

Serotype: O  
WRL Ref No: Mongolia/2004  
Date collected: 2004  
Date received by WRLFMD: 19/10/2004  
Species: not known  
Material used: Epithelium  
Region sequenced: VP1  
RT-PCR primers: not known  
No. of Nt determined: 637  
No. of ambiguities: 2  
Gene length: 639

Report date: 13/07/2005  
Topotype: SEA  
Genotype/strain: Mya98  
Sequence filename: MOG04--A.SEQ  
Date sequence last updated: 19/10/2004  
Total no. of comparisons: 1702  
Min. no. of nt for comparison: 300

Comments: VP1 sequence received from Alexei Sherbakov, ARRIAH, 19/10/2004

### Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/MYA/1/04* [TRRL]	MYA04-AA	637	622	2	97.65	2.35
2	O/MYA/2/04* [TRRL]	MYA04-AB	637	622	2	97.65	2.35
3	O/VIT/9/05* [TRRL]	VIT05-AI	637	619	2	97.17	2.83
4	O/VIT/4/05* [TRRL]	VIT05-AD	637	619	2	97.17	2.83
5	O/VIT/4/2005	VIT05-04	637	619	2	97.17	2.83
6	O/TAI/36/04* [TRRL]	TAI04-AB	637	618	2	97.02	2.98
7	O/VIT/6/05* [TRRL]	VIT05-AF	637	618	2	97.02	2.98
8	O/VIT/10/05* [TRRL]	VIT05-AJ	637	614	2	96.39	3.61
9	O/MYA/4/98	MYA98-04	351	335	8	95.44	4.56
10	O/MYA/1/98	MYA98-01	628	595	11	94.75	5.25

### Relationships to Reference Virus Strains

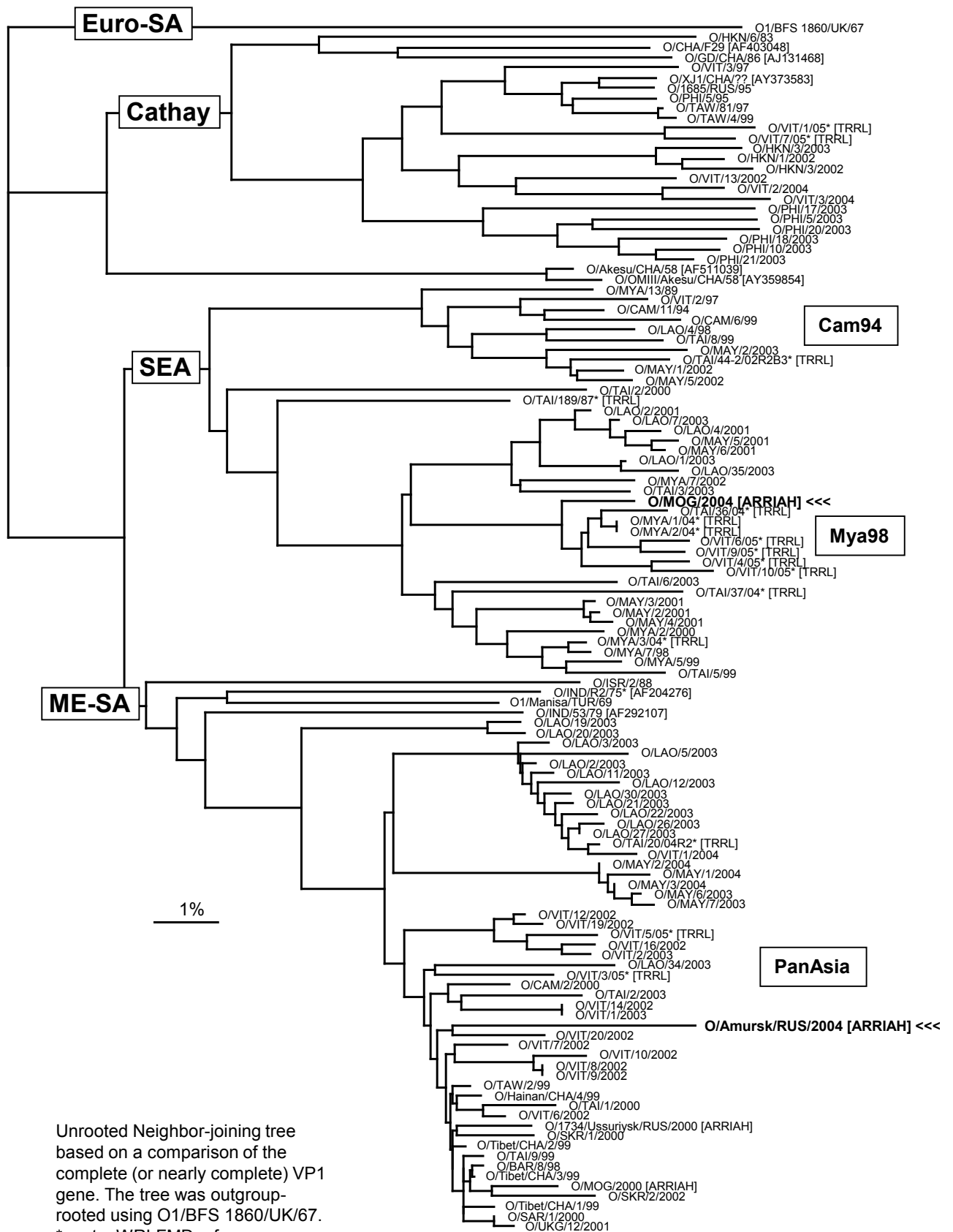
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/TAI/189/87* [TRRL]	TAI87-AC	637	581	2	91.21	8.79
2	O/TAW/2/99	TAW99-02	637	549	2	86.19	13.81
3	O/IND/R2/75* [AF204276]	IND75--A	637	545	2	85.56	14.44
4	O1/Manisa/TUR/69	TUR69--E	637	534	2	83.83	16.17
5	O/IND/53/79 [AF292107]	IND79A53	637	532	2	83.52	16.48
6	O/MOR/1/91	MOR91-01	637	528	2	82.89	17.11
7	O/ISR/2/88	ISR88-02	637	526	2	82.57	17.43
8	O/PHI/5/95	PHI95-05	637	506	2	79.43	20.57
9	O1/BFS 1860/UK/67	UKG67--A	637	505	2	79.28	20.72
10	O/HKN/6/83	HKN83-06	635	503	4	79.21	20.79

nt, nucleotides

\*, not a WRLFMD reference number

TRRL, sequence from Thailand Regional Reference Laboratory

Report on: FMDV O/Amursk/Russia 2004 & O/Mongolia/2004



Unrooted Neighbor-joining tree based on a comparison of the complete (or nearly complete) VP1 gene. The tree was outgroup-rooted using O1/BFS 1860/UK/67. \*, not a WRLFMD ref. no.