



WRLFMD

INSTITUTE FOR ANIMAL HEALTH

Director: Professor Martin W. Shirley, PhD

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Ash Road,

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Surrey,

GU24 0NF

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Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00022

Sender Details:

Date Received: 30th April 2009

Country of Origin: Kenya

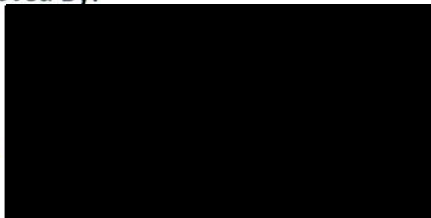
Date Reported: 17th August 2009

Dear 

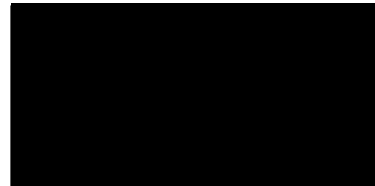
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

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

Results Approved By:

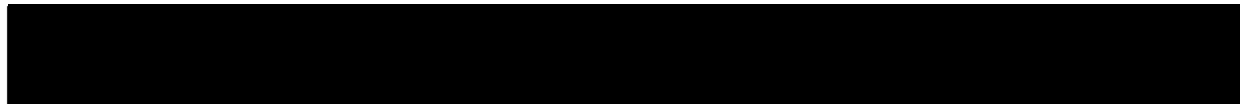


Official Stamp:



Date:

17/08/09



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.byrom@bbsrc.ac.uk)

Molecular Epidemiology Report Form

IAH-P-EP-MEG-FOR-005-1

Page 1 of 1

Serotype: A WRL RefNo: KEN/28/2008 Sender Ref: K73/08 Date collected: 01/08/2008 Date received by WRLFMD: 30/04/2009 Date received for sequencing: 01/06/2009 Species: CATTLE Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 13/08/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: AFRICA Genotype/strain: G-I Sequence filename: KEN08-28.SEQ Date sequence last updated: 07/08/2009 Total no. of comparisons: 1183 Min. no. of nt for comparison: 300 Total turn-around time: 105 days Sequencing time: 73 days
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Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/KEN/22/2009	KEN09-22	639	631	0	98.75	1.25
2	A/KEN/3/2006	KEN06-03	639	605	0	94.68	5.32
3	A/KEN/12/2005 (K44/2005)	KEN05-12	639	600	0	93.9	6.1
4	A/KEN/7/2008	KEN08-07	639	598	0	93.58	6.42
5	A/KEN/8/2008	KEN08-08	639	596	0	93.27	6.73
6	A/MAL/5/81	MAL81-05	639	556	0	87.01	12.99
7	A/K49/84*	KEN84-AC	639	555	0	86.85	13.15
8	A/K16/74*	KEN74-AA	639	552	0	86.38	13.62
9	A/BUN/2/80	BUN80-02	639	550	0	86.07	13.93
10	A/KEN/42/66 (K18/66)	KEN66-42	639	549	0	85.92	14.08

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A22/IRQ/24/64 (AJ251474)	IRQ64-24	639	514	0	80.44	19.56
2	A/IRN/2/87 (EF208770)	IRN87-02	636	509	0	80.03	19.97
3	A/IRN/22/99 (EF208772)	IRN99-22	636	506	0	79.56	20.44
4	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	639	505	0	79.03	20.97
5	A/IRN/1/96 (EF208771)	IRN96-01	638	501	1	78.53	21.47
6	A/TAI/2/97 (EF208778)	TAI97-02	636	499	0	78.46	21.54
7	A/TAI/118/87* (EF208777)	TAI87-AD	636	497	0	78.14	21.86
8	A/IRN/1/2005 (EF208769)	IRN05-01	639	499	0	78.09	21.91
9	A/SAU/41/91	SAU91-41	636	496	0	77.99	22.01
10	A/SAU/23/86 (EU414536)	SAU86-23	639	490	0	76.68	23.32

nt, nucleotides

*, not a WRLFMD reference number

Molecular Epidemiology Report Form

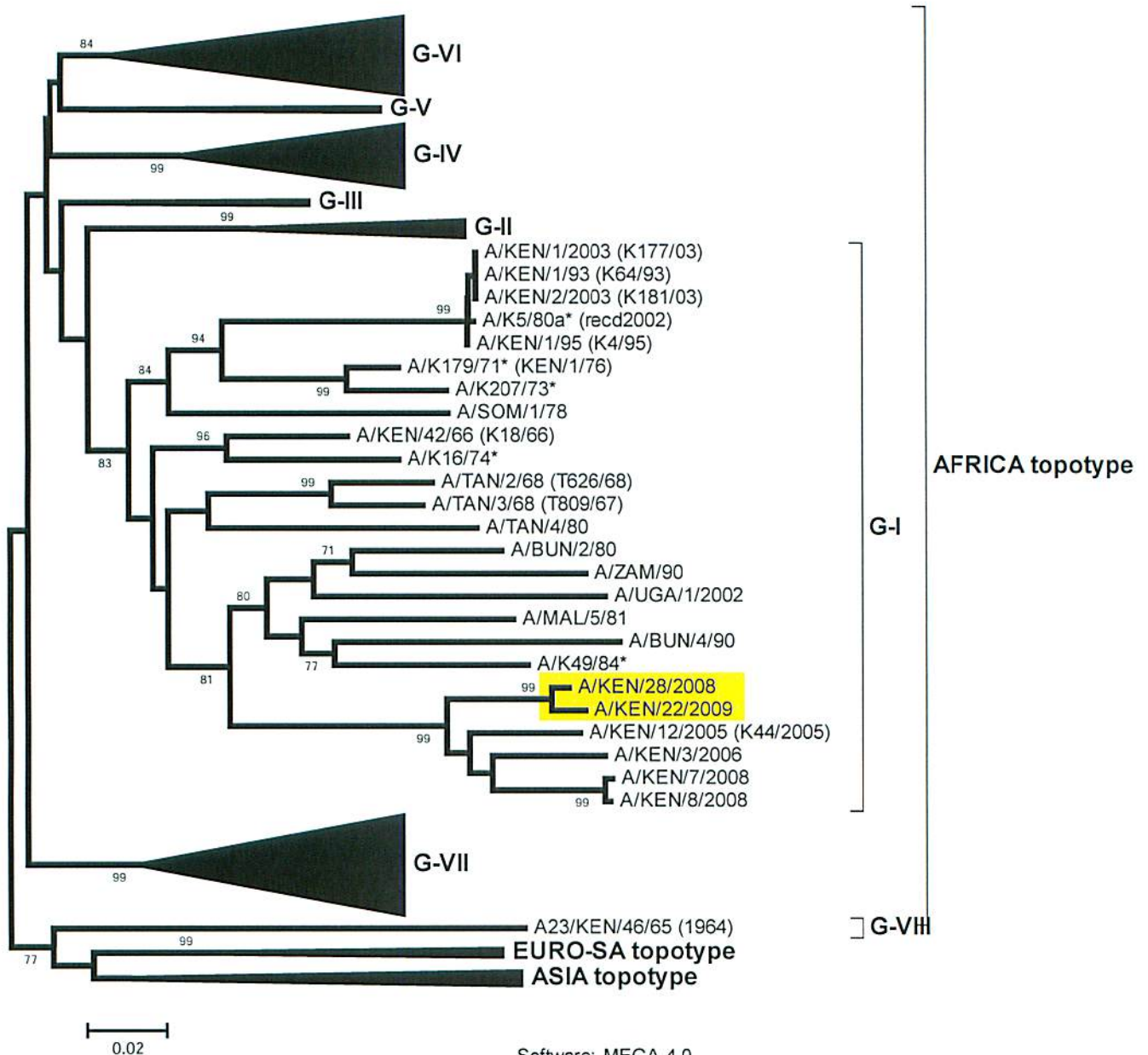
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Report on FMDV A in Kenya in 2008 and 2009

Batch: WRLFMD/2009/00022



N.J. Knowles & J. Wadsworth, 13 August 2009

Software: MEGA 4.0
 No. of Taxa : 124
 Data File : n:\evd\meg\db\fmdv\la\KEN2009a.meg
 Data Title : A Kenya 2008-2009
 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.