

FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

Report Date for this Batch: 13 October 2013

FMDV type SAT 2

Country: Kenya

Period: 2012

No. of samples: 1

BATCH: WRLFMD/2013/00019



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IAH-P-EP-MEG-FOR-005-3

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Serotype: SAT2 WRLFMD Ref No: KEN/4/2012 Batch No: WRLFMD/2013/00019 Sender Ref: K126/12 Location: Rongai, Nakuru District, Rift Valley Province, Kenya Date collected: 01/01/2012 Date received by WRLFMD: 25/09/2013 Date received for sequencing: 01/10/2013 Species: Bovine Material used: BTy1 27/09/2013 Region sequenced: VP1 RT-PCR primers: SAT2-1C445F/SAT-2B208R SAT2-P1-1223F/SAT-2B208R	Report date: 13/10/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: IV Genotype/strain: unnamed Sequence filename: KEN12-04.SEQ Date sequence last updated: 13/10/2013 No. of Nt determined: 648 No. of ambiguities: 0 Gene length: 648 Total no. of comparisons: 637 Min. no. of nt for comparison: 600 Total turn-around time: 18 days Sequencing time: 12 days
Comments:	

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT2/KEN/12/2011	KEN11-12	648	643	0	99.23	0.77	IV	unnamed
2	SAT2/KEN/19/2011	KEN11-19	648	643	0	99.23	0.77	IV	unnamed
3	SAT2/KEN/18/2011	KEN11-18	648	642	0	99.07	0.93	IV	unnamed
4	SAT2/KEN/21/2011	KEN11-21	648	642	0	99.07	0.93	IV	unnamed
5	SAT2/TAN/3/2011	TAN11-03	648	642	0	99.07	0.93	IV	unnamed
6	SAT2/TAN/4/2011	TAN11-04	648	642	0	99.07	0.93	IV	unnamed
7	SAT2/TAN/6/2011	TAN11-06	648	642	0	99.07	0.93	IV	unnamed
8	SAT2/KEN/20/2011	KEN11-20	648	641	0	98.92	1.08	IV	unnamed
9	SAT2/TAN/7/2011	TAN11-07	648	641	0	98.92	1.08	IV	unnamed
10	SAT2/TAN/8/2011	TAN11-08	648	641	0	98.92	1.08	IV	unnamed

Most Closely Related Reference Viruses

(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT2/KEN/1/84 (K7/84) (AY344505)	KEN84-AB	648	563	0	86.88	13.12	IV	unnamed
2	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	648	549	0	84.72	15.28	IV	unnamed
3	SAT2/RHO/1/48 (AY593847)	ZAM48B01	648	521	0	80.40	19.60	III	unnamed
4	SAT2/MAL/1/2003	MAL03-01	648	514	0	79.32	20.68	I	unnamed
5	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	513	1	79.29	20.71	III	unnamed
6	SAT2/ZIM/14/2002 (KF219689)	ZIM02-14	648	510	0	78.70	21.30	I	unnamed
7	SAT2/SA/106/59 (AY593848)	RSA59--A	648	508	0	78.40	21.60	I	unnamed
8	SAT2/ZIM/7/83 (AF136607)	ZIM83A07	648	487	0	75.15	24.85	II	unnamed
9	SAT2/ZIM/5/81 (EF134951)	ZIM81-AA	648	486	0	75.00	25.00	II	unnamed
10	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	481	0	74.23	25.77	V	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV SAT2 in Kenya in 2013

Batch: WRLFMD/2013/00019

◆ indicates viruses in this batch

Software: MEGA 5.2

Analysis

Analysis ----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

Test of Phylogeny ----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment ----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 651

No Of Bootstrap Reps = 1000

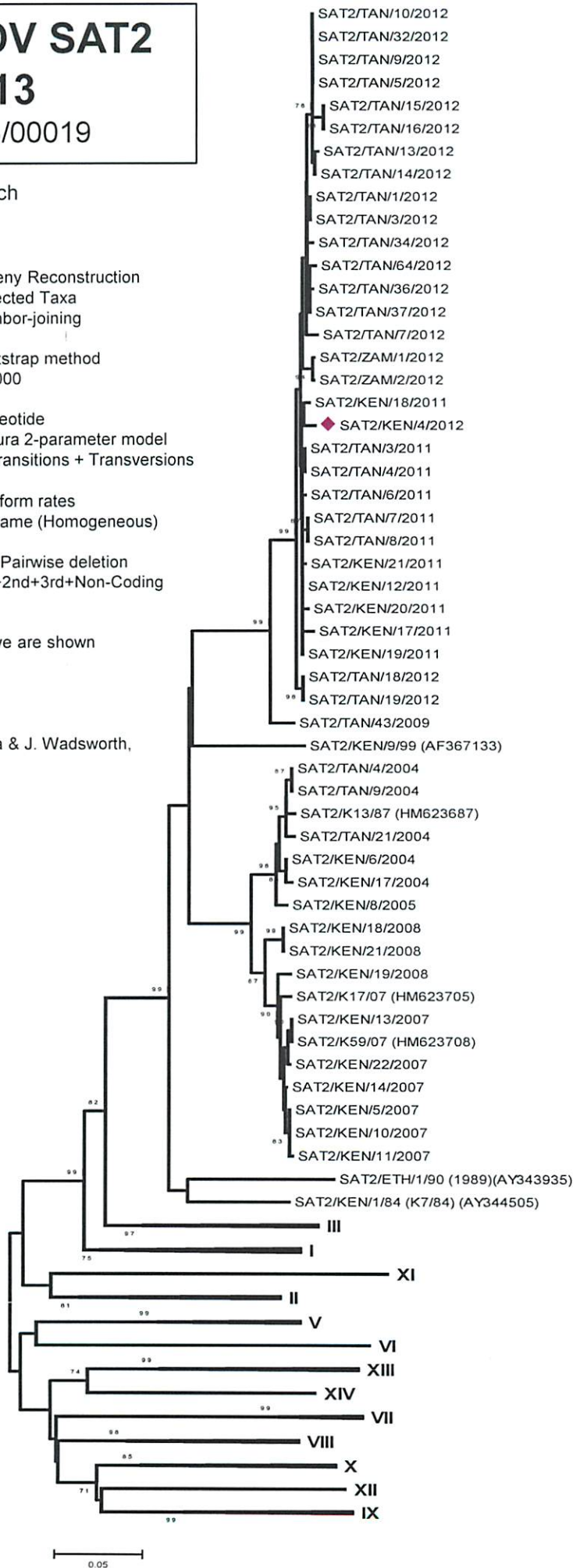
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, K. Bachanek-Bankowska & J. Wadsworth,
13 October 2013

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