

Serotype: SAT2	Report date: 29/07/2008
WRL Ref No: NMB/1/2008	Reported by: N.J. Knowles
Sender Ref: NAM 01/08	Checked by: D.J. Paton
Date collected: Jan 2008	
Date received by WRLFMD: 09/06/2008	Topotype: none defined
Date received for sequencing: 16/06/2008	Genotype/strain: none designated
Species: Cattle	Sequence filename: NMB08-01.SEQ
Material used: BTy1	Date sequence last updated: 29/07/2008
Region sequenced: VP1	Total no. of comparisons: 411
RT-PCR primers: SAT2-1C445F/SAT-2B208R; SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 300
No. of Nt determined: 648	Total turn-around time: 50 days
No. of ambiguities: 0	Sequencing time: 43 days
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/NMB/4/2007	NMB07-04	648	641	0	98.92	1.08
2	SAT2/ZAM/1/2007	ZAM07-01	648	641	0	98.92	1.08
3	SAT2/ZAM/3/2007	ZAM07-03	648	641	0	98.92	1.08
4	SAT2/NMB/1/2007	NMB07-01	648	640	0	98.77	1.23
5	SAT2/ZAM/2/2007	ZAM07-02	648	640	0	98.77	1.23
6	SAT2/ZAM/8/2008	ZAM08-08	648	636	0	98.15	1.85
7	SAT2/BOT/24/2006 (buffalo)	BOT06-24	648	618	0	95.37	4.63
8	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	564	1	87.17	12.83
9	SAT2/BOT/2/2005	BOT05-02	648	564	0	87.04	12.96
10	SAT2/BOT/4/2005	BOT05-04	648	564	0	87.04	12.96

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/RHO/1/48 [AJ251475]	ZAM48A01	648	546	0	84.26	15.74
2	SAT2/K52/84 (Kenya)	KEN84K52	648	519	0	80.09	19.91
3	SAT2/K183/74 (Kenya)	KEN74183	648	509	0	78.55	21.45
4	SAT2/SA/106/59 (AY593848)	RSA59--A	648	505	0	77.93	22.07
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	492	0	75.93	24.07
6	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	483	0	74.54	25.46
7	SAT2/KEN/3/57	KEN57-03	648	475	0	73.3	26.7
8	SAT2/ANG/4/74 [AF479417]	ANG74-04	648	474	0	73.15	26.85
9	SAT2/SAU/6/2000 [AF367135]	SAU00A06	647	467	1	72.18	27.82
10	SAT2/GAM/8/79 [AF479410]	GAM79-08	648	465	0	71.76	28.24

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV SAT 2 from Namibia in 2008

Software: MEGA 4.0

No. of Taxa : 126

Data File : n:\levd\meg\db\fmdv\sat2\NMB2008a.meg

Data Title : Namibia 2008

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

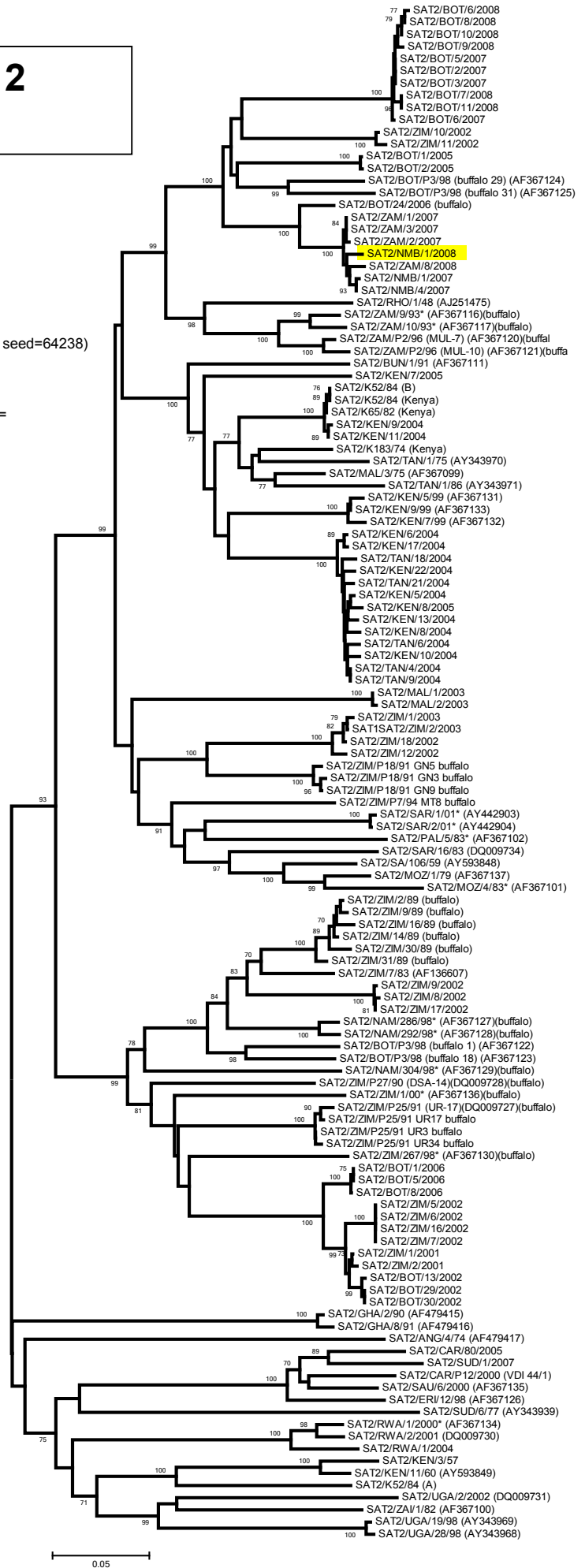
No. of Sites : 648

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, K. Ebert & J. Wadsworth, 29 July 2008



0.05