



INSTITUTE FOR ANIMAL HEALTH  
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## FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00031

Sender Details:



Date Received: 8<sup>th</sup> August 2012  
Country of Origin: TANZANIA  
Date Reported: 16<sup>th</sup> November 2012

Dear Dr S. M. Das,

Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

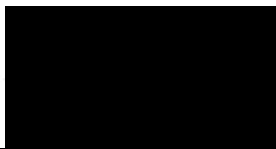
<http://www.wrlfmd.org/>

's

Results Approved By:



Official Stamp:



Date:

16 / 11 / 12

A UKAS accredited testing laboratory No. 4025.

To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: [trish.ryder@p.ac.uk](mailto:trish.ryder@p.ac.uk). IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

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

## Genotyping Report

Report Date for this Batch: 9 November 2012

FMDV type A

Country: Tanzania

Period: 2012

No. of samples: 2

BATCH: WRLFMD/2012/00031



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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: TAN/40/2012 Batch No: WRLFMD/2012/00031 Sender Ref: 7686 Location: Maaloni, Ngorongoro district, Arusha region, Tanzania Date collected: 01/06/2012 Date received by WRLFMD: 08/08/2012 Date received for sequencing: 26/09/2012 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 09/11/2012 Reported by: N.J. Knowles Checked by: D.P. King Topotype: AFRICA Genotype/strain: G-I Sequence filename: TAN12-40.SEQ Date sequence last updated: 17/10/2012 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 1502 Min. no. of nt for comparison: 600 Total turn-around time: 93 days Sequencing time: 44 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/TAN/41/2012	TAN12-41	639	639	0	100.00	0.00	AFRICA	G-I
2	A/KEN/22/2009	KEN09-22	639	615	0	96.24	3.76	AFRICA	G-I
3	A/KEN/28/2008	KEN08-28	639	613	0	95.93	4.07	AFRICA	G-I
4	A/TAN/42/2009	TAN09-42	639	613	0	95.93	4.07	AFRICA	G-I
5	A/TAN/47/2009	TAN09-47	639	610	0	95.46	4.54	AFRICA	G-I
6	A/TAN/11/2009	TAN09-11	639	606	0	94.84	5.16	AFRICA	G-I
7	A/TAN/4/2009	TAN09-04	639	606	0	94.84	5.16	AFRICA	G-I
8	A/COD/10/2011	COD11-10	639	603	0	94.37	5.63	AFRICA	G-I
9	A/COD/11/2011	COD11-11	639	603	0	94.37	5.63	AFRICA	G-I
10	A/COD/12/2011	COD11-12	639	603	0	94.37	5.63	AFRICA	G-I
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/KEN/42/66 (K18/66)	KEN66-42	639	540	0	84.51	15.49	AFRICA	G-I
2	A21/Lumbwa/KEN/64 (AY593761)	KEN64-AA	639	535	0	83.72	16.28	AFRICA	G-III
3	A/GHA/16/73	GHA73-16	636	521	0	81.92	18.08	AFRICA	G-VI
4	A/EGY/1/72 (EF208756)	EGY72-01	639	520	0	81.38	18.62	AFRICA	G-II
5	A/NGR/2/73	NGR73-02	639	520	0	81.38	18.62	AFRICA	G-V
6	A/UGA/13/66	UGA66-13	639	520	0	81.38	18.62	AFRICA	G-VII
7	A/SUD/3/77 (GU566064)	SUD77-03	639	519	0	81.22	18.78	AFRICA	G-IV
8	A12/UK/119/32 (M10975)	UKG32119	639	516	0	80.75	19.25	EURO-SA	A <sub>12</sub>
9	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	509	0	80.03	19.97	EURO-SA	A <sub>5</sub>
10	A/IRN/22/99 (EF208772)	IRN99-22	636	508	0	79.87	20.13	ASIA	Iran-99

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

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# Report on FMDV A in Tanzania in 2012

Batch: WRLFMD/2012/00031

◆ indicates viruses in this batch

Software: MEGA 5.1

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

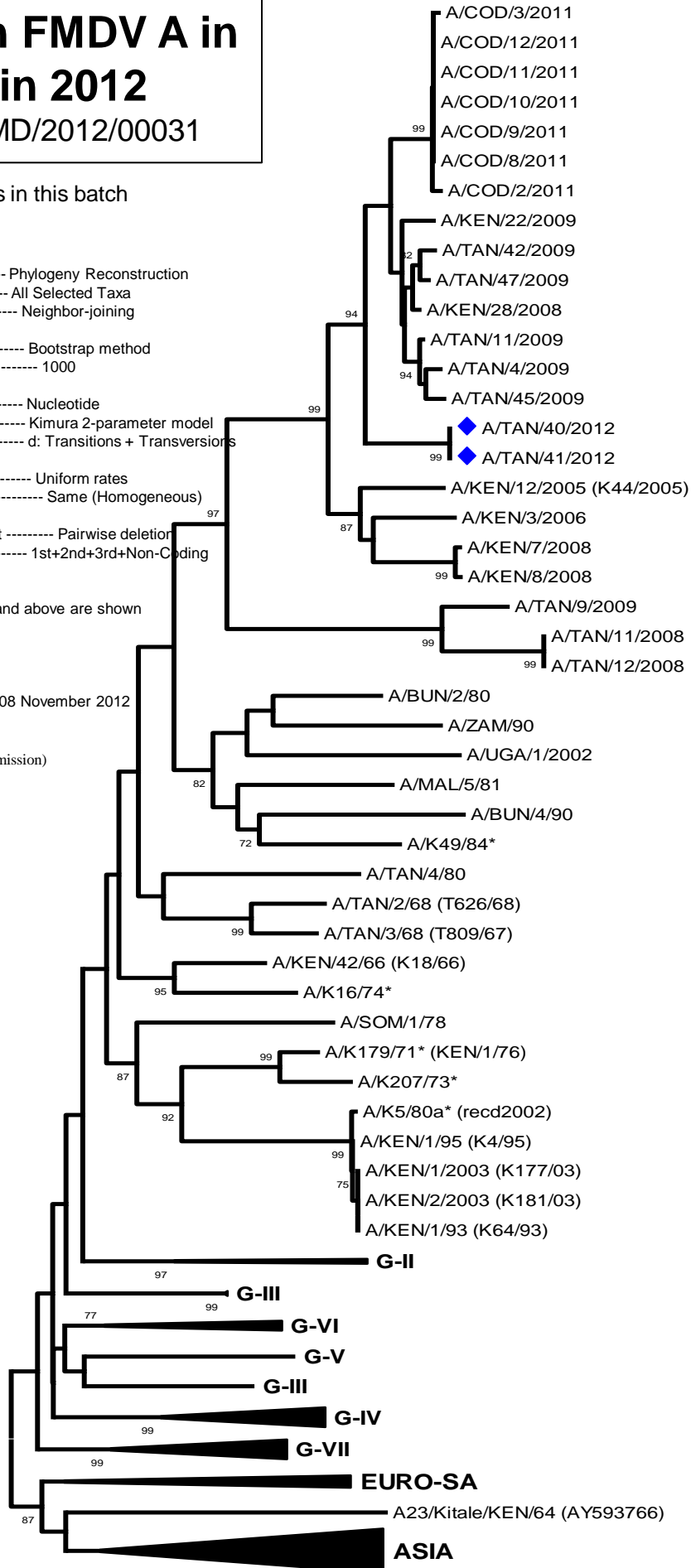
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 08 November 2012

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G-I

AFRICA

0.02