

Serotype: O	Report date: 18/04/2006
WRL Ref No: SEN/8/2006	Reported by: N.J. Knowles
Sender Ref: 0147	Checked by: D. Paton
Date collected: 23/01/2006	
Date received by WRLFMD: 11/02/2006	Topotype: West Africa
Date received for sequencing: 16/02/2006	Genotype/strain: none designated
Species: Cattle	Sequence filename: SEN06-08.SEQ
Material used: BTy2	Date sequence last updated: 11/04/2006
Region sequenced: VP1	Total no. of comparisons: 1798
RT-PCR primers: O-1C272F/NK61	Min. no. of nt for comparison: 300
No. of Nt determined: 639	Total turn-around time: 66 days
No. of ambiguities: 0	Sequencing time: 61 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/CIV/8/99	CIV99-08	639	608	0	95.15	4.85
2	O/GNA/4/99	GNA99-04	638	606	1	94.98	5.02
3	O/ALG/2/99	ALG99-02	639	605	0	94.68	5.32
4	O/MOR/2/99	MOR99-02	333	315	3	94.59	5.41
5	O/GNA/10/99	GNA99-10	443	416	13	93.91	6.09
6	O/GNA/6/99	GNA99-06	328	308	7	93.9	6.1
7	O/ALG/1/99	ALG99-01	630	591	9	93.81	6.19
8	O/TOG/1/2004	TOG04-01	639	598	0	93.58	6.42
9	O/NGR/11/2001	NGR01-11	639	597	0	93.43	6.57
10	O/TOG/4/2005	TOG05-04	639	596	0	93.27	6.73

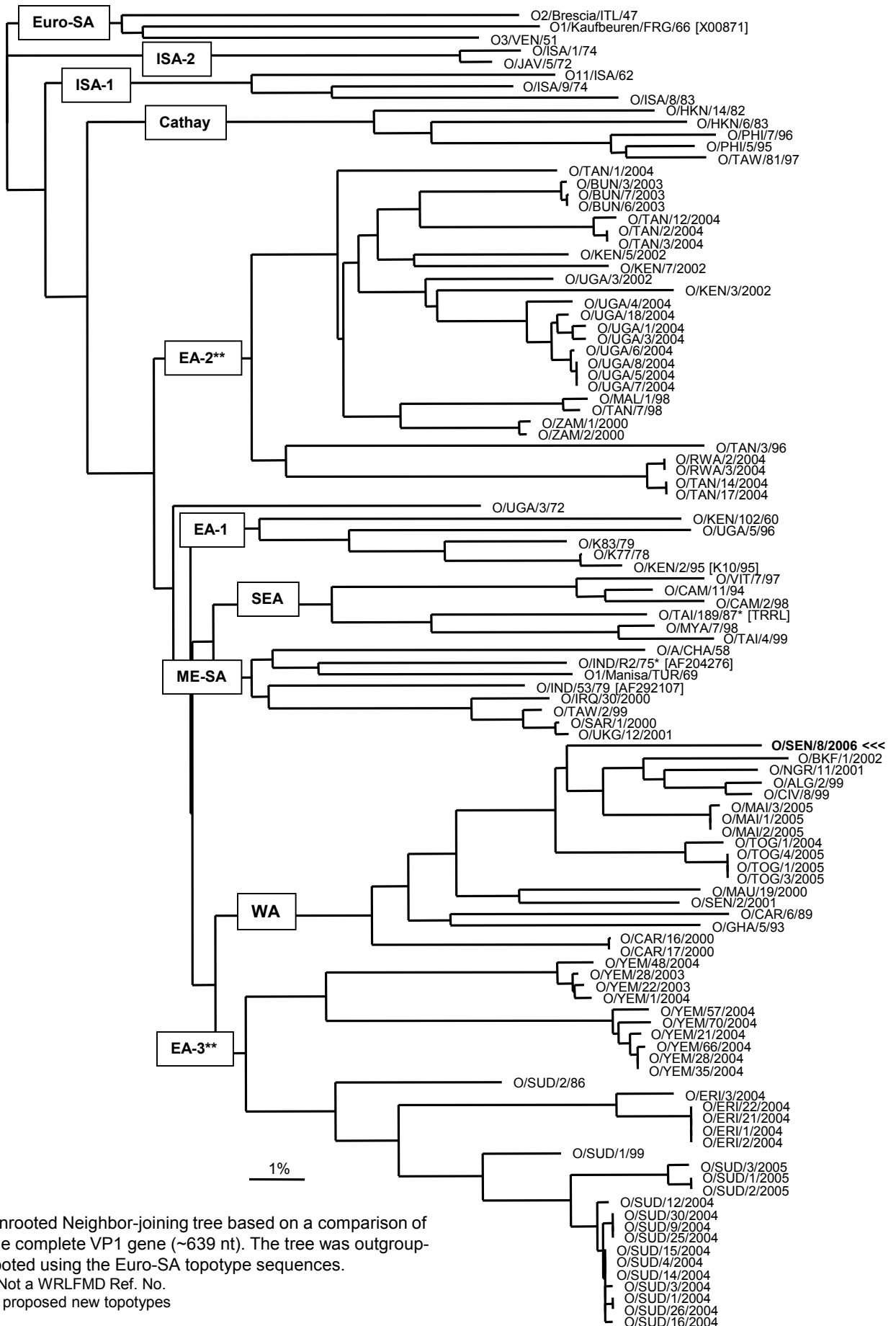
Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/IND/53/79 [AF292107]	IND79A53	639	540	0	84.51	15.49
2	O/IND/R2/75* [AF204276]	IND75--A	639	534	0	83.57	16.43
3	O1/Manisa/TUR/69	TUR69--E	639	530	0	82.94	17.06
4	O/TAW/2/99	TAW99-02	639	526	0	82.32	17.68
5	O/MOR/1/91	MOR91-01	639	523	0	81.85	18.15
6	O/ISR/2/88	ISR88-02	639	523	0	81.85	18.15
7	O/TAI/189/87* [TRRL]	TAI87-AC	639	519	0	81.22	18.78
8	O1/BFS 1860/UK/67	UKG67--A	639	508	0	79.5	20.5
9	O/PHI/5/95	PHI95-05	639	504	0	78.87	21.13
10	O/HKN/6/83	HKN83-06	637	501	2	78.65	21.35

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV O from Senegal in 2006



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (~639 nt). The tree was outgroup-rooted using the Euro-SA topotype sequences.

* Not a WRLFMD Ref. No.

** proposed new topotypes