

Molecular Epidemiology Report Form

IAH-P-EP-MEG-FOR-005-1

Page 1 of 1

Serotype: SAT2 WRL Ref No: ZAM/8/2008 Sender Ref: ZAM 08/08 Date collected: 2008 Date received by WRLFMD: 17/04/2008 Date received for sequencing: 24/04/2008 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: 19/05/2008 Reported by: N.J. Knowles Checked by: D.P. King Topotype: none defined Genotype/strain: none designated Sequence filename: ZAM08-08.SEQ Date sequence last updated: 16/05/2008 Total no. of comparisons: 410 Min. no. of nt for comparison: 300 Total turn-around time: 32 days Sequencing time: 25 days																																																																																								
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Ten Most Closely Related Viruses																																																																																									
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nt, nucleotides *, not a WRLFMD reference number																																																																																									

Report on FMDV SAT2 in Zambia in 2008

Software: MEGA 4.0

No. of Taxa : 159

Data File : n:\levd\meg\db\fmdv\sat2\ZAM2008a.meg

Data Title : Zambia 2008

Data Type : Nucleotide (Coding)

Analysis : Phylogeny reconstruction

Tree Inference : =====

->Method : Neighbor-Joining

->Phylogeny Test and options : Bootstrap (1000 replicates; seed=84007)

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 reference number

N.J. Knowles, J. Wadsworth & K. Ebert, 12 June 2008



0.05