

Serotype: SAT2	Report date: 25/09/2006
WRL Ref No: KEN/32/2004	
Sender Ref: K52/2004	
Date collected: 23/02/2004	Topotype: none defined
Date received by WRLFMD: 26/05/2006	Genotype/strain: none designated
Date received for sequencing: 07/06/2006	Sequence filename: KEN04-32.SEQ
Species: Cattle	Date sequence last updated: 21/06/2006
Material used: BTy1	Total no. of comparisons: 338
Region sequenced: VP1	Min. no. of nt for comparison: 300
RT-PCR primers: SAT2-P1-1223F/SAT-2B208R	Total turn-around time: 122 days
No. of Nt determined: 648	Sequencing time: 110 days
No. of ambiguities: 0	
Gene length: 648	

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/KEN/22/2004	KEN04-22	648	643	0	99.23	0.77
2	SAT2/TAN/4/2004	TAN04-04	648	641	0	98.92	1.08
3	SAT2/TAN/9/2004	TAN04-09	648	641	0	98.92	1.08
4	SAT2/KEN/5/2004	KEN04-05	648	640	0	98.77	1.23
5	SAT2/TAN/21/2004	TAN04-21	648	640	0	98.77	1.23
6	SAT2/TAN/6/2004	TAN04-06	648	640	0	98.77	1.23
7	SAT2/KEN/8/2004	KEN04-08	648	638	0	98.46	1.54
8	SAT2/KEN/10/2004	KEN04-10	648	638	0	98.46	1.54
9	SAT2/TAN/18/2004	TAN04-18	648	638	0	98.46	1.54
10	SAT2/KEN/13/2004	KEN04-13	648	638	0	98.46	1.54

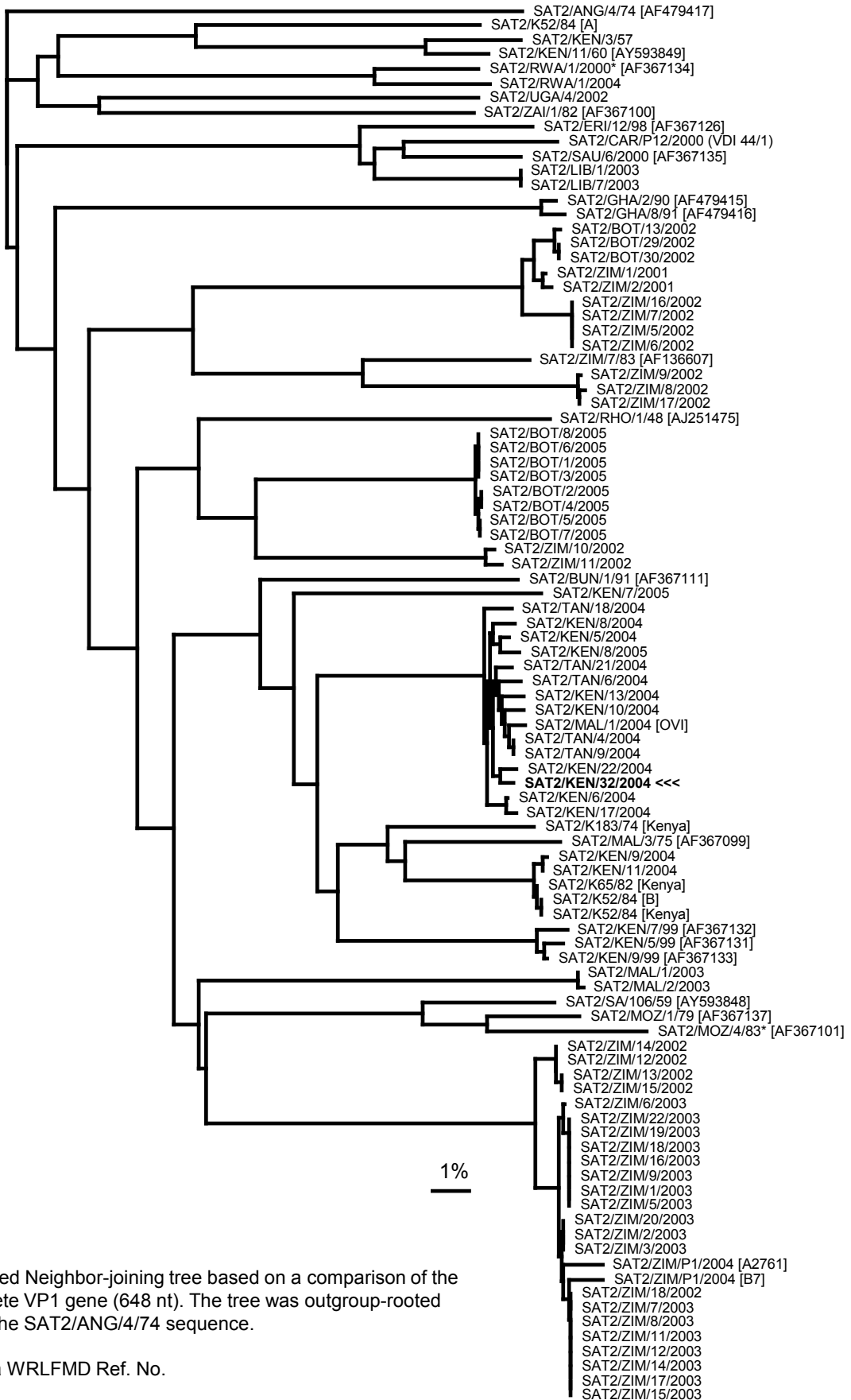
Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/K183/74 (Kenya)	KEN74183	648	575	0	88.73	11.27
2	SAT2/K65/82 (Kenya)	KEN82K65	648	575	0	88.73	11.27
3	SAT2/SA/106/59 [AY593848]	RSA59--A	648	513	0	79.17	20.83
4	SAT2/RHO/1/48 [AJ251475]	ZAM48A01	648	513	0	79.17	20.83
5	SAT2/ZIM/9/89	ZIM89-09	218	169	1	77.52	22.48
6	SAT2/ZAM/3/81 (OVI)	ZAM81V03	198	153	6	77.27	22.73
7	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	486	0	75	25
8	SAT2/K52/84 (A)	KEN84-AA	648	464	0	71.6	28.4
9	SAT2/KEN/11/60 [AY593849]	KEN60--A	648	459	0	70.83	29.17
10	SAT2/KEN/3/57	KEN57-03	648	453	0	69.91	30.09

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV SAT 2 isolate from Kenya in 2004



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (648 nt). The tree was outgroup-rooted using the SAT2/ANG/4/74 sequence.

*; not a WRLFMD Ref. No.