

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

Genotyping Report

Report Date for this Batch: 16 June 2014

FMDV type A

Country: Ethiopia

Period: 2001

No. of samples: 2

BATCH: WRLFMD/2014/00013



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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: ETH/10/2001 Batch No: WRLFMD/2014/00013 Sender Ref: 10a ETH 10/13 Location: Konso, Konso special woreda, SNNPR, Ethiopia Date collected: 2000/2001 Date received by WRLFMD: 27/02/2014 Date received for sequencing: 19/05/2014 Species: Bovine Material used: BTy1 20/03/2014 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 06/06/2014 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: AFRICA Genotype/strain: G-VII Sequence filename: ETH01-10.SEQ Date sequence last updated: 06/06/2014 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 1933 Min. no. of nt for comparison: 600 Total turn-around time: 99 days Sequencing time: 18 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/ETH/11/2001	ETH01-11	639	639	0	100.00	0.00	AFRICA	G-VII
2	A/ETH/6/2000 (FJ798147)	ETH00-06	639	637	0	99.69	0.31	AFRICA	G-VII
3	A/ETH/10/2005 (2002)(FJ798149)	ETH05-10	639	635	0	99.37	0.63	AFRICA	G-VII
4	A/ETH/9/2005 (2000)(FJ798148)	ETH05-09	639	635	0	99.37	0.63	AFRICA	G-VII
5	A/ETH/16/2005 (2000/01)(EF208764)	ETH05-16	639	632	0	98.90	1.10	AFRICA	G-VII
6	A/K60/01 (KJ440867)	KEN01-AA	639	632	0	98.90	1.10	AFRICA	G-VII
7	A/K73/01 (KJ440866)	KEN01-AB	639	627	0	98.12	1.88	AFRICA	G-VII
8	A/ETH/3/2005 (year nk)(EF208762)	ETH05-03	639	624	0	97.65	2.35	AFRICA	G-VII
9	A/ETH/4/2005 (2000)(EF208763)	ETH05-04	639	624	0	97.65	2.35	AFRICA	G-VII
10	A/ETH/1/94 (EF208766)	ETH94-01	639	611	0	95.62	4.38	AFRICA	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/UGA/13/66 (KF561705)	UGA66-13	639	565	0	88.42	11.58	AFRICA	G-VII
2	A/KEN/42/66 (K18/66)(KF561699)	KEN66-42	639	544	0	85.13	14.87	AFRICA	G-I
3	A21/Lumbwa/KEN/64 (AY593761)	KEN64-AA	639	535	0	83.72	16.28	AFRICA	G-III
4	A/NGR/2/73 (KF561704)	NGR73-02	639	533	0	83.41	16.59	AFRICA	G-V
5	A/GHA/16/73 (KF561698)	GHA73-16	636	527	0	82.86	17.14	AFRICA	G-VI
6	A/EGY/1/72 (EF208756)	EGY72-01	639	524	0	82.00	18.00	AFRICA	G-II
7	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	524	0	82.00	18.00	ASIA	A15
8	A/SUD/3/77 (GU566064)	SUD77-03	639	523	0	81.85	18.15	AFRICA	G-IV
9	A/IRN/2/87 (EF208770)	IRN87-02	636	514	0	80.82	19.18	ASIA	Iran-87
10	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	512	0	80.50	19.50	EURO-SA	A ₅

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.2

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Assembled with Report Generator v4.2

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Report on FMDV A in Ethiopia in 2001

Batch: WRLFMD/2014/00013

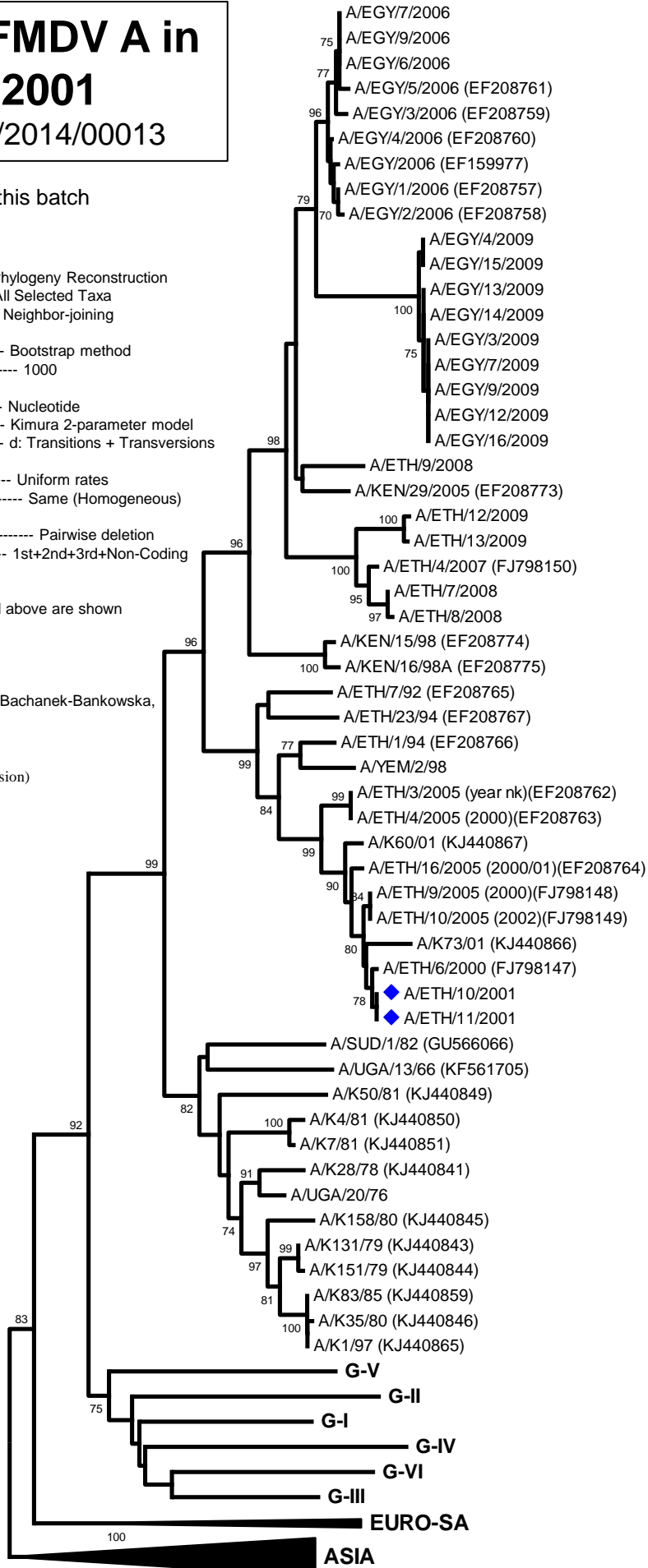
◆ indicates viruses in this batch

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 June 2014

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G-VII

AFRICA

0.02