

Serotype: A	Report date: 24/06/2006
WRL Ref No: KEN/12/2005	
Sender Ref: K44/2005	
Date collected: 15/07/2005	
Date received by WRLFMD: 24/01/2006	Topotype: Africa
Date received for sequencing: 08/02/2006	Genotype/strain: none designated
Species: Cattle	Sequence filename: KEN05-12.SEQ
Material used: BTy2	Date sequence last updated: 15/05/2006
Region sequenced: VP1	Total no. of comparisons: 909
RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 300
No. of Nt determined: 639	Total turn-around time: 151 days
No. of ambiguities: 0	Sequencing time: 136 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	A/K49/84*	KEN84-AC	639	558	0	87.32	12.68
2	A/MAL/5/81	MAL81-05	639	554	0	86.7	13.3
3	A/BUN/2/80	BUN80-02	639	546	0	85.45	14.55
4	A/KEN/42/66 (K18/66)	KEN66-42	639	543	0	84.98	15.02
5	A/K16/74*	KEN74-AA	639	540	0	84.51	15.49
6	A/UGA/1/2002	UGA02-01	639	539	0	84.35	15.65
7	A/BUN/4/90	BUN90-04	639	539	0	84.35	15.65
8	UG 1/02/2 (Onderstepoort)	UGA02-AA	378	318	0	84.13	15.87
9	A/TAN/2/68 (T626/68)	TAN68-02	639	537	0	84.04	15.96
10	A/TAN/3/68 (T809/67)	TAN68-03	639	536	0	83.88	16.12

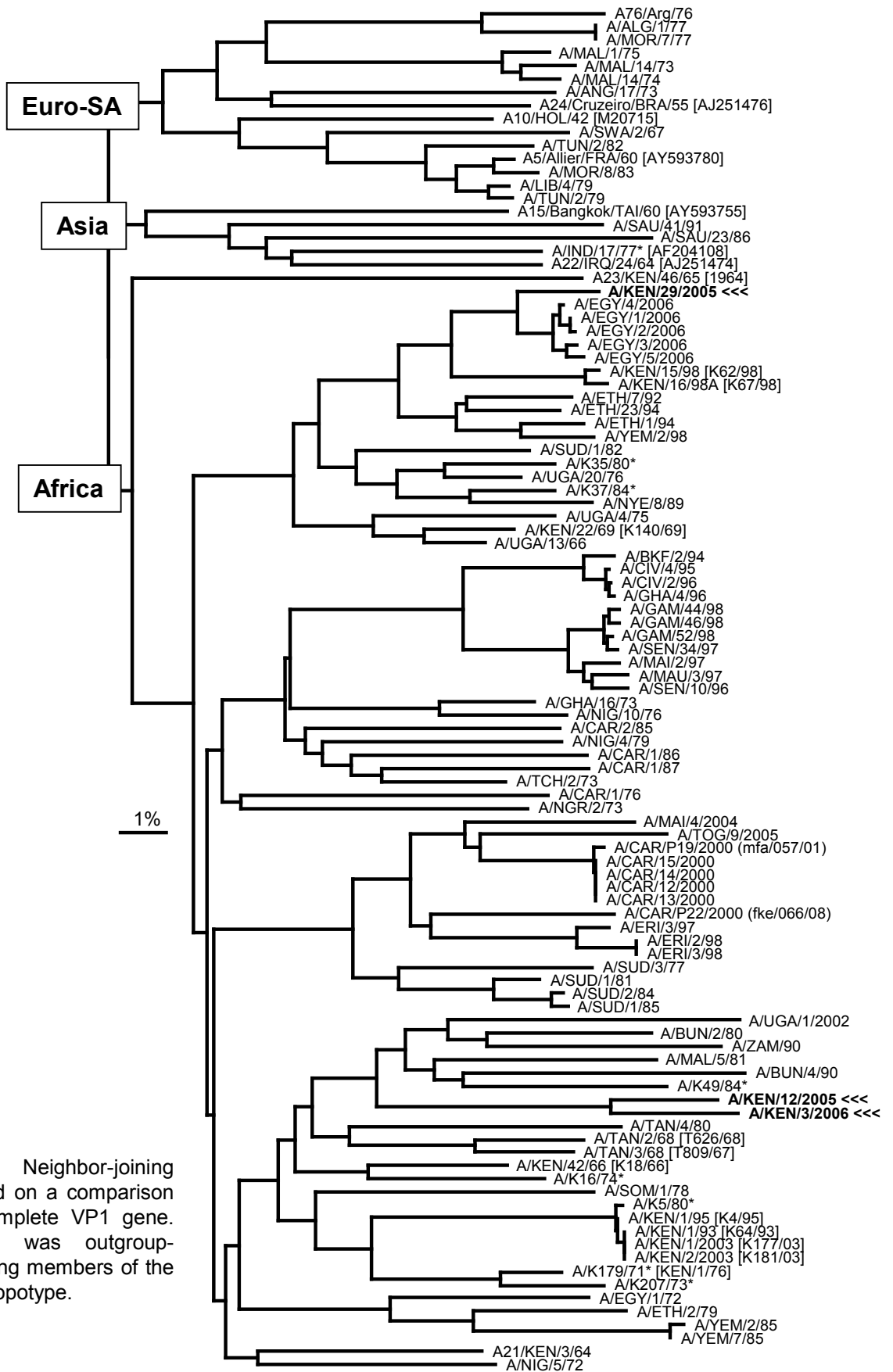
Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A22/IRQ/24/64 (AJ251474)	IRQ64-24	639	508	0	79.5	20.5
2	A/IRN/22/99	IRN99-22	636	504	0	79.25	20.75
3	A/IRN/87	IRN87--M	634	500	2	78.86	21.14
4	A/IRN/1/96	IRN96-01	638	500	1	78.37	21.63
5	A/SAU/41/91	SAU91-41	636	496	0	77.99	22.01
6	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	639	498	0	77.93	22.07
7	A/TAI/118/87*	TAI87-AD	636	493	0	77.52	22.48
8	A/TAI/2/97	TAI97-02	636	492	0	77.36	22.64
9	A/IND/7/82 (1980)	IND82-07	639	493	0	77.15	22.85
10	A/SAU/23/86	SAU86-23	639	482	0	75.43	24.57

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV type A in Kenya 2005-2006



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene. The tree was outgroup-rooted using members of the Euro-SA toptotype.