



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

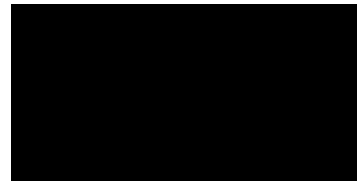
Dear 

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 

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

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<p>Serotype: O WRL Ref No: KEN/24/2008 Sender Ref: K63/08 Date collected: 01/07/2008 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: O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639</p>	<p>Report date: 14/08/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: EA-2 Genotype/strain: none designated Sequence filename: KEN08-24.SEQ Date sequence last updated: 07/08/2009 Total no. of comparisons: 2096 Min. no. of nt for comparison: 300 Total turn-around time: 106 days Sequencing time: 74 days</p>																																																																																								
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3	O/K77/78* (DQ165072)	KEN78-77	639	633	0	99.06	0.94
4	O/KEN/5/95 (K36/95)(AJ303516)	KEN95-05	639	633	0	99.06	0.94
5	O/KEN/10/95 (AY283389)	KEN95A10	495	490	0	98.99	1.01
6	O/KEN/77/78 (AF300812)	KEN78A77	495	490	0	98.99	1.01
7	O/K70/77*	KEN77-70	639	624	0	97.65	2.35
8	O/K83/79* (AJ303511)	KEN79B83	638	603	1	94.51	5.49
9	O/BUN/10/86	BUN86-10	638	582	1	91.22	8.78
10	O/BUN/1/84	BUN84-01	638	580	1	90.91	9.09
Relationships to Reference Virus Strains							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/IND/53/79 [AF292107]	IND79A53	639	559	0	87.48	12.52
2	O/IND/R2/75* [AF204276]	IND75-A	639	552	0	86.38	13.62
3	O1/Manisa/TUR/69 (AJ251477)	TUR69-E	639	548	0	85.76	14.24
4	O/ISR/2/88 (DQ164899)	ISR88-02	639	542	0	84.82	15.18
5	O/MOR/1/91	MOR91-01	639	538	0	84.19	15.81
6	O/TAI/189/87* [TRRL]	TAI87-AC	639	538	0	84.19	15.81
7	O/TAW/2/99 (AJ294927)	TAW99-02	639	538	0	84.19	15.81
8	O/HKN/6/83 (AJ294919)	HKN83-06	637	506	2	79.43	20.57
9	O1/BFS 1860/UK/67 (J02185)	UKG67-A	639	506	0	79.19	20.81
10	O/PHI/5/95 (DQ164946)	PHI95-05	639	504	0	78.87	21.13
nt, nucleotides *, not a WRLFMD reference number							

Molecular Epidemiology Report Form

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Page 1 of 1

Serotype: O WRL Ref No: KEN/6/2009 Sender Ref: K16/09 Date collected: 01/02/2009 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: O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 14/08/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: EA-2 Genotype/strain: none designated Sequence filename: KEN09-06.SEQ Date sequence last updated: 07/08/2009 Total no. of comparisons: 2096 Min. no. of nt for comparison: 300 Total turn-around time: 106 days Sequencing time: 74 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	O/KEN/24/2008	KEN08-24	639	639	0	100	0
2	O/KEN/36/2008	KEN08-36	639	627	0	98.12	1.88
3	O/KEN/7/2002	KEN02-07	639	600	0	93.9	6.1
4	O/KEN/30/2004	KEN04-30	639	598	0	93.58	6.42
5	O/KEN/26/2005	KEN05-26	639	597	0	93.43	6.57
6	O/KEN/4/2005	KEN05-04	639	596	0	93.27	6.73
7	O/KEN/6/2005	KEN05-06	639	595	0	93.11	6.89
8	O/KEN/3/2007	KEN07-03	639	588	0	92.02	7.98
9	O/KEN/17/2007	KEN07-17	639	587	0	91.86	8.14
10	O/KEN/20/2007	KEN07-20	639	587	0	91.86	8.14

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/ISR/2/88 (DQ164899)	ISR88-02	639	538	0	84.19	15.81
2	O/TAW/2/99 (AJ294927)	TAW99-02	639	538	0	84.19	15.81
3	O/IND/R2/75* [AF204276]	IND75-A	639	537	0	84.04	15.96
4	O/MOR/1/91	MOR91-01	639	537	0	84.04	15.96
5	O/IND/53/79 [AF292107]	IND79A53	639	532	0	83.26	16.74
6	O1/Manisa/TUR/69 (AJ251477)	TUR69-E	639	526	0	82.32	17.68
7	O/TAI/189/87* [TRRL]	TAI87-AC	639	519	0	81.22	18.78
8	O1/BFS 1860/UK/67 (J02185)	UKG67-A	639	511	0	79.97	20.03
9	O/HKN/6/83 (AJ294919)	HKN83-06	637	508	2	79.75	20.25
10	O/PHI/5/95 (DQ164946)	PHI95-05	639	501	0	78.4	21.6

nt, nucleotides
 *, not a WRLFMD reference number

Molecular Epidemiology Report Form

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Page 1 of 1

Serotype: O WRL Ref No: KEN/10/2009 Sender Ref: K29/09 Date collected: 01/02/2009 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: O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 14/08/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: EA-2 Genotype/strain: none designated Sequence filename: KEN09-10.SEQ Date sequence last updated: 07/08/2009 Total no. of comparisons: 2096 Min. no. of nt for comparison: 300 Total turn-around time: 106 days Sequencing time: 74 days																																																																																								
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nt, nucleotides *, not a WRLFMD reference number																																																																																									

Report on FMDV O in Kenya in 2008-2009

Batch: WRLFMD/2009/00022

Software: MEGA 4.0
No. of Taxa : 144
Data File : n:\evd\meg\dblfmdv\o\KEN2009a.meg
Data Title : O Kenya 2008-2009
Data Type : Nucleotide (Coding)
Analysis : Phylogeny reconstruction
Tree Inference : =====
->Method : Neighbor-Joining
->Phylogeny Test and options : Bootstrap (1000 replicates; seed=56488)
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, 14 August 2009

