa-197/2013 (KJ754939)	BAN13-AB	639	608	0	95.15	4.85	ASIA	genotype VII
4	A/IND/161/2003* (HQ832578)	IND03-AD	639	596	0	93.27	6.73	ASIA	genotype VII
5	A/IND/249/2004* (HQ832582)	IND04-AF	639	596	0	93.27	6.73	ASIA	genotype VII
6	A/BHU/27/2003 (FJ755013)	BHU03-27	639	595	0	93.11	6.89	ASIA	genotype VII
7	A/IND/243/04* (FJ617245)	IND04-AA	639	595	0	93.11	6.89	ASIA	genotype VII
8	A/IND/249/2004* (HQ127680)	IND04-AD	639	595	0	93.11	6.89	ASIA	genotype VII
9	A/BHU/41/2002 (EU414525)	BHU02-41	639	594	0	92.96	7.04	ASIA	genotype VII
10	A/BHU/42/2003	BHU03-42	639	594	0	92.96	7.04	ASIA	genotype 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	A22/IRQ/64 (AY593763)	IRQ64--A	639	544	0	85.13	14.87	ASIA	A ₂₂
2	A/IRN/1/96 (EF208771)	IRN96-01	638	541	1	84.80	15.20	ASIA	Iran-96
3	A/IRN/2/87 (EF208770)	IRN87-02	636	531	0	83.49	16.51	ASIA	Iran-87
4	A12/UK/119/32 (M10975)	UKG32119	639	531	0	83.10	16.90	EURO-SA	A ₁₂
5	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	528	0	82.63	17.37	ASIA	A ₁₅
6	A/IRN/9/2011	IRN11-09	639	527	0	82.47	17.53	ASIA	Iran-05 ^{QAZ-11}
7	A/IRN/22/99 (EF208772)	IRN99-22	636	524	0	82.39	17.61	ASIA	Iran-99
8	A/TUR/1/2008 (FJ755133)	TUR08-01	639	526	0	82.32	17.68	ASIA	Iran-05 ^{ARD-07}
9	A/AFG/10/2010	AFG10-10	639	524	0	82.00	18.00	ASIA	Iran-05 ^{HER-10}
10	A/TAI/118/87* (EF208777)	TAI87-AD	636	521	0	81.92	18.08	ASIA	Thai-87

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV A in Turkey in 2015

Batch: WRLMEG/2015/00019

◆ 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

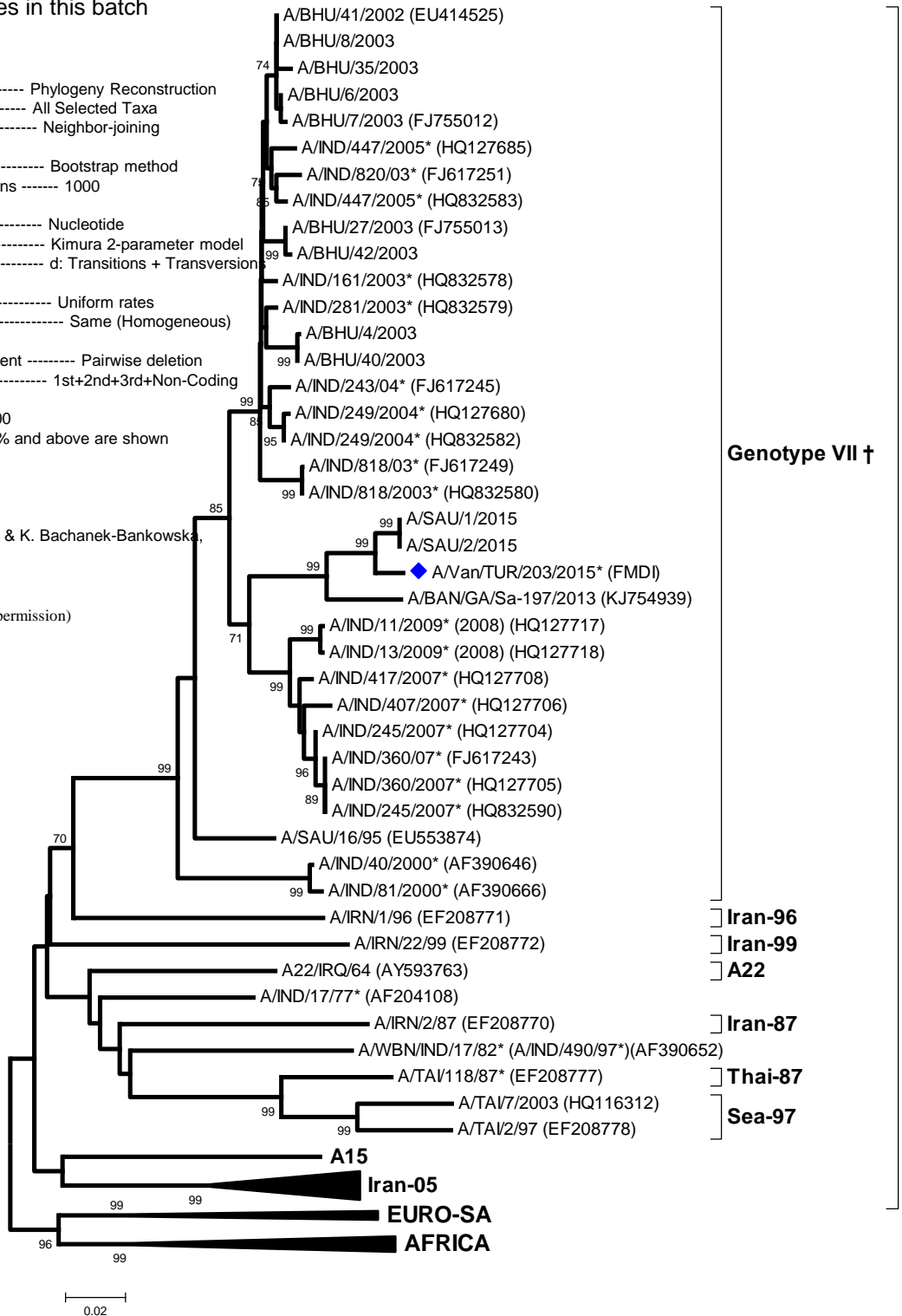
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

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

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† genotype designation assigned by PD-FMD: Tosh, C., Sanyal, A., Hemadri, D., Venkataramanan, R. (2002). Phylogenetic analysis of serotype A foot-and-mouth disease virus isolated in India between 1977 and 2000. Arch. Virol. 147: 493-513.