

Molecular Epidemiology Report Form

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

Serotype: O	Report date: 09/08/2007
WRL Ref No: UGA/18/2007	
Sender Ref: KABERAMAIDO K/01/01	
Date collected: 24/04/2007	
Date received by WRLFMD: 03/07/2007	Topotype: EA-2
Date received for sequencing: 18/07/2007	Genotype/strain: none designated
Species: Cattle	Sequence filename: UGA07-18.SEQ
Material used: BTy2	Date sequence last updated: 08/08/2007
Region sequenced: VP1	Total no. of comparisons: 1634
RT-PCR primers: O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 300
No. of Nt determined: 639	Total turn-around time: 37 days
No. of ambiguities: 0	Sequencing time: 22 days
Gene length: 639	

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/UGA/5/2004	UGA04-05	639	627	0	98.12	1.88
2	O/UGA/7/2004	UGA04-07	639	627	0	98.12	1.88
3	O/UGA/8/2004	UGA04-08	639	627	0	98.12	1.88
4	O/UGA/6/2004	UGA04-06	639	626	0	97.97	2.03
5	O/UGA/18/2004	UGA04-18	639	625	0	97.81	2.19
6	O/UGA/1/2004	UGA04-01	639	623	0	97.5	2.5
7	O/UGA/4/2004	UGA04-04	639	623	0	97.5	2.5
8	O/UGA/3/2004	UGA04-03	639	622	0	97.34	2.66
9	O/COD/3/2006	COD06-03	639	620	0	97.03	2.97
10	O/COD/68/2006	COD06-68	639	619	0	96.87	3.13

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/MOR/1/91	MOR91-01	639	541	0	84.66	15.34
2	O/ISR/2/88 (DQ164899)	ISR88-02	639	540	0	84.51	15.49
3	O/TAW/2/99	TAW99-02	639	540	0	84.51	15.49
4	O/IND/53/79 [AF292107]	IND79A53	639	539	0	84.35	15.65
5	O/IND/R2/75* [AF204276]	IND75--A	639	539	0	84.35	15.65
6	O1/Manisa/TUR/69 (AJ251477)	TUR69--E	639	537	0	84.04	15.96
7	O/TAI/189/87* [TRRL]	TAI87-AC	639	523	0	81.85	18.15
8	O/HKN/6/83	HKN83-06	637	511	2	80.22	19.78
9	O1/BFS 1860/UK/67 (J02185)	UKG67--A	639	510	0	79.81	20.19
10	O/PHI/5/95 (DQ164946)	PHI95-05	639	508	0	79.5	20.5

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV O/Uganda/18/2007

Software: MEGA 3.1

No. of Taxa : 127

Data File : n:\levd\meg\db\fmdv\o\UGA2007a.meg

Data Title : UGA 2007

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

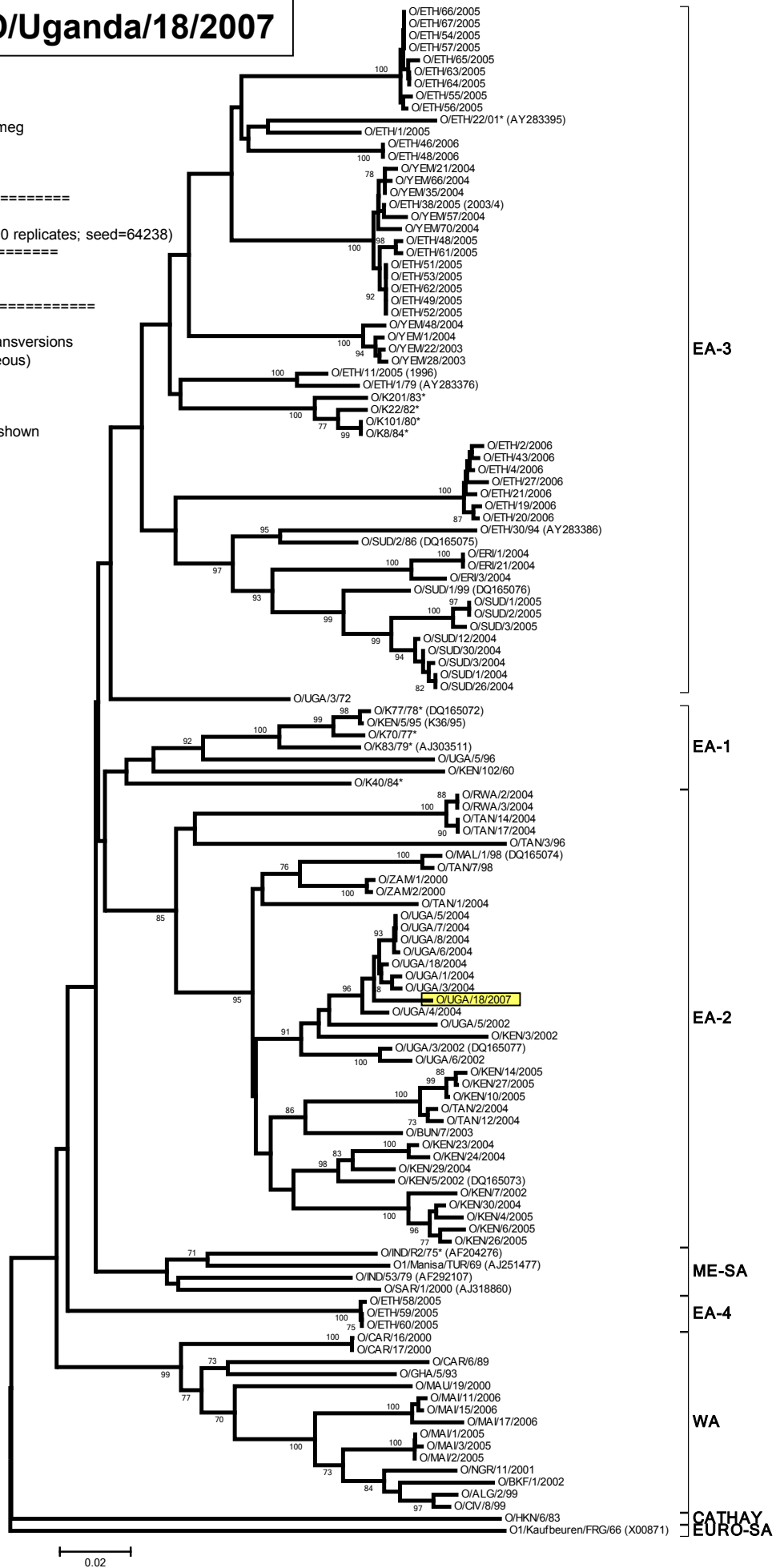
No. of Sites : 642

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 9 August 2007



EA-3

EA-1

EA-2

ME-SA

EA-4

WA

CATHAY
EURO-SA