

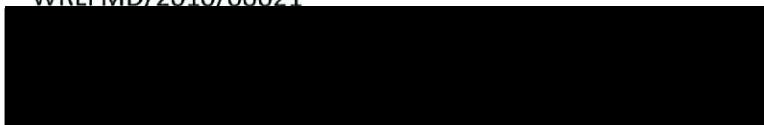


**INSTITUTE FOR ANIMAL HEALTH**  
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## FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00021

Sender Details:



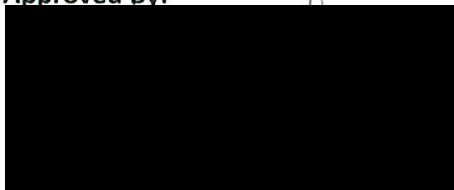
Date Received: 6<sup>th</sup> April 2010  
Country of Origin: Kenya  
Date Reported: 18<sup>th</sup> June 2010

Dear Dr. Sabenzia Nabalayo Wekesa,

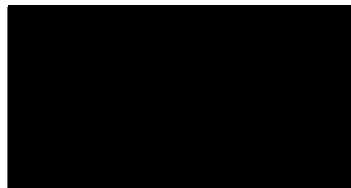
**Re.: Serotype O**

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/>

Results Approved By:

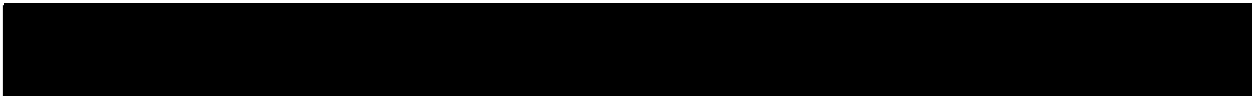


Official Stamp:



Date:

18/6/10



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: [elizabeth.wilson@bbsrc.ac.uk](mailto:elizabeth.wilson@bbsrc.ac.uk))

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

## Genotyping Report

Date: 18 June 2010

FMDV type O

Country: Kenya

Period: 2010

No. of isolates: 1

BATCH: WRLFMD/2010/00021



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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: KEN/69/2010 Batch No: WRLFMD/2010/00021 Sender Ref: K33/10 Location: Korisa, Kenya Date collected: 07/02/2010 Date received by WRLFMD: 06/04/2010 Date received for sequencing: 27/05/2010 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 16/06/2010 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: EA-1 Genotype/strain: unnamed Sequence filename: KEN10-69.SEQ Date sequence last updated: 16/06/2010 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2447 Min. no. of nt for comparison: 300 Total turn-around time: 71 days Sequencing time: 20 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/KEN/65/2009	KEN09-65	639	639	0	100.00	0.00	EA-1	unnamed
2	O/KEN/62/2009	KEN09-62	639	638	0	99.84	0.16	EA-1	unnamed
3	O/KEN/63/2009	KEN09-63	639	638	0	99.84	0.16	EA-1	unnamed
4	O/KEN/64/2009	KEN09-64	639	638	0	99.84	0.16	EA-1	unnamed
5	O/KEN/66/2009	KEN09-66	639	638	0	99.84	0.16	EA-1	unnamed
6	O/KEN/67/2009	KEN09-67	639	638	0	99.84	0.16	EA-1	unnamed
7	O/K77/78* (AF300812)	KEN78A77	495	494	0	99.80	0.20	EA-1	unnamed
8	O/K77/78* (DQ165072)	KEN78-77	639	637	0	99.69	0.31	EA-1	unnamed
9	O/KEN/2/95 (K10/95)(AJ303514)	KEN95-02	639	637	0	99.69	0.31	EA-1	unnamed
10	O/KEN/37/2008	KEN08-37	639	637	0	99.69	0.31	EA-1	unnamed
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	O/K83/79* (AJ303511)	KEN79B83	638	607	1	95.14	4.86	EA-1	unnamed
2	O/UGA/5/96 (AJ296327)	UGA96-05	639	572	0	89.51	10.49	EA-1	unnamed
3	O/K40/84*	KEN84-40	639	567	0	88.73	11.27	EA-1	unnamed
4	O/IND/53/79 (AF292107)	IND79A53	639	561	0	87.79	12.21	ME-SA	unnamed
5	O/ETH/1/2007 (FJ798137)	ETH07-01	639	556	0	87.01	12.99	EA-3	unnamed
6	O/SUD/2/86 (DQ165075)	SUD86-02	639	554	0	86.70	13.30	EA-3	unnamed
7	O/IND/R2/75* (AF204276)	IND75--A	639	553	0	86.54	13.46	ME-SA	unnamed
8	O/IRN/61/2001 (DQ164896)	IRN01-61	638	549	1	86.05	13.95	ME-SA	Irn-2001
9	O/PAK/16/2003 (DQ165068)	PAK03-16	639	549	0	85.92	14.08	ME-SA	Pak-98
10	O/ETH/58/2005 (FJ798141)	ETH05-58	639	548	0	85.76	14.24	EA-4	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v3.1

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# Report on FMDV O in Kenya in 2010

Batch: WRLFMD/2010/00021

Software: MEGA 4.0  
 No. of Taxa : 272  
 Data File : n:\evd\meg\db\fmvd\o\KEN2010a.meg  
 Data Title : O Tanzania 2008-2009 & Kenya 2010  
 Data Type : Nucleotide (Coding)  
 Analysis : Phylogeny reconstruction  
 Tree Inference : =====  
 ->Method : Neighbor-Joining  
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)  
 Include Sites : =====  
 ->Gaps/Missing Data : Pairwise Deletion  
 ->Codon Positions : 1st+2nd+3rd+Noncoding  
 Substitution Model :  
 =====  
 ->Model : Nucleotide: Kimura 2-parameter  
 ->Substitutions to Include : d: Transitions + Transversions  
 ->Pattern among Lineages : Same (Homogeneous)  
 ->Rates among sites : Uniform rates  
 No. of Sites : 642  
 No Of Bootstrap Reps = 1000  
 Only bootstrap values of 70% and above are shown

\* , not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 18 June 2010

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