

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

Genotyping Report

Report Date for this Batch: 18 April 2016

FMDV type A

Country: Ethiopia

Period: 2015

No. of samples: 1

BATCH: WRLFMD/2016/00010



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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: 06/04/2016
WRLFMD Ref No: ETH/19/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2016/00010	Checked by: K. Bachanek-Bankowska
Sender Ref: Eth-31055/15	
Location: Guna, Arsi, Oromia, Ethiopia	Topotype: AFRICA
Date collected: 20/12/2015	Genotype/strain: G-IV
Date received by WRLFMD: 25/02/2016	Sequence filename: ETH15-19.SEQ
Date received for sequencing: 24/03/2016	Date sequence last updated: 06/04/2016
Species: Bovine	No. of Nt determined: 639
Material used: BTy1 18/03/2016	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 2128
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 41 days
	Sequencing time: 13 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/CAR/P19/2000 (mfa/057/01)	CRC00-01	639	564	0	88.26	11.74	AFRICA	G-IV
2	A/CAR/12/2000	CAR00-12	639	562	0	87.95	12.05	AFRICA	G-IV
3	A/CAR/13/2000	CAR00-13	639	562	0	87.95	12.05	AFRICA	G-IV
4	A/CAR/14/2000	CAR00-14	639	562	0	87.95	12.05	AFRICA	G-IV
5	A/CAR/15/2000 (EF208755)	CAR00-15	639	562	0	87.95	12.05	AFRICA	G-IV
6	A/SUD/12/2011	SUD11A12	639	562	0	87.95	12.05	AFRICA	G-IV
7	A/SUD/12/2011	SUD11B12	639	562	0	87.95	12.05	AFRICA	G-IV
8	A/SUD/12/2011	SUD11C12	639	562	0	87.95	12.05	AFRICA	G-IV
9	A/SUD/12/2011	SUD11D12	639	562	0	87.95	12.05	AFRICA	G-IV
10	A/SUD/1/2011	SUD11A01	639	561	0	87.79	12.21	AFRICA	G-IV
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/SUD/3/77 (GU566064)	SUD77-03	639	544	0	85.13	14.87	AFRICA	G-IV
2	A/KEN/42/66 (K18/66)(KF561699)	KEN66-42	639	534	0	83.57	16.43	AFRICA	G-I
3	A/NGR/2/73 (KF561704)	NGR73-02	639	532	0	83.26	16.74	AFRICA	G-V
4	A/GHA/16/73 (KF561698)	GHA73-16	636	526	0	82.70	17.30	AFRICA	G-VI
5	A/EGY/1/72 (EF208756)	EGY72-01	639	524	0	82.00	18.00	AFRICA	G-II
6	A21/Lumbwa/KEN/64 (AY593761)	KEN64-AA	639	522	0	81.69	18.31	AFRICA	G-III
7	A/UGA/13/66 (KF561705)	UGA66-13	639	518	0	81.06	18.94	AFRICA	G-VII
8	A/IRN/22/99 (EF208772)	IRN99-22	636	512	0	80.50	19.50	ASIA	Iran-99
9	A12/UK/119/32 (M10975)	UKG32119	639	513	0	80.28	19.72	EURO-SA	A ₁₂
10	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	509	0	80.03	19.97	EURO-SA	A ₅

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.4

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Report on FMDV A in Ethiopia in 2015

Batch: WRLFMD/2016/00010

◆ 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

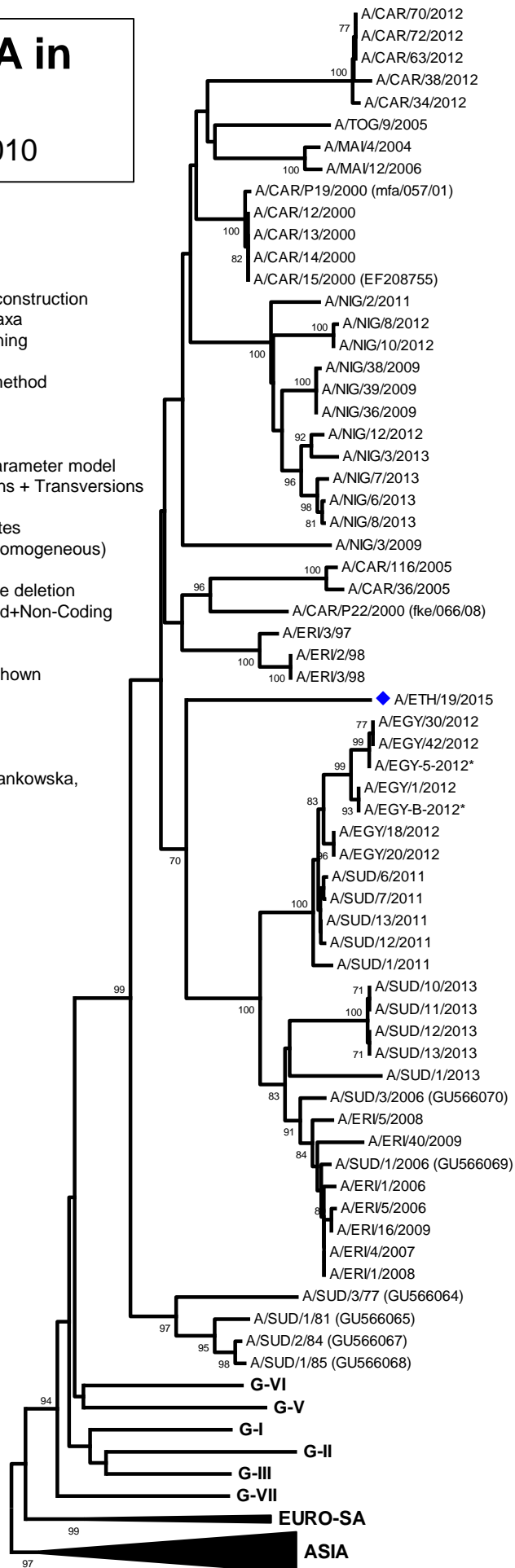
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
18 April 2016

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G-IV

AFRICA

0.02