

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

Genotyping Report

Report Date for this Batch: 13 October 2013

FMDV type A

Country: Kenya

Period: 2012

No. of samples: 2

BATCH: WRLFMD/2013/00019



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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: KEN/5/2012 Batch No: WRLFMD/2013/00019 Sender Ref: K160/12 (88) Location: Esageri, Koibatek District, Rift Valley Province, Kenya Date collected: 23/12/2012 Date received by WRLFMD: 25/09/2013 Date received for sequencing: 01/10/2013 Species: Bovine Material used: BTy1 27/09/2013 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 13/10/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: AFRICA Genotype/strain: G-I Sequence filename: KEN12-05.SEQ Date sequence last updated: 13/10/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 1669 Min. no. of nt for comparison: 600 Total turn-around time: 18 days Sequencing time: 12 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/KEN/6/2012	KEN12-06	639	639	0	100.00	0.00	AFRICA	G-I
2	A/KEN/22/2009 (KF561703)	KEN09-22	639	616	0	96.40	3.60	AFRICA	G-I
3	A/KEN/28/2008 (KF561702)	KEN08-28	639	616	0	96.40	3.60	AFRICA	G-I
4	A/TAN/47/2009 (KF561697)	TAN09-47	639	615	0	96.24	3.76	AFRICA	G-I
5	A/TAN/42/2009 (KF561695)	TAN09-42	639	614	0	96.09	3.91	AFRICA	G-I
6	A/TAN/11/2009 (KF561694)	TAN09-11	639	609	0	95.31	4.69	AFRICA	G-I
7	A/TAN/4/2009 (KF561692)	TAN09-04	639	609	0	95.31	4.69	AFRICA	G-I
8	A/COD/10/2011	COD11-10	639	606	0	94.84	5.16	AFRICA	G-I
9	A/COD/11/2011	COD11-11	639	606	0	94.84	5.16	AFRICA	G-I
10	A/COD/12/2011	COD11-12	639	606	0	94.84	5.16	AFRICA	G-I

Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/find_genotyping/prototypes.htm)									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/KEN/42/66 (K18/66)(KF561699)	KEN66-42	639	541	0	84.66	15.34	AFRICA	G-I
2	A/UGA/13/66 (KF561705)	UGA66-13	639	519	0	81.22	18.78	AFRICA	G-VII
3	A21/Lumbwa/KEN/64 (AY593761)	KEN64-AA	639	518	0	81.06	18.94	AFRICA	G-III
4	A/NGR/2/73 (KF561704)	NGR73-02	639	516	0	80.75	19.25	AFRICA	G-V
5	A12/UK/119/32 (M10975)	UKG32119	639	515	0	80.59	19.41	EURO-SA	A ₁₂
6	A/GHA/16/73 (KF561698)	GHA73-16	636	512	0	80.50	19.50	AFRICA	G-VI
7	A/EGY/1/72 (EF208756)	EGY72-01	639	514	0	80.44	19.56	AFRICA	G-II
8	A/SUD/3/77 (GU566064)	SUD77-03	639	512	0	80.13	19.87	AFRICA	G-IV
9	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	505	0	79.40	20.60	EURO-SA	A ₅
10	A/IRN/22/99 (EF208772)	IRN99-22	636	504	0	79.25	20.75	ASIA	Iran-99

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Serotype: A WRLFMD Ref No: KEN/6/2012 Batch No: WRLFMD/2013/00019 Sender Ref: K160/12 (196) Location: Esageri, Koibatek District, Rift Valley Province, Kenya Date collected: 24/12/2012 Date received by WRLFMD: 25/09/2013 Date received for sequencing: 01/10/2013 Species: Bovine Material used: BTy1 27/09/2013 Region sequenced: VPI RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 13/10/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: AFRICA Genotype/strain: G-I Sequence filename: KEN12-06.SEQ Date sequence last updated: 13/10/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 1669 Min. no. of nt for comparison: 600 Total turn-around time: 18 days Sequencing time: 12 days
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Most Closely Related Reference Viruses

(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

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Assembled with Report Generator v4.1

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Report on FMDV A in Kenya in 2012

Batch: WRLFMD/2013/00019

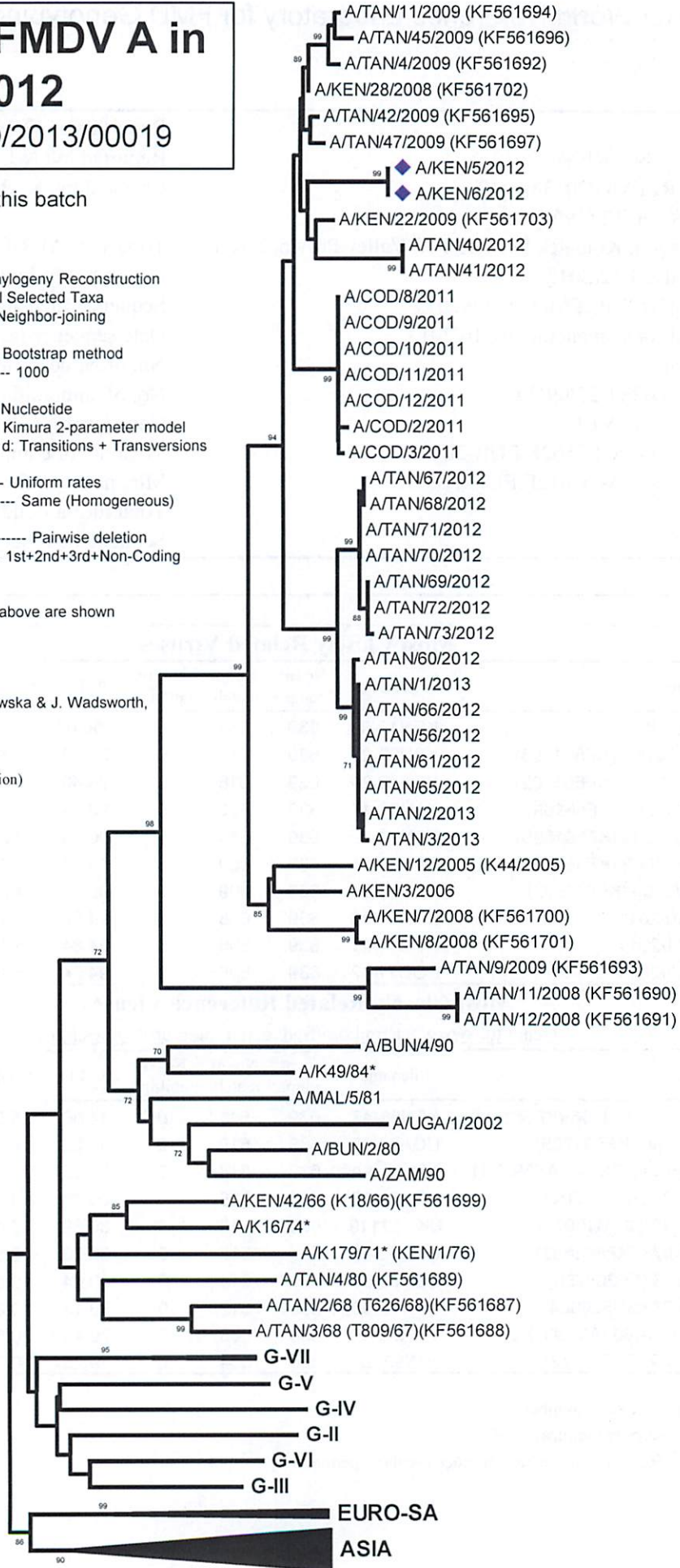
◆ indicates viruses in this batch

Software: MEGA 5.2
 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, K. Bachanek-Bankowska & J. Wadsworth,
 13 October 2013

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G-I

AFRICA