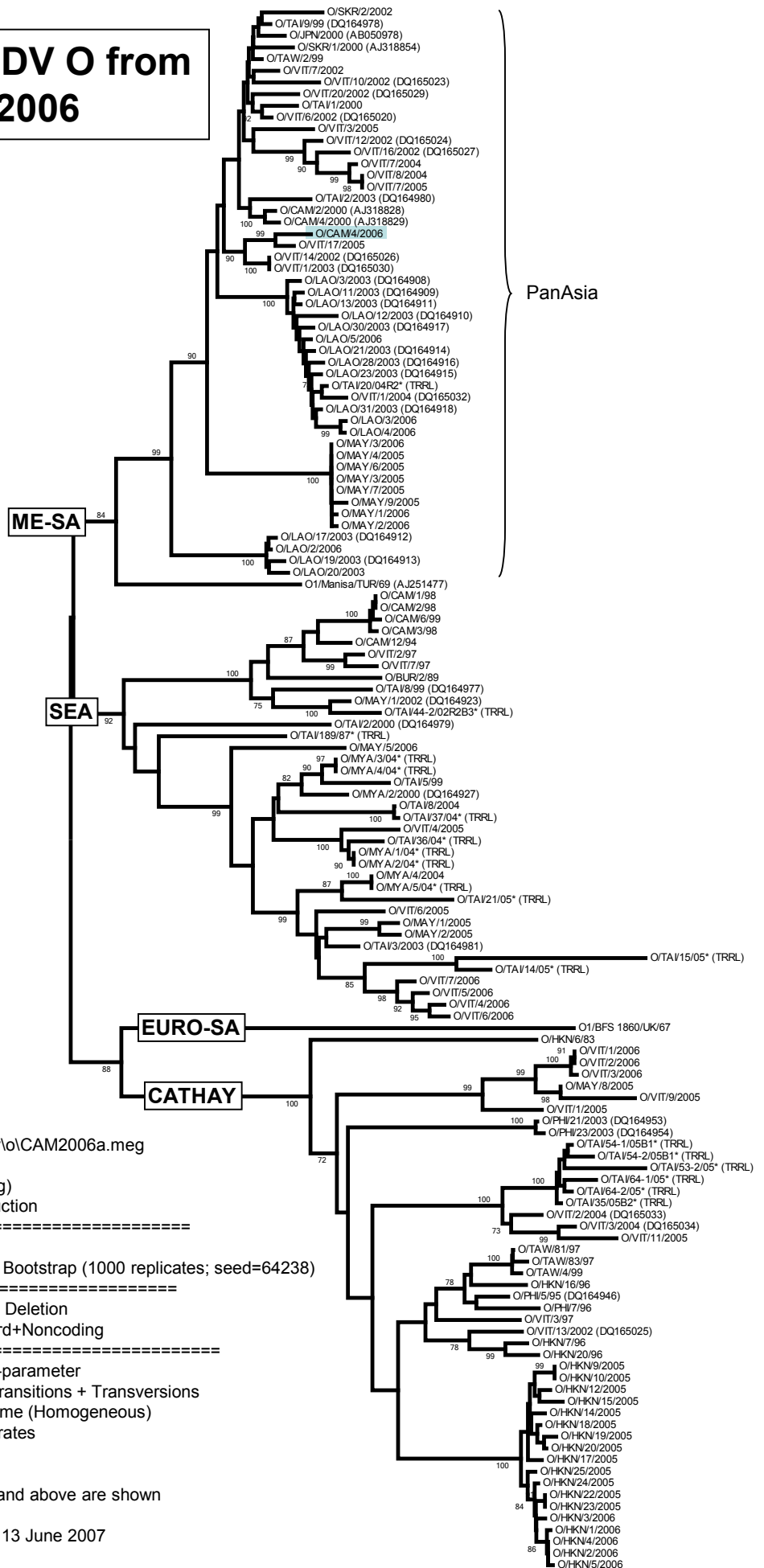


Serotype: O	Report date: 13/06/2007						
WRL Ref No: CAM/4/2006							
Sender Ref: CAM 16/06							
Date collected: 28/07/2006							
Date received by WRLFMD: 27/05/2007	Topotype: ME-SA						
Date received for sequencing: 04/06/2007	Genotype/strain: PanAsia						
Species: Cattle	Sequence filename: CAM06-04.SEQ						
Material used: LK1 BHK1 BTy1	Date sequence last updated: 13/06/2007						
Region sequenced: VP1	Total no. of comparisons: 1584						
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: 17 days						
No. of ambiguities: 0	Sequencing time: 9 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/VIT/17/2005	VIT05-17	639	628	0	98.28	1.72
2	O/VIT/1/2003 (DQ165030)	VIT03-01	639	621	0	97.18	2.82
3	O/VIT/14/2002 (DQ165026)	VIT02-14	639	621	0	97.18	2.82
4	O/BAR/1/99	BAR99-01	323	311	0	96.28	3.72
5	O/VIT/2/2002	VIT02-02	488	469	4	96.11	3.89
6	O/NEP/4/98 (DQ164935)	NEP98-04	639	613	0	95.93	4.07
7	O/SKR/2000 (AF428246)	SKR00-AC	639	613	0	95.93	4.07
8	O/SKR/2000 (AJ539139)	SKR00-AA	639	613	0	95.93	4.07
9	O/TAW/2/99	TAW99-02	639	613	0	95.93	4.07
10	O/Tibet/CHA/3/99	CHA99-03	639	613	0	95.93	4.07
Relationships to Reference Virus Strains							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/TAW/2/99	TAW99-02	639	613	0	95.93	4.07
2	O/IND/53/79 [AF292107]	IND79A53	639	570	0	89.2	10.8
3	O/IND/R2/75* [AF204276]	IND75--A	639	569	0	89.05	10.95
4	O1/Manisa/TUR/69 (AJ251477)	TUR69--E	639	568	0	88.89	11.11
5	O/TAI/189/87* [TRRL]	TAI87-AC	639	564	0	88.26	11.74
6	O/ISR/2/88 (DQ164899)	ISR88-02	639	560	0	87.64	12.36
7	O/MOR/1/91	MOR91-01	639	558	0	87.32	12.68
8	O/HKN/6/83	HKN83-06	637	525	2	82.42	17.58
9	O/PHI/5/95 (DQ164946)	PHI95-05	639	526	0	82.32	17.68
10	O1/BFS 1860/UK/67	UKG67--A	639	523	0	81.85	18.15
nt, nucleotides							
*, not a WRLFMD reference number							

Report on FMDV O from Cambodia in 2006



Software: MEGA 3.1
 No. of Taxa : 134
 Data File : n:\levd\meg\db\fmdv\o\CAM2006a.meg
 Data Title : Cambodia 2006
 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 : 639
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and above are shown

N.J. Knowles & J. Wadsworth, 13 June 2007

