

Serotype: SAT2 Report date: 15/01/2008
WRL Ref No: NMB/1/2007
Sender Ref: NAM 11/07 #1
Date collected: 11/2007
Date received by WRLFMD: 18/12/2007 Topotype: none defined
Date received for sequencing: 03/01/2008 Genotype/strain: none designated
Species: Cattle Sequence filename: NMB07-01.SEQ
Material used: BTy1 Date sequence last updated: 15/01/2008
Region sequenced: VP1 Total no. of comparisons: 380
RT-PCR primers: SAT2VP3-AB/SAT-2B208R; Min. no. of nt for comparison: 300
SAT-1D209F/SAT-2B208R Total turn-around time: 28 days
No. of Nt determined: 648 Sequencing time: 12 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/NMB/4/2007	NMB07-04	648	647	0	99.85	0.15
2	SAT2/ZAM/1/2007	ZAM07-01	648	643	0	99.23	0.77
3	SAT2/ZAM/3/2007	ZAM07-03	648	643	0	99.23	0.77
4	SAT2/ZAM/2/2007	ZAM07-02	648	642	0	99.07	0.93
5	SAT2/BOT/24/2006 (buffalo)	BOT06-24	648	620	0	95.68	4.32
6	SAT2/BOT/2/2005	BOT05-02	648	567	0	87.5	12.5
7	SAT2/BOT/4/2005	BOT05-04	648	567	0	87.5	12.5
8	SAT2/BOT/P3/98 (buff 29)	BOW98-15	366	320	6	87.43	12.57
9	SAT2/BOT/1/2005	BOT05-01	648	566	0	87.35	12.65
10	SAT2/BOT/3/2005	BOT05-03	648	566	0	87.35	12.65

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/K65/82 (Kenya)	KEN82K65	648	521	0	80.4	19.6
3	SAT2/K183/74 (Kenya)	KEN74183	648	508	0	78.4	21.6
4	SAT2/SA/106/59 (AY593848)	RSA59--A	648	505	0	77.93	22.07
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	493	0	76.08	23.92
6	SAT2/KEN/11/60 (AY593849)	KEN60--A	648	479	0	73.92	26.08
7	SAT2/KEN/3/57	KEN57-03	648	474	0	73.15	26.85
8	SAT2/K52/84 (A)	KEN84-AA	648	471	0	72.69	27.31

nt, nucleotides

*, not a WRLFMD reference number

Serotype: SAT2
WRL Ref No: NMB/4/2007
Sender Ref: NAM 11/07 #5
Date collected: 11/2007
Date received by WRLFMD: 18/12/2007
Date received for sequencing: 03/01/2008
Species: Cattle
Material used: BTy1
Region sequenced: VP1
RT-PCR primers: SAT2VP3-AB/SAT-2B208R;
SAT-1D209F/SAT-2B208R
No. of Nt determined: 648
No. of ambiguities: 0
Gene length: 648

Report date: 15/01/2008
Topotype: none defined
Genotype/strain: none designated
Sequence filename: NMB07-04.SEQ
Date sequence last updated: 15/01/2008
Total no. of comparisons: 380
Min. no. of nt for comparison: 300
Total turn-around time: 28 days
Sequencing time: 12 days

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/NMB/1/2007	NMB07-01	648	647	0	99.85	0.15
2	SAT2/ZAM/1/2007	ZAM07-01	648	644	0	99.38	0.62
3	SAT2/ZAM/3/2007	ZAM07-03	648	644	0	99.38	0.62
4	SAT2/ZAM/2/2007	ZAM07-02	648	643	0	99.23	0.77
5	SAT2/BOT/24/2006 (buffalo)	BOT06-24	648	621	0	95.83	4.17
6	SAT2/BOT/2/2005	BOT05-02	648	567	0	87.5	12.5
7	SAT2/BOT/4/2005	BOT05-04	648	567	0	87.5	12.5
8	SAT2/BOT/P3/98 (buff 29)	BOW98-15	366	320	6	87.43	12.57
9	SAT2/BOT/1/2005	BOT05-01	648	566	0	87.35	12.65
10	SAT2/BOT/3/2005	BOT05-03	648	566	0	87.35	12.65

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	547	0	84.41	15.59
2	SAT2/K65/82 (Kenya)	KEN82K65	648	522	0	80.56	19.44
3	SAT2/K183/74 (Kenya)	KEN74183	648	509	0	78.55	21.45
4	SAT2/SA/106/59 (AY593848)	RSA59--A	648	506	0	78.09	21.91
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	492	0	75.93	24.07
6	SAT2/KEN/11/60 (AY593849)	KEN60--A	648	480	0	74.07	25.93
7	SAT2/KEN/3/57	KEN57-03	648	475	0	73.3	26.7
8	SAT2/K52/84 (A)	KEN84-AA	648	471	0	72.69	27.31

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV SAT2 from Namibia and Zambia in 2007

Software: MEGA 3.1

No. of Taxa : 154

Data File : n:\levd\meg\db\fmv\sat2\ZAM2007a.meg

Data Title : Zambia & Namibia 2007

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)

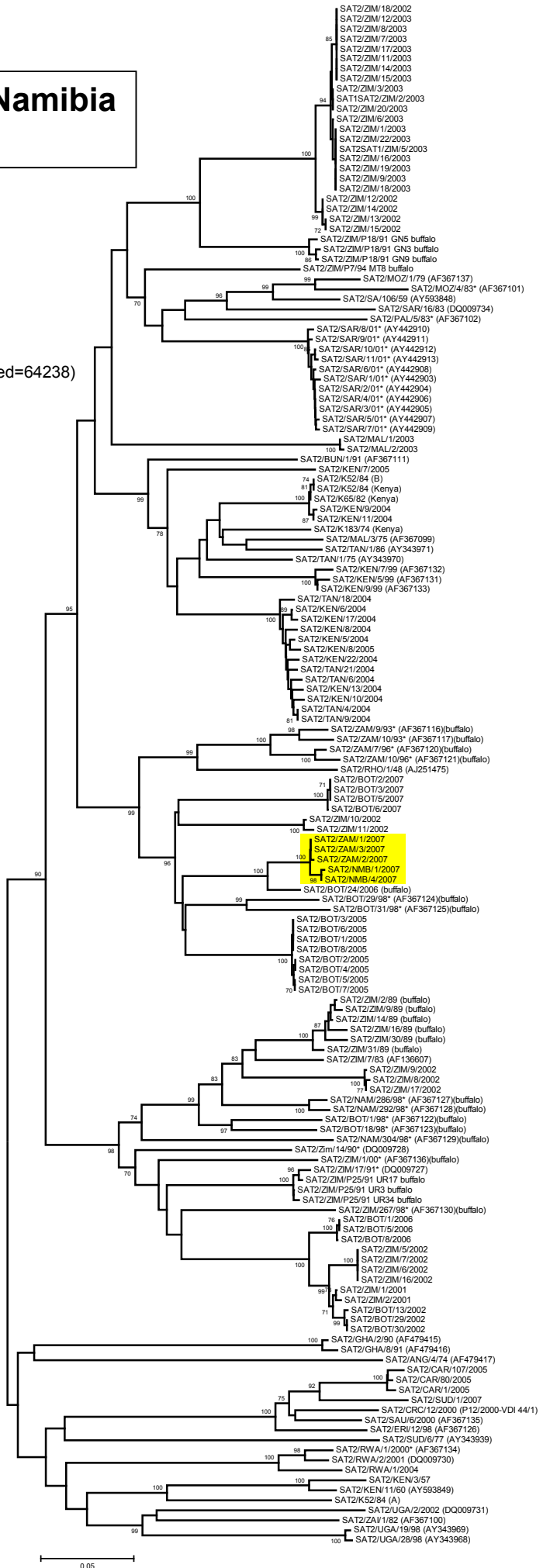
Rates among sites : Uniform rates

No. of Sites : 648

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% or greater are shown

N.J. Knowles & Jemma Wadsworth, 15 January 2008



0.05